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Maximum Match 100%
Listing first 45 summaries
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length: 2000000000
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WPI; 2001-112459/12. N-PSDB; AAF30046.

Thonnard J;

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AAB35813	ABB61097	ABB60228	ABB61241	AAG90704	AAE18359	ABP25889	AAE18363	AAW93408	AAU33228	AAB82349	AAU04591	AAY56967	AAG67365	AAM52321	AAY95030	AAR85287	AAE16323 .	AAY13492	AAE18360	AAE18364	AAB94053	AAR85291	AAW95501	AAG92487	AAY44646	AAR24147	AAY31384	AA017657	ABB54367	ABB06928	AAR85285	AA017656	76	AAR73913
Rat nerve growth f		Drosophila melanog	Drosophila melanog	77	Streptococcus pyog	Streptococcus poly		Swine HEV ORF 1 pr	i Se	Human NOGO-A prote	Human Nogo protein	Human MAGI polypep	acid	Las17 protein. Sa		Lysin carboxy term	Active cellulase p	Truncated cellulas	Streptococcus pyog	Streptococcus pyog	Human protein sequ	Enterococcus hirae	. subtilis	-	phromobacte:			H influenzae BASB2	Lactococcus lactis	g	Lysin. Lactococcu	uenzae BASB		Listeria monocytog

ALIGNMENTS

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RESULT 1
AAB20106
                                           25-JUN-1999;
                                                                                  23-JUN-2000; 2000WO-EP05854.
                                                                                                                                                                                                                                         Misc-difference
                                                                                                                                                                                                                                                                                                                                                     BASB110; infection; otitis media; pneumonia; therapy; diagnosis; antibacterial; antimicrobial; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-APR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB20106;
                                                                                                                                04-JAN-2001.
                                                                                                                                                                         WC200100838-A1.
                                                                                                                                                                                                                                                                                                         Moraxella catarrhalis.
                                                                                                                                                                                                                                                                                                                                                                                                                     Moraxella catarrhalis BASB110 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB20106 standard; Protein; 322 AA
(SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
                                           99GB-0015031.
                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                    /note= "Gly in translation of BASB110 PCR product"
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PINARARA

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The present sequence is that of BASB110 protein from Moraxella CC catarrhalis strain Mc2931 (ATCC 43617), a causative agent of otitis CC media in children and pneumonia in adults. The sequence is a causative agent of otitis CC differs by 1 residue from the predicted polypeptide sequence (see AB20107) of a BASB110 pen product, having Ser rather than Gly at CC polynucleotides encoding them, as well as expression vectors, host CC cells and methods. Also claimed is a vaccine composition comprising a BASB110 polypeptide an immunogenic fragment of a ccid sequence identity to BASB110, or comprising a tleast as amino caid sequence identity to BASB110, or comprising a polypeptide. A claimed therapeutic composition acid sequence identity to BASB110, or comprising a polypeptide or antibody. A claimed therapeutic composition useful infection involves identifying a BASB110 polypeptide or comprising a polypeptide or antibody. A claimed therapeutic composition useful in treating composition useful in reating antibody antibody at least as a claim or actarrhalis infection comprises at least 1 antibody antibody in raising specific antibodies, and in screening for antibacterial drugs.
                                                      BASB110; infection; otitis media; pneumonia; therapy; diagnosis; antibacterial; antimicrobial; vaccine.
                                                                                                                          Moraxella catarrhalis BASB110 protein.
                                                                                                                                                                                                                                           AAB20107 standard; Protein; 322
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel BASB110 polypeptides of Moraxella catarrhalis, useful as vaccine for treating Moraxella catarrhalis infections -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 VAPPVTEAPFATGSSGVMQFRYFVGATNFVVRRFGTATVAGSTVTSNGMWFSGRDGDLIN 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 KVRERSISSGVNTAHTESBVAVQSSRÞÞVQQHBAVQKÞTBÞVVVVKKÞTÞTBÞVVQQBAÞ 180
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Pred. No. 5.2e-134;
D; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence is that of BASB110 protein from Moraxella CC catarrhalis strain Mc2931 (ATCC 43617), a causative agent of otitis media in children and pneumonia in adults. The sequence is a creative form of a BASB10 pCR product. The sequence is a constitute from the predicted polypeptide sequence (see AAB2016) of CC 104. The invention provides BASB10 pCR product sequence (see AAB2016) of CC polynuclectides encoding them, as well as expression vectors, host cc leis and methods for producting BASB10 polypeptides, and cc cells and methods for producing BASB10 polypeptides, or comprising a BASB110 polypeptide, an immunogenic fragment of a cid sequence identity to BASB10, or comprising a BASB10 polypeptide. The composition cc ancided such a polypeptide. A claimed having at least 88% amino CC Moraxella infection involves identifying a BASB10 polypeptide or cc directed against a BASB10 polypeptide or cc directed against a BASB10 polypeptide. A claimed method of diagnosing a cc directed against a BASB10 polypeptide or cc directed against a BASB10 polypeptide or cc directed against a BASB10 polypeptide. BASB110 polypeptide also cc directed against a BASB110 polypeptide. BASB110 polypeptide as also cc antibacterial drugs.
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                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 83-84; 88pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel BASB110 polypeptides of Moraxella catarrhalis, useful vaccine for treating Moraxella catarrhalis infections -
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N-PSDB; AAF30047.
241 AŚNAGTVIOADHNIDGAŚIVIOHTNIGEVŚSYIHIKDAGVKTGDTVRTGORIAŚNIKNOEŚG
                                                                                                            181
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                                                                                                                                            121 KVRERSISSGVNTAHTÞSÞVAVQSSRÞÞVQQHÞAVQKÞ†ÞÞVVVVKKÞTÞTÞÞVVQQÞAÞ. 180
                                                                                                                                                                         121 KVRERSISSGVNTAHTPSPVAVQSSRPPVQQHPAVQKPTPPVVVXKFTPTPPVVQQPAP 180
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Misc-difference
                                                                                                                                                                                                                61 QVITDSQGVDNRYQVKQGDTVSKIAQRYGLNWREIGHINNLNSGYTIYTGQWLTLWSGDL 120
                                                                                                                                                                                                                                                  61 QVITDSQGVPNRYQVKQGDTVSKIAQRYGLNWRBIGHINNLNSSYTIYTGQWLTLWSGDL 120
                                                                                                                                                                                                                                                                                                                                                                                                         321,
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                      ASNAGTVIQADHNWDGASIVIQHTNGFVSSYIHIKDAQVKTGDTVRTGQRIASMKNQPSG 300
                                                                   vapoviteápeátássavná erkevatnevvekeátátvástvisnammesardadlin 240
                                                                                               VAPPVTEAPFATGSSGVMQFRYPVGATNPVVRRFGTATVAGSTVTSNGMWFSGRDGDLIN 240
                                                                                                                                                                                                                                                                                                                                                                                                  Similarity 99.7
21, Conservative
                                                                                                                                                                                                                                                                                                   MTVTÍAHNSONOKÞÍKRLGLÍFGVÍTTÓLLÁGCÁSKÞTYNSTSGSGSHRTSGSGGLÁÍGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  322 AA;
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                                                                                                                                                                                                                                                                                                                                                                            99.8%; Score 1666; DB 22; Length 322; 99.7%; Pred. No. 1.1e-133; tive 0; Mismatches 1; Indels 0
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Matches

322,

Similarity

19 61 Query Match Best Local !

Sequence

322 AA;

RESULT 2
AAB20107
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23-APR-2001

(first entry)

Moraxella catarrhalis

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                                                                                                                                                                                           The present sequence is the Haemophilus somnus lipoprotein LppB.

Recombinant vaccines containing H. somnus lipoproteins LppA, LppB
and LppC have been described. H. somnus transferrin-binding proteins Tbp1
and Tbp2 have also been found to be effective in vaccines against
H. somnus infection. Clones expressing Tbp epitopes were identified by
screening a genomic expression library of H. somnus strain HS25 in
E. coli with polyclonal antiserum raised against affinity-purified Tbp1
and Tbp2 of H. somnus. The genes coding for Tbp1 and Tbp2 were obtained
by inverse PCR. The nucleotide sequence encoding Tbp1 and Tbp2 may be
used for the recombinant production of Tbp1 and Tbp2, which may then be
used to manufacture vaccine compositions for immunising against H. somnus
infections. The antibodies raised against the transferrin binding
proteins may also be used diagnostically to identify the presence of
that causes a number of diseases in cattle such as thromboembolic
meningencephalitis (ITEME), myocarditis, septicaemia, arthritis and
                                                                                                                                          Query Match
Best Local (
                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 11; 67pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   myocarditis and pneumonia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acids encoding Haemophilus somnus transferrin binding proteins useful for vaccinating against and diagnosing H. somnus infections e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-565601/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Potter AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-MAR-1999;
24-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200053765-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Haemophilus somnus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                arthritis; pneumonia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Haemophilus somnus; lipoprotein B; lppB; transferrin-binding protein; tbp; antibacterial; vaccine; infection; tbromboembolic meningoencephalitis; ITEME; myocarditis; septicaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB21225;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB21225 standard; Protein; 345 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (UYSA-) UNIV SASKATCHEWAN
180
                                                                                           73
                                                                                                                            63;
                                                                                                                                           Similarity
                                                         YKVRKGDTMFLIAYISGMDIKELATLNNMSEPYHLSIGQVLKIANNIPDSNMIPTQTINE
SEVTQNTVNE-TWNANKPTNEQMKPVATPTHSTMPINK---TPPATSNIAWIWP-----
                          GVNTAHTPSPVAVQSSRPPVQQHPAVQKPTPPVVVVKKPTPTPPVVQQPAPVAPPVTEAP
                                                                                           YOVKOGDTVSKIAORYGLNWREIGHINNLNSSYTIYTGOWLTLWSG----DLKVRERSISS
                                                                                                                                                                                           345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rioux C,
                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               somnus LppB.
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                                                                                                                                                                                           AA;
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99US-0405728.
                                                                                                                                        12.5%; Score 209; DB 21; 24.8%; Pred. No. 1.4e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schryvers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   in cattle
                                                                                                                           49;
                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B
                                                                                                                           106;
                                                                                                                                                       Length 345;
                                                                                                                         Indels
                                                                                                                           36;
                                                                                                                       'Gaps
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                            189
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229
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RESULT 4
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Thersen J, P
represent novel Neisseria meningitis and N. gonorrheae polymucleotides and polypeptides. ARZ54537 to ARZ54576 and ARZ54616 to ARZ55473 represent PCR primers used in the exemplification of the present invention. The polypeptides, the polymucleotides, antibodies and compositions of the invention can be used as vaccines, as diagnostic reagents, and as immunogenic compositions. The polypeptides can be used in the manufacture of medicaments for treating or preventing infection due to Neisserial bacteria (e.g. meningitis and septicaemia), to detect the presence of Neisseria bacteria, or to raise antibodies. They may also be used to screen for agonists or antagonists, which may themselves have use as antibacterial agents. The polynucleotides of the invention may also be used in gene therapy protocols.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Neisseria meningitidis; Neisseria gonorrheae; antigenic; diagnosis; immunogenic; infection; antibacterial; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                        Claim 2; Page 207; 1453pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel Neisserial polypeptides predicted to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB;
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31-JUL-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Neisseria meningitidis ORF 025 protein sequence SEQ ID NO:112-1
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                                                                                                                                                                                                                                                                                                                                     AAZ53015 to AAZ54536, AAZ54577 to AAZ54615, and AAY74253 to AAY75941
                                                                                                                                                                                                                                                                                                                                                                                                                                                       vaccines
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)B; AAZ53075.
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INST GENOMIC
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, Pizza M, Rappuoli
, Venter JC;
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98US-0103796
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98US-0099062.
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99US-0121528.
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Rappuoli R,
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                                                                                                                                                                                                                                                                                                                                                                                           English.
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Ratti
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meningitis;
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Scalato E, Scarselli
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RESULT 5
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09-OCT-1998;
09-OCT-1998;
25-FEB-1999;
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Petersen i
Tettelin I
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                                                Novel Neisserial polypeptides predicted vaccines and diagnostics -
Claim 2; Page 206- ; 1453pp; English
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                                                                                                                     2000-062150/05.
DB; AAZ53073.
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INST GENOMIC RES.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----ekaaavk-srpavp--aavotpv-----kpaaqppvqsapqpaapaaenkavpa 278
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LAAADGKVVYAGSGLRGYGNLVIIQHNSSFLTAYGHNQKLLVGEGQQVKRGQQVALMGNT 388
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98US-0094869.
98US-0098994.
98US-0099062.
98US-0103749.
98US-0103794.
98US-0121528.
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Pred. No. 5.8e-09;
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Ratti
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                                                                      þe
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Scalato E, Scarselli
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Best Local S
Matches 66
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FEVRONGKPVNP 331
                                  FRISRNGVYVDP 317
                                                                                                               IQADHNMDGAS--IVIQHTNGFVSSYIHIKDAQVKTGDTVRTGQRIASMKNQPSGAALFE
                                                                                                                                                                                            -PFATGSSGVMQFRYPVGATNPVVRRFGTATVAGSTVTSNGMWFSGRDGDLINASNAGTV
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                                                                          VYAGSGLRGYGNLVIIQHNSSFLTAYGHNQKLLVGEGQQVKRGQQVALMGNTDASRTQLH 319
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AAY74312 standard; Protein; 351 AA

AAY74312;

21-MAR-2000 (first entry)

Neisseria meningitidis ORF 025 protein sequence SEQ ID NO:110-1.

Neisseria meningitidis; Neisseria gonorrheae; antigenic; diagnosis; immunogenic; infection; antibacterial; gene therapy. meningitis; septicaemia;

Neisseria meningitidis.

WO9957280-A2.

11-NOV-1999.

30-APR-1999; 99WO-US09346

RESULT 6
AAY74312
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RESULT 7
ABB4871
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DT 05-P
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                 WO200177335-A2
                                                                              Antibacterial; gene therapy; vaccine; blosynthesis; biodegradation; vitamin Bl2; bacterial infection; disease.
                                                                                                                                Listeria monocytogenes protein #1425
                                                                                                                                                                 05-FEB-2002
                                                                                                                                                                                                                                   ABB48721 standard; Protein; 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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                                              Listeria monocytogenes
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INST GENOMIC RES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----PVTEAPFA----TGSSGVMQFRYPVGATNPVVRRFGTATVAGSTVTSNGMWFSGR 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VKVKPAGYAAPKTAAVESRPAVP---AAVQTPV-----KPAAQPPVQSAPQPAAPAAEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---VNTAHTPSP-VAVQSSRPPVQQHPAVQKPTPPVVVVKKPTPTPPVVQQPAPVAP----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YQVKQGDTVSKIAQRYGLNWREIGHINNLNSSYTIYTGQWLTLWSGDLKVRERSISSG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Page 206; 1453pp; English
                                                                                                                                                                                                                                                                                                                                                                                   AGQPVLAAADGKVVYAGSGLRGYGNLVIIQHNSSFLTAYGHNQKLLVGEGQQVKRGQQVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        351 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Galeotti C, Grandi G,
Pizza M, Rappuoli R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 198; DB 21;
Pred. No. 1.3e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                   B
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Ratti G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Masignani V, Mora M;
Scalato E, Scarselli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 351;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60;
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RESULT 8
AAR45178
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                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B12. The genome sequence and proteins encoded by it are also useful for selecting compounds that regulate gene expression and cell replication and modulate L. monocytogenes-related diseases. In addition, the genome sequence and proteins encoded by it are useful in pharmaceutical and vaccines compositions for the treatment or prevention of infections by L. monocytogenes and related organisms.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to the genome sequence of Listeria monocytogenes EGD-e (see ABA03041). The genome sequence and fragments of it are useful for selecting probes and primers for detecting genes in L. monocytogenes and related organisms, and for studying genetic polymorphisms and other genomes. The present sequence is a protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dominguez-Bernal G, Garri
Chakraborty T, Domann B,
Perez-Diaz J, Baquero F,
Maduenio E, De Pablos B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   encoded by the genome sequence of the present invention. Proteins expressed from the genome sequence are useful for raising specific antibodies, identification of L. monocytogenes and related organisms, an for biosynthesis and biodegradation, especially biosynthesis of Vitamin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genomic sequence for Listeria monocytogenes, useful e.g. and prevention of Listeria and related bacterial infectic related polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Buchrieser C, Frangeul L, Couve E, Rusnick C, Fishi H, Dehoux P
Dussurget O, Chetouani F, Nedjari H, Glaser P, Kunst F, Cossart
Danials J, Gosbel W, Kreft J, Kuhn M, Ng E, Vazquez-Boland JA;
Dominguez-Bernal G, Garrido-Garcia P, Tierrez-Martinez A, Amend A
Chakraborty T, Domann B, Hain T, Berche P, Charbit A, Durant L;
Perez-Diaz J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N;
Perez-Diaz J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N;
Madduenio E, De Pablos B, Wehland J, Kaerst U, Entian K, Hauf J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                 301
408
                                                                                                                                                                                                           196
                                                                                                                                                                                                                                                                                         136 TPSPVAVQSSRPPVQQHPAVQKPTPPVVVVKKPTPTPPVVQQPAPVAPPVTEAPFATGSS 195
                                                                                                                                                                                                                                                                                                                                                                          76 KQGDTYSKIAQRYGLNWREIGHINNLNSSYTIYTGQWLTLWSGDLKVRERSISSGVNTAH 135
                                                                                                                                                                                                                                                                                                                                                                                                                      66;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                     NAGTVIQADHNMDGAS-----IVIQHTNGFVSSYIHIKDAQVK--TGDTVRTGQRIAS
MGSTGQSTGQHL-HFEIHKNGIPVDP 432
                                                                                                                                                                                                      GVMQFRYPVGA-----TNPVVRRF----GTATVAGSTVTSNGMWFSGRDGDLINAS 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID No 1426; 192pp;
                                       M--KNOPSGAALFEFRISRNGVYVDP 317
                                                                                ASGTVVFSGFGASGSGFGGYGYVVKIDHGNGFQTLYGHMRAGSLKVVTGQQVSQGQPIGI
                                                                                                                                                                 GGGQFIKPASGILTSGFSERTNPVTGKYESHKGQDIAGGGTVT
                                                                                                                                                                                                                                                  AKQEAAIKAAEEKRMQEAAAASSAKSAAVVK------QPSSSSNEATE----TVSS
                                                                                                                                                                                                                                                                                                                                   EKNDLVMALANKKDLT------KSEQTLLASE-----QGALTDEEKRLASNIAGEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      436 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000FR-0004629
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                                                                                                                                                                                                                                                                                                                                                                                                                                       9.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                      33;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 158.5; DB : Pred. No. 3.8e-05
                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     French
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  bacterial infections,
                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fsihi H, want F,
                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     for treatment
                                                                                                                                                                                                                                                                                                                                                                                                                      67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dehoux P;
Cossart P;
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                                                                                                                                                                 347
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Matches
                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                  The sequence is that of the Listeria p60 protein. Antibodies generated against the protein can be used in the detection of Listeria by immunoassay (partic. ELISA). The detection method allows determination of individual Listeria species, esp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure, Fig 4; 19pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New primers for PCR detection of Listeria - including individual speciles, also new peptide(s) for raising antibodies for immunochemical detection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1993-406956/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Schubert P, Neumann S, Pawelzik M, Linxweiler W,
Hofmann G, Bubert A, Goebel W, Koehler B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-JUN-1992;
25-NOV-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MERE ) MERCK PATENT GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-JUN-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Listeria monocytogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Immunogenic polypeptide; antibodies; immunoassay; conjugate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-DEC-1993.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-JUN-1994 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR45178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR45178 standard; Protein; 478
          431
                               289
                                                      374
                                                                                                                                               150 QQHPAVQKPTBPVV-----APFATG
                                                                                                                                                                                       220
                                                                                                                                                                                                              160 ttqqaabvaetktevkqttqattpabkvaetketpvidquatthavksgdtiwalsvkyg
                                                                                                                                                                                                                                                           102 írtsíkgg--tkytvettesnöwhkityndöktgfungkyltdkavstpvaptgevkket
                                                                                                                                                                                                                                    66 --SQGVP------SKIAQRYG
                                                                                                                                                                                                             90
                                                                                                                                                                                                                                                                               25 ITTCILAGCASKPTYNSTSGSGSHRTSGSGGLA--IGSQVITP----------
                  QRIASMKNQPSGAALFEF--RISRNGVYV 315
                                                                                                                                                                                                                                                                                                                         83;
                                   LGKAYSWGGNGPTTFDCSGYTKYVFAKAGISLPRTSGAQYASTTRISESQAKPGDLV---
                                                                            NANKTINTINTINTINTPSKYTINTINSNTINTINSNTINANQGSSININSNSSASATTAEAQKH 373
                                                                                                  SSGVMQFRYFVGATNFVVRRFGTATVAGSTVTSNGMWFSGRDGDLINASNAGTVIQADHN 253
                                                                                                                        - EAPÄAEKQAAPVVKENTINTATTEKKETATQ----QOTÁPKÁP--ŤEAAKPAPÁPSTINT 313
                                                                                                                                                                   VSVQDIMSWNNISSS-SIYVGQKLAI------KQTANTATPKÅEVKT----
                                                                                                                                                                                         LNWREIGHINNLNSSYTIYTGOWLTLWSGDLKVRERSISSGVNTAHTPSPVAVQSSRPPV 149
                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                   478 AA;
                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92DE-4219111.
92DE-4239567.
-----FFDYGSGİSHVĞIYV 445
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                                                                                                                                                                                                                                                                                                              9.1%; Scu
21.3%; Pre
1ve 46;
                                                       Score 151.5; DB 14; Length 478;
Pred. No. 0.0017;
6; Mismatches 117; Indels 143; Gaps
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Best Local Si
Matches 69;
                                                                                                                                                                                                                                                                                                             The present invention is related to a Lactococcus lactis nucleotide sequence (ABA90521) and related proteins (ABB53300-ABB55621). The nucleic acid sequence is useful in the detection and/or amplification of related species. The proteins of the invention are useful for the biosynthesis or biodegradation of a composition of interest. The production helps research in lactic bacteria, particularly useful in the production of yogurt and cheese.

Note: The sequence data for this patent is based on equivalent patent format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 6; SEQ ID No 280; 2504pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New nucleotide sequence useful in the identification lactis and related species -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bolotine A, Sorokine A, Renault P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-043418/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (INRG ) INRA INST NAT RECH AGRONOMIQUE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biosynthesis; biodegradation; lactic bacterium; yogurt; cheese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lactococcus lactis protein acmA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABB53578 standard; Protein; 439
                   383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABB53578;
                    249 QADHNMDGASIVIQHTNGFVSSYIHIKDAQVKTGDTV-----RTGQRIASMK 295
                                                                  337
                                                                                                                                        133
                                                                                                                                            243 YTVKSGDTLWGISOKYGISVAQIQSANNLKST-VIYIGOKLVLTTSSSSSSNTNSSTSSGN
                                                                                                                                                                                           184 TAALTGKYÄTDENYGASLNRIISQYNLTREDGASSAGTSNSGG-STATNTNNNSNTSSTT 242
                                                                                                                                                                                        73
                                                                                                                                                                                                                   26 TTCILAGCASKPTYNST------SGSGSHRTSGSGGLAIGSQVITDSQGVPNR 72
                                                                                                                                                                                                                                                              1 Similarity
69; Conserv
       SSTSNSSAAS-----NTSIH---
                                             KYKTTIAOLKSWNHLNSDTIFIGQNLIVSQSAGSSSSTG-----SSSAST--
                                                                    PFATGSSGVMQFRYPVGATNPVVRRFGTATVAGSTVTSNGMWFSGRDGDLINASNAGTVI 248
                                                                                                                    TAHTPSPVAVQSSRÞFVQQHFAVQKPTPPVVVVKKPTPTPPVVQQPAPVAPPVT----EA 188
                                                                                                           SAGTTTPTT----
                                                                                                                                                                 YQVKQGDTVSKIAQRYGLNWREIGHINNLNSSYTIYTGQWLTLWSGDLKVRERSISSGVN 132
                                                                                                                                                                                                                                                                                                            439 AA;
                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                 8.8%; Score 146.5; DB 23; 23.6%; Pred. No. 0.00041; tive 39; Mismatches 107;
                                                                                             ------SVTPAKPASQTTIKVKSGDTLWGLSV 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B
-KVVKGDTLWGLSQKSGSPIASIK 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ehrlich SD;
                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                        Length 439;
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                                               382
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ABB4B4B
AC ABB4B
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                                                                                                                                                                                                                                                                                                                                                               The present invention relates to the genome sequence of Listeria commonocytogenes EGD-e (see ABA03041). The genome sequence and fragments of it are useful for selecting probes and primers for detecting genes in L. commoncytogenes and related organisms, and for studying genetic polymorphisms and other genomes. The present sequence is a protein concottogenes and other genomes. The present invention. Proteins composes of from the genome sequence of the present invention. Proteins composes of from the genome sequence are useful for raising specific antibodies, identification of L. monocytogenes and related organisms, and for biosynthesis and biodegradation, especially biosynthesis of Vitamin CC antibodies, identification of L. monocytogenes and related organisms, and for biosynthesis and biodegradation, especially biosynthesis of Vitamin CC and modulate L. monocytogenes-related diseases. In addition, the genome sequence and proteins encoded by it are also useful for selecting compositions for the treatment or prevention of infections by L. compositions for the treatment or prevention of infections by L. compositions for this patient did not form part of the printed specification, but was obtained in electronic format directly from WIPO at figure in the genome sequence adata for this patient did not form part of the printed specification, but was obtained pot_sequences.
                                                                                                                                                                                                                     Query Match
Best Local (
                                                                                                                                                                                              Matches
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                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 6; SEQ ID No 1364; 192pp; French
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Maduenio E, De
Rose M, Voss H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chakraborty T, Domann E,
Perez-Diaz J, Baquero F,
Maduenio E, De Pablos B,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antibacterial; vitamin B12; ba
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Listeria monocytogenes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dominguez-Bernal G,
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                                                                                                                                                                                                                        Similarity
                                                              IITSIKGG--TKVTVETTESNGWHKITYNDGKTGFVNGKYLTDKAVSTPVAPTQEVKKET
                                                                                                                         ITTCILAGCASKPTYNSTSGSGSHRTSGSGGLA--IGSQVITD------
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                                                                                                                                                                                                                                                                                                                    482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C. Frangeul L. Couve E. Rusniok C. Fsihi H. Dehoux P.
D. Chetcuani F. Nedjari H. Glaser P. Cossart P.
Goebel W. Kreft J. Kuhn M. Ng E. Vazquez-Boland JA.
Bernal G. Garrido-Garcia P. Tierrez-Martinez A. Amend A.
T. Domann E. Hain T. Berche P. Charbit A. Durant L.
J. Baquero F. Garcia Del Portillo F. Gomez-Lopez N.
De Pablos B. Wehland J. Kaerst U. Entian K. Hauf J.
                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PASTEUR

    gene therapy; vaccine; biosynthesis; biodegradation;
bacterial infection; disease.

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                                                                                                                                                                                                                        8.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein #1363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          482
                                                                                                                                                                                        Score 146.5; DB 2
Pred. No. 0.00046;
6; Mismatches 121
                                                                                                                                                                                    121;
                                                                                                                                                                                                                                                      DB 23;
   --NRYQVKQGDTVSKIAQRYG
                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                      Length 482;
                                                                                                                                                                                                                                                                                                                                                                                                             part of the printed directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  for treatment
                                                                                                                                                                                        145;
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                                      AAR73913 is the Listeria monocytogenes protein P60 precursor. It contains the meningitis related antigenic sequences (MRHAS) claimed in AAR73891-R73894 and AAR73903-R73906, which are recognised by a monoclonal antibody from the hybridoma Rubella virus (RV)-1. The claimed MRHAS peptides may be used in immunoassays to diagnose the presence of bacterial and/or viral meningitis agents in a sample, or in prophylactic and therapeutic meningitis treatments. The
                                                                                                                                                                                                                      New peptide(s) and corresp. antibodies for the treatment of meningitis - the peptide(s) corresp. to homologous antigenic sites on bacterial and viral agents and on chemokine(s), used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Listeria monocytogenes; protein P60 precursor; vaccine; meningitis related homologous antigenic sequence; MRHAS; RV immunoassay; diagnosis; treatment; prophylactic; bacterial;
                                                                                                                                                                       Claim 47; Fig 7/10; 98pp; English.
                                                                                                                                                                                                                                                                                     WPI; 1995-147431/19.
                                                                                                                                                                                                                                                                                                                    Sharma LR,
                                                                                                                                                                                                                                                                                                                                                  (SHAR/)
(VALS/)
                                                                                                                                                                                                                                                                                                                                                                                                    28-SEP-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                    28-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Listeria monocytogenes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Listeria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR73913 standard; protein; 484 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      158 TTQQAAPAAETKTEVKQTTQATTPAPKVAETKETPVVDQNATTHAVKSGDTIWALSVKYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90
                                                                                                                                                                                                                                                                                                                                                  SHARMA L R.
VAN ALSTYNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             monocytogenes protein P60 precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NKTNTNTNTNTNTNTNTTNTPSKNTNTNSNTNTNSNTNANQGSSNNNSNSSASAI I AE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QQHPAVQKPTPPVV------VVKKPTPTPPVVQQPAPVAPPVTEAPFATGSSGVMQ 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LNWREIGHINNLNSSYTIYTGQWLTLWSGDLKVRERSISSGVNTAHTPSPVAVQSSRPPV 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VRTGQRIASMKNQPSGAALFEF--RISRNGVYV 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FRYPVGA-----TNPVVRRFGTATVAGSTVTSNGMWFSGRDGDLINASNAGTVIQ 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AQXHLGKAYSWGGNGPTTFDCSGYTKYVFAKAGISLPRTSGAQYASTTRISESQAKPGDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      - EAPAAEKQAAPVVKENTNTNTATTEKKETATQ - - -
                                                                                                                                                                                                     and preventing meningitis
                                                                                                                                                                                                                                                                                                                    Van Alstyne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                    93US-0127499
                                                                                                                                                                                                                                                                                                                                                                                                                                    94WO-CA00516.
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peptides may also be used as vaccines against meningitis. NB: Identified by matching corresponding MRHAS peptides.

ÖS

Sequence

484

B

Query Match Best Local

Matches

81;

Conservative

Similarity

8.8%;

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160 TTQQAAPAAETKTEVKQTTQATTPAPKVAETKETPVVDQNATTHAVKSGDTIWALSVKYG 90 LNWREIGHINNLNSSYTIYTGQWLTLWSGDLKVRERSISSGVNTAHTPSPVAVQSSRPPV 149

66 --SQGVP-----NRYQVKQGDTVSKIAQRYG

25 ITTCILAGCASKPTYNSTSGSGSHRTSGSGGLA--IGSQVITP----------

; Score 146.5; DB 16; Length 484; ; Pred. No. 0.00046; 46; Mismatches 121; Indels 145;

Gaps

14;

65

IITSİKGG--TKVTVETTESNGWHKITYNDGKTGFVNGKYLTDKAVSTPVAPTQEVKKET 159

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RESULT 12
AAO17658
ID AAO17
New isolated non-typeable Haemophilus influenzae BASB201 polypeptides,
                          WPI; 2002-426267/45.
N-PSDB; AAL46626.
                                                     Thonnard J;
                                                                                  13-OCT-2000; 2000GB-0025169.
                                                                                                  05-OCT-2001; 2001WO-EP11561
                                                               (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS
                                                                                                                                                                                  Key
Domain
                                                                                                                                       WO200230967-A2
                                                                                                                                                                  Domain
                                                                                                                                                                                                                BASB201; otitis media; pneumonia; sinusitis; nos auditive nerve damage; delayed speech learning; antibacterial; auditory; antiinflammatory.
                                                                                                                                                                                                      Haemophilus influenzae.
                                                                                                                                                                                                                                                         H influenzae BASB201 #3.
                                                                                                                                                                                                                                                                        05-AUG-2002 (first entry)
                                                                                                                                                                                                                                                                                                       AAO17658 standard; Protein; 410 AA
                                                                                                                                       301..400
/label= peptidase_M37-like_domain
                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                              32..300

'label= KEQ_rich_domain

301..400
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Best Local s
Matches 62
                                                                                                                                                                                                                                                                                                                                                                        The present invention provides the protein and coding sequences of several versions of the BASB201 protein from non-typeable Haemophilus influenzae. These can be used in the production of vaccines against H. Children, pneumonia in elders, simusitis, nosocomial infections, or invented in the middle ear, simusitis, nosocomial infections, or accumulation in the middle ear, auditive nerve damage, delayed speech the middle ear. The present sequence is a version of the BASB201 protein sequence of the invention.
                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    useful as components of vaccines for treating bacterial infection such as otitis media, delayed speech learning and inflammation of middle ear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 3; Page 88; 90pp; English.
     394
                                306
                                                              335
                                                                                                  279 STSGUGAAKKQYSLPVSGS--ILHTEG--SIQAGEVRWKGMVIGASAGTPVKAIAAGRVI
                                                                                                                            193 GSSGV----MOFRYPYGATNEVVRRFGTATVAGSTYTSNGMWFSGRDGDLINASNAGTYI 248
                                                                                                                                                           237 AEQAAREQEKREREALAGROKAEEKRT-------SKPYQPTVQERQLLN 278
                                                                                                                                                                                      134 AHTESPVAVQSSREEV-QQHEAVQXETEEVVVVXXETETEVVVQQEAEVAPEVTEAEEAT 192
                                                                                                                                                                                                                    188 ÓKKÓOOALOKAOÓEHOFS-----LNELNKNLALDODK-----LNALKANEQALRQEIOR 236
                                                                                                                                                                                                                                                 74 QVKQGDTVSKIAQRYGLNWREIGHINNLNSSYTIYTGQWLTLWSGDLKVRERSISSGVNT 133
                                                                                                                                                                                                                                                                                     ch
1 Similarity 24.6%; Score 134; DB 23;
62; Conservative 37; Mismatches 111;
                                    LAGYLNGYGYMVIVKHGETDLSLYGFNQAVSVKVGQLVSAGQVIAQVGNTGEISRSALY- 393
                                                                 OADH-NWDGASIVIQHTNGEVSSYIHIKDAQVKTGDTVRTGQRIASMKN--OPSGAALFE 305
FGISRKGTPVNP
                         FRISRNGVYVDP 317
                                                                                                                                                                                                                                                                                                                                                                410 AA;
405
                                                                                                                                                                                                                                                                                                                    Length 410;
                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                     42;
                                                                                                                                                                                                                                                                                  Gaps
                                                                                                    334
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맑 Ś В Ś B Ś 밁 Ş

376 AQKHLGKAYSWGGNGPTTFDCSGYTKYVFAKAGISLPRTSGAQYASTTRISESQAKPGDL

-----GASIVIOHTNGF-VSSYIHIKDAQVKTGDT 284

316 NKTVINTNITNINTNINTPSKNININSNITVINSNITVANOGSSNNNSNSSASAIIAB 200 FRYPVGA-----TNPVVRREGTATVAGSTVTSNGMWFSGRDGDLINASNAGTVIQ

249

259

219 89

- EAPÄAEKOAAPVVKENTNTNTATTEKKETATQ----QQTAPKAPTEAAKPAPAPSTNTNA QQHPAVQKPTPPVV------VVKKPTPTPVVQQQAAVQABAPAAFAATG88GVMQ 199 VSVQDIMSWNYLSSS-SIYVGQKLAI------KQTANTATPKAEVKT----

250 ADHNMD-----

260 150 220

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RESULT 13
AAO17656
13-OCT-2000; 2000GB-0025169
               05-OCT-2001; 2001WO-EP11561
                                      18-APR-2002.
                                                     WO200230967-A2.
                                                                                                                             BASB201, otitis media, pneumonia, sinusitis, nosocomial infection, auditive nerve damage; delayed speech learning, vaccine, antibacterial, auditory, antiinflammatory.
                                                                                                                       Haemophilus influenzae.
                                                                                                 Domain
                                                                                                                                                                        H influenzae BASB201 #1.
                                                                                                                                                                                            05-AUG-2002
                                                                                                                                                                                                             AA017656;
                                                                                                                                                                                                                      AAO17656 standard; Protein; 410 AA.
                                                                                                                                                                                        (first entry)
                                                            /label= KEQ_rich_domain
301..400
/label= peptidase_M37-like_domain
                                                                                              Location/Qualifiers 32..300
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RESULT 14
AAR85285
ID AAR85285
AC AAR85
AC AAR85
XX 01-AP
DT 01-AP
XX Lysin
XX Lysin
XX chees
XX chees
XX Uscto
XX Usoto
XX Usoto
XX Usoto
XX Usoto
XX Usoto
XX Lacto
XX Lacto
XX Isono
PN W0953
XX PN W0953
XX 12-MA
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                         23-NOV-1995.
                                               WO9531561-A1
                                                                      Lactococcus
                                                                                                       Lysin; autolysis;
                                                                                                                                                      01-APR-1996
                                                                                                                                                                             AAR85285;
                                                                                                                                                                                                   AAR85285 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated non-typeable Haemophilus influenzae BASB201 polypeptides, useful as components of vaccines for treating bacterial infection such as otitis media, delayed speech learning and inflammation of middle ea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Thonnard
  12-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
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                                                                                                                                                                                                                                                             394
                                                                                                                                                                                                                                                                                   306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QVKQGDTVSKIAQRYGLNWREIGHINNLNSSYTIYTGQWLTLWSGDLKVRERSISSGVNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of the invention.
                                                                                                                                                                                                                                                                                FRISRNGVYVDP 317
                                                                                                                                                                                                                                                                                                          LAGYLNGYGYMVIVKHGETDLSLYGPNQAVSVKVGQLVSAGQVIAQVGNTGEISRSALY-
                                                                                                                                                                                                                                                                                                                                QADH-NMDGASIVIQHTNGFVSSYIHIKDAQVKTGDTVRTGQRIASMKN--QPSGAALFE
                                                                                                                                                                                                                                                                                                                                                      STSGLGAAKKQYSLPVSGS--ILHTFG--SIQAGEVRWKGMVIGASAGTPVKAIAAGRVI
                                                                                                                                                                                                                                                                                                                                                                                                     AEQAAREQEKREREALAQRQKAEEKRT
                                                                                                                                                                                                                                                                                                                                                                                                                          QKKQQQALQKAQQEHQ-----STLNELNKNLALDQDK-----LNALKANEQALRQEIQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Page 87; 90pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                410 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                      (first
  95WO-NL00170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is a version of the BASB201 protein
                                                                                                       culture, lactic
                                                                      (Strain MG1363)
                                                                                                                                                      entry)
                                                                                            induction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7.8%;
24.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36;
                                                                                                                                                                                                   437
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5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 131;
Pred. No. (
                                                                                                                                                                                                   A
                                                                                                       acid
                                                                                                       bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 23;
0.0078;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 410;
                                                                                                       fermentation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                     ---SKPYQPTVQERQLLN
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le ear
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ABBOGA

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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                In situ production of a homologous autolysin or a heterologous autolysin from a food grade Gram positive bacteria, can be used a process for the lysis of a culture of lactic acid bacteria. The process can be used in the manufacture of products containing cultures of lactic acid bacteria e.g. cheese, where the culture lysed following the completion of fermentation. The enhanced induction of the autolysin is performed some hours after the fermentation is finished. No extra lysin needs to be added and lysin does not need to be isolated or encapsulated. The time of lysis can be precisely controlled.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                      02-AUG-2001
                                                           WO200155180-A2
                                                                                                                                                         Micromonospora carbonacea; antibiotic; everninomicin; biosynthesis;
                                                                                                                                                                                                Micromonospora carbonacea everninomicin locus protein ORF
                                                                                                                                                                                                                                       18-JUN-2002
                                                                                                                                                                                                                                                                                                                   ABB06928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 15; Page 55-57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lysis of a culture of lactic acid bacteria in, production - by in situ prodn. of an auto:lys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAT06135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              inducible promoter.
                                                                                                                                       cluster;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               346
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QUEST INT BV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WNHLSSDTIYIGQNLIVSQSAAASNP----STGSGSTATNNSNSTSSNSNASIHKVV 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGSNNS-----ASTTPTTSVTPA--KPTSQTTVKVKSGDTLWALSVKYKTSIAQLKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SSTTYTVKSGDTLWGISQRYGISVAQIQSANNLKST-IIYIGQKLVLTGS----ASSTNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---RYQVKQGDTVSKIAQRYGLNWREIGHINNLNSSYTIYTGQWLTLWSGDLKVRERSIS 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTCILAGCASKPTYNST-----
                                                                                                                                                                                                                                                                                                                 standard; Protein; 518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EAPFATGSSGVMQ---FRYPVGATNPVVRRFGTATVAGSTVTSNGMWFSGRDGDLINASN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SGVNTAHTPSPVAVQSSRPPVQQHPAVQKPTPPVVVVKKPTPT--PPVVQQPAPVAPPVT 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TAALTGRYATDPSYGASLNRIISQYNLTRFDGASSAGNTNSGG---STTTITNNNSGTNS
                                                                                                                                                                                                                                                                                                                                                                                                                      KGDTLWGLSQKSGSPI----ASIKAWNHL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGTVIQADHNMDGASIVIQHTNGFVSSYIHIKDAQVKTGDTVRTGQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               437 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                       genetic
                                                                                                                                                                                                                                       (first entry)
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24.1%;
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                                                                                                                                       manipulation;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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                                                                                                                                       contig
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auto:lysin, regulated by
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RESULT 16
ABB54;367
XX ABB54;
XX ABB54;
XX ABB54;
XX Lacto
XX Biosy
XX Biosy
XX Lacto
XX FR280
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                             Lactococcus lactis IL1403
                                                               Biosynthesis;
                                                                               Lactococcus lactis protein pi244.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local !
                                                                                                                    16-MAY-2002
                                                                                                                                                ABB54367;
                                                                                                                                                             ABB54367 standard; Protein; 894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABL50555 to ABL50562 represent contigs 1 to 8 from the Micromonospora carbonaces everninomicin biosynthetic locus gene cluster. The contigs encode the protein sequences designated ORF (open reading frame) 1 to a protein of the everninomicin antibiotic in overproducing strains, and to allow chemical modifications of everninomicin to enhance certains, gene cluster can be used to produce wis genetic manipulation or combinational biosynthesis. The gene cluster can be used to produce genetic systems and genet manipulation or combinational biosynthesis. The novel enzyme activities, and avoid the problems of low yield and quality of everninomicins produced by chemical synthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 15; Fig 1; 181pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel isolated gene cluster encoding polypeptides involved in everninomicin biosynthesis useful for construction of everninomicin of everninomicin strains, and to allow chemical modifications of everninomicin to enhance certain properties.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Staffa A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-476185/51.
N-PSDB; ABL50562.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-JAN-2000; 2000US-0177711.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-JAN-2001; 2001WO-CA00128.
                                                                                                                                                                                                                                                223
                                                                                                                                                                                                                                                            233 GR-PGDLINASNAGTV 247
                                                                                                                                                                                                                                                                     169 T--PPPTTPPPTGAAPALKVSG----NRLVTASGATYRLLGVNRASGEPACVQGKGMNDS
                                                                                                                                                                                                                                                                                                                            175
                                                                                                                                                                                                                                                                                                                                                       118
                                                                                                                                                                                                                                                                                                                                                                                 116
                                                                                                                                                                                                                                                                                                                                                                                                     64 -----TDSQGVPNRYQV----KQGDTVSKIAQRYGLNWREIGHINNLNSSYTIYTGQWLTL 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                         20 LIFGVITTCILAGCASKPTYNSTSGSG-----SHRTSG-SGGLAI---GSQVI---- 63
                                                                                                                                                                                                                                                                                                                                                                                                                                8 LAVGTTATLVAÅGLÅGLIFFPASAAATGCSVAYTVQSQWTGGFSGNVÅLTNLGSALIGWTL 67
                                                                                                                                                                                                                                   GPVDQASVNAMKAWNI 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    69;
                                                                                                                                                                                                                                                                                           VQQPAPVAPPVTEAPFATGSSGVMQFRYPVGATNPVVRRFGTATVAG--STVTSNGMWFS 232
                                                                                                                                                                                                                                                                                                                       WŚGSNPVPKSFALNGTTCTGSVTŚPTPEPTTTPP-----PTTPPPTTPPPTTPPPT 168
                                                                                                                                                                                                                                                                                                                                                WSGDLKVRERSISSGVN-TAHTESPVAVQSSRPPVQQHDAVQKPTPPVVVVKKPTPTPPV 174
                                                                                                                                                                                                                                                                                                                                                                           TFDFPTSGQQVTQGMSATWSQSGTSVSAAS----LSWN--GSLGTGGSTTIGFNGS---- 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity 27.0%;
                                                                                                           (first entry)
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                                                 biodegradation; lactic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zazopoulos E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 130.5; DB 22; Length Pred. No. 0.012; Length 2; Mismatches 112; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mercure S,
                                                                                                                                                                8
                                         bacterium; yogurt;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nowacki P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 518;
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RESULT 17
AAO17657
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AAO171
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AAO171
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Best Local S
Matches 69
                                                                            BASB201; otitis media; pneumonia; sinusitis; nos auditive nerve damage; delayed speech learning; antibacterial; auditory; antiinflammatory.
                                                 Haemophilus influenzae.
                                                                                                                                                                                            H influenzae BASB201 #2.
                                                                                                                                                                                                                                                         05-AUG-2002
                                                                                                                                                                                                                                                                                                                                      AAO17657 standard; Protein;
                                                                                                                                                                                                                                                                                                           AAO17657;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention is related to a Lactococcus lactis nucleotide nucleic acid sequence (ABA90521) and related proteins (ABB53300-ABB55521). The nucleic acid sequence is useful in the detection and/or amplification of related species. The proteins of the invention are useful for the biosynthesis or biodegradation of a composition of interest. The production helps research in lactic bacteria, particularly useful in the production of yogurt and cheese.

Note: The sequence data for this patent is based on equivalent patent format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New nucleotide sequence useful in the identification or Lactococcus lactis and related species -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-043418/06.
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                                                                                                                                                                                                                                                                                                                                                                                                                                 807 QVVQAGSNYYDWYGNYTVIKHADGLYTGYAHQSRIDVSVGQNVKKGQQIGLM 858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-APR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-OCT-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             246 TYIQADHY---MDGASIYIQHTNGFVSSYIHIKDAQYKTGDTVRTGQRIASM 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                771 EMĠ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           194 SSGVMQFRYFVGATNFVVRRFGTATVAGSTVTSNGMVFSGRDGDLIN-----ASNAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    138 SPVAVOSSRPPVOOHPA----VQKETPPVVVVKKPTPTPPVVQQPAPVAPPVTEAPFATG 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              620 LLGNAQGESDANPTADEG----GGRPGFGYGVWQWTDSSGASSGRVYMINLMTRAGVTDN 675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               78 GDTVSKIAQRYGLNWREIGHINNLNSSYTIYTGQWLTLWSGDLKVRERSISSGVNTAHTP 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29 ILAGCASKPTYNSTSGSGSHRTSGSGGLAIGSQVITDSQGVPNR--YQVK-----Q 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6; SEQ ID No 1069; 2504pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TQAFVANFERÞLNGHÞERSTWAQEWYNKFVNLKIÞSGGGGYI---ÀÞISSÞIÍ----VÍS 770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           h 7.8%; Score 130.5; DB 23; Similarity 23.6%; Pred. No. 0.023; 69; Conservative 32; Mismatches 112;
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                                                                                                 nosocomial infection; ng; vaccine;
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             12-OCT-1999
                                         AAY31384;
                                                               AAY31384 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 3;
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                                                                                                                                 Y-FGISRKGTPVNP
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Pred. No. 0.0094;
3; Mismatches 111;
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The invention provides a method for detecting a US (sub)type hepatitis E virus (US-HEV), or its naturally occurring variants in a sample by treatment with a binding partner specific for a marker of the virus, and then detecting any complex formed. The method is used to diagnose infection with US-HEV. Polypeptides from US-HEV, antibodies specific for open reading frames (ORF) in US-HEV and host cells expressing these ORFs are useful in vaccines or for passive immunisation. The polypeptides are also used to raise specific antibodies (useful as immunoassay reagents). Fragments of nucleic acid from US-HEV are useful as immunoassay reagents) usual hybridisation and amplification assays for detecting infection. The present sequence represents a HEV-US2 ORF1 protein.
Sequence
                                                                                                                                                 Claim 6; Page 216-221; 260pp; English.
                                                                                                                                                                                                      WPI; 1999-288017/24.
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1708 AA
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                                                                                                                                                                                                     The protein sequence of the beta lytic peptidase from Achromobacter lyticus was deduced from the DNA sequence obtd. by PCR using primers based on the sequence of the L. enzymogenes beta-protease. The beta-lytic protease is expected to be an enzyme which can decompose not only Gram-positive bacteria but also some Gram-negative bacteria.
                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                     Beta-lytic protease gene and DNA encoding it - Gram-positive and some Gram-negative bacteria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1992-171653/21.
N-PSDB; AAQ25083.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-APR-1992.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JP04108387-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Achromobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gram-negative;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Beta-lytic protease.
                                                                                                                                                                                                                                                                                                                                                                   Claim 2; Fig 1; 13pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-AUG-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29-AUG-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-NOV-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR24147 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (WAKP ) WAKO PURE CHEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    748
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             574 TTVVDGAHLEANGPEEYVLSFDASRQSMGAGSHSLTYELTPAGLQVKISSNGLDCTATFP
  117 SGDLKVRERSISSGVNTAHTPSPVAVQSSRPPVQQHPAVQKPTPPVVVVKKPTPTPPVVQ 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        260 VIQHTNGFVSSYIHIKDAQVKTGDTVRTGQRIASMKNQP-SGAALFEFRISRN 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            634 XGGAPSAAPGEVXAFCSALYRYNRFTQRHSLTGGLWLHPEGLLGIFPPFSPGHIWESANP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           77 QGDTVS----EIGHI----NN 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27 TCILAGC---ASKPTYNSTSGSGSHRTSGSGGLAI-----GSQVITDSQGVPNRYQVK
                                                    50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LNSSYTIYTGQWLTL-WSGDLKVRERSISSGVNTAHTPSPVAVQSSRPPV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -LCH----AFYORFPEAFYSTEFIMREGLAAYTLTPRPIIHAVAPDYRVEON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YTYPDGA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EESHVDAASVPSVPEPAGLTSPIVLT--PPPPPPPPVRKPATSPPPRTRR-----LL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FCGEGTLYTRTWSTSGFSSDFSPPEAAAPASAAAPGLPYPT-----PPVSDIWVLPPPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FRYPVGATNPVVRRFGTATVAGSTVTSNGMWFSGRDGDLINASNAGTVIQADHNMDGASI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -QQH-----PAVQKP----TPPVVVVKPTPTPVVVQQPAPVAPPVTEAPFATGSSGVMQ
                                                                                                                                                     374 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ilarity 22.7%; P: Conservative 37;
                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              lyticus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gram-positive; bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90JP-0225136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90JP-0225136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein;
                                                                         7.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----KVYAGSLXESDCDW--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IND
                                                    29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 0.11;
7; Mismatches 120;
                                                                            Score 126.5; DB 13; Pred. No. 0.017;
                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                decomposition.
                                                    65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels 116; Gaps
                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                decomposing
                                                                                                      Length
                                                    49;
                                                    Gaps
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                                                    7;
                                                                                                                                                                                                       ARYSULT 20
ARYA44
XX ARYA44
AC ARYA44
XX ARYA4
AC ARAYA4
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                                                                                                                           Query Match
Best Local S
                                                                                                      Matches
                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-147208/13.
N-PSDB; AAZ49721.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bramley JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-JUN-1998;
21-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY44646;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY44646 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Achromobacter lyticus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9967381-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (UYVE-) UNIV
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  154 AGGRAARRRVPAGL
                                                                                                                                 Similarity
                                                 SGDLKVRERSISSGVNTAHTPSPVAVQSSRPPVQQHPAVQKPTPPVVVVKKPTPTPPVVQ 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TATANPANTOAOA
                                                                                                                                                                                                          374 AA;
                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plaut KI,
                                                                                                                              7.6%;
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The present sequence is a Achromobacter lyticus beta-lytic protease which has anti-staphylococcal activity. The beta-lytic protease gene is used in the production of altered genes which allow expression and preferably secretion of active protein in mammalian cells/tissues. The altered gene is produced by operably linking the beta-lytic protease coding sequence with mammalian promoter, signal peptide and translation initiation sequences. The modified sequence is used in gene therapy to treat staphylococcal mastitis infections runinants, e.g. goats, sheep, and cows. It is also used to produce transgenic animals which are resistant to staphylococcal infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Beta-lytic protease; antibiotic; anti-staphylococcal; gene therapy; mastitis; staphylococcal infection; rum transgenic animal; altered beta-lytic protease gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Treatment of Staphylococcal infections, such as animals, especially cows -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Achromobacter lyticus beta-lytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Fig 14B; 61pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               229 MWFSGRDGDLINASNAGTVIQADHNMDGASIVIQHTNGFVSSYIHIKDAQVKTGDTVRTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QRIASMKNOPSGA 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GWGSNQNGNWVSASAAGSFKR--HSSCFAEIV--HTGGWSTTYYHLMNIQYNTGANVSMN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QGRP-----GRAAVSPNGLLQFPFPRGASWHV---GGAHTNTGSGNYPMSSLDMSRGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QPAPVAPPVTEAPFATGSSGVMQFRYPVGATNPVVRRFGTATVAGS-----TVTSNG
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99US-0337079.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                374
Score 126.5; DB
Pred. No. 0.017;
9; Mismatches
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                                                    DB 21; Length
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                                                           374;
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  Query Match
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Matches 52
                                                                                                                                                                                           mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a protein described in the exemplification of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutanicum. Tare useful for identifying the mutation point of a gene derived from mutant of corvneform bacterium, measuring expression amount and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 17;
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N-PSDB; AAH67706.
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Tateishi N,
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     l Similarity 52; Conserv
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7.5%;
llarity 33.8%;
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; 2000JP-0159162.
; 2000JP-0280988.
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Senoh A,
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Score 125.5; DB 22;
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            CC The invention relates to RP-factors which are substances that can CC resuscitate dormant, moribund or latent cells, possibly also having CC growth-stimulating activity. Host cells containing a vector comprising CC the RP-factor or its receptor encoding nucleic acid can be used for the CC convertases, antibodies (against the RP-factors, their receptors or CC convertases, antibodies (against the RP-factors and RP-factor receptors or CC convertases), antagonists and agonists, are useful in vaccines and for CC excipients, generally as antimicrobials and especially for infections CC associated with latency. They can be used as potentiators of antibiotics such as isoniazid, streptomycin etc., in treatment of tuberculosis. CC RP-factor can also be used: to determine the microbiological quality of foods, pharmaceuticals, medical products; as culture additive for CC produce libraries of biomolecules and microorganisms (which may then be creened for useful products). Probes complementary to the RP-factor culcic acid are used identify and clone other RP-factor genes. The CC inventions may also be used to prevent bacterial resuscitation. Breaking CC dormancy with RP-factor facilitates detection, culture and enumeration of the contractor of the contractor of the contractor of the contractor of the contractor of the contractor of the contractor of the contractor of the contractor of the contractor of the contractor of the contractor of the contractor of the contractor of the contractor of the contractor of the contractor of the contractor of the contractor of the contractor of the contractor of the contractor of the contractor of the contractor of the contractor of the contractor of the contractor of the contractor of the contractor of the contractor of the contractor of the contractor of the contractor of the contractor of the contractor of the contractor of the contractor of the contractor of the contractor of the contractor of the contractor of the contractor of the contractor of the contractor of the contractor of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New bacterial resuscitation factors - useful for stimulating bacteria and growth, particularly for use as antimicrobials, vaccines comprising bacteria with mutations in resuscitation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure;
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04-JUN-1997;
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In situ production of a homologous autolysin or a heterologous autolysin from a food grade Gram positive bacteria, can be used in process for the lysis of a culture of lactic acid bacteria. The cultures of lactic acid bacteria the manufacture of products containing lysed following the completion of fermentation. The enhanced induction of the autolysin is performed some hours after the fermentation is finished. No extra lysin needs to be added and the lysin does not need to be isolated or encapsulated. The time of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                          Disclosure; Page 69-72; 103pp; English.
                                                                                                                                                                                                                                                                                                      Lysis of a culture of lactic acid bacteria in, e.g. cheese production - by in situ prodn. of an auto:lysin, regulated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (UNIL )
                                                                                                                                                                                                                                                                                                   inducible promoter.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lysin; autolysis; culture; lactic acid bacteria; fermentation; cheese; foodstuffs; induction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Enterococcus hirae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Enterococcus hirae autolysin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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rocal Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       116 WSGDLKVRERSISSGVNTAHTESEVAVQSSREPVQQHEAVQKFTEEVVVVKKETETEEVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QUEST INT BV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              56 LAIGSQVITDSQGVPNRYQVKQGDTVSKIAQRYGLNWREIGHINNLNSSYTIYTGQWLTL 115
                                                                                                                                                                                                                                                                                                                                                                                                                                         Kok J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PEKSSA 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NOPSGA 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GIDLNKNPNAKVIAVDPN-----VIPLGSKVYVEGYGEATTA-ADTGGAIK-GNKIDVFV 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GDLINASNAGTVIQADHNNDGASIVIQHTNGFVSSYIHIKDAQVKTGDTVRTGQRIASMK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QQPAPVAPPVTEAPFATGSSGVMQFRYPVGATNPVVRRFGTATVAGSTVTSNGMWFSGRD
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Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Venema
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The present invention describes primer sets for synthesising 5602 (C full-length cDNAs defined in the specification. Where a primer set (C comprises: (a) an oligo-dry primer and an oligonucleotide complementary for the following primer and an oligonucleotide which comprises one of the temperature strand of a polymucleotide which comprises one of complementary strand of a polymucleotide which comprises one of an oligonucleotide comprises at least 15 nucleotides; or (b) a combination complementary strand of a polymucleotide which comprises a 5'-end comprises and an oligonucleotide comprising a sequence complementary to a complementary strand of a polymucleotide which comprises a 5'-end complementary to a comprise which comprises a 3'-end sequence complementary to a coligonucleotide comprises a 3'-end sequence, where the coligonucleotide comprises at least 15 nucleotides and the combination of the specification. The primers set can be used in antisense therapy and confidence of the specification. The primers are useful for synthesising polymucleotides, and the comprises at least 15 nucleotides and the combination of the specification. The primers are useful for synthesising polymucleotides, and the comprise of the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 24
AAB94053
ID AAB94
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Best Local S
Matches 36
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Ishii S,
                                                                                                                                                                                                                                              Claim 8; SEQ ID 14222; 2537pp +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-JUL-1999;
27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
                                                                                                                                                                                                                                                                                 Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs -
                                                                                                                                                                                                                                                                                                                                                                                                                               (HELI-) HELIX RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-JUL-2000; 2000EP-0116126.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-FEB-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EP1074617-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB94053 standard; Protein;
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hirae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31
                                                                                                                                                                                                                                                                                                                                                                                  Isogai T, Nishikawa T,
Sugiyama T, Wakamatsu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       can be precisely controlled. This is the Enterococcus autolysin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YGLNWREIGHINNLNSSYTIYTGQWLTLWSGDLKVRERSISSGVNTAHTPSPVA 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGSSTTNTGNNASSGNTSGNTNTSGSTGQATGA------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGCASKPTYNSTSG---SGSHRTSGSGGLAIGSQVITDSQGVPNRYQVKQGDTVSKIAQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; 2000JP-0118776.
; 2000JP-0183767.
; 2000JP-0241899.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           666 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence SEQ
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99JP-0300253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          detection; diagnosis; antisense therapy;
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Pred. No. 0.063;
1; Mismatches
                                                                                                                                                                                                                                              CD ROM; English.
                                                                                                                                                                                                                                                                                                                                                                              Hayashi K,
A, Nagai K,
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                                                                                                                                                                                                                                                                                                                                                                              Saito K,
Otsuki
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T;
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                                                                                                                                                                                                                                                                                                                          BVH-P1 gene; streptococcal infection; pharyngitis; erysipelas; impetigo; scarlet fever; bacteraemia; necrotising fascitis; toxic shock; vaccine; immune response; anti-inflammatory; immunisation; antibacterial.
 The invention relates to antigens,
                         Claim 21; Fig 16;
                                                  New Streptococcus pyogenes antigen useful for diagnosing, treating streptococcal infection, e.g. pharyngitis, erysimpetigo, scarlet fever, and invasive diseases
                                                                                                                                            Martin D,
                                                                                                                                                                                                06-JUL-2000; 2000US-216465P
                                                                                                                                                                                                                        06-JUL-2001; 2001WO-CA01001
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                                                                                                                                                                                                                                                                                                   Streptococcus pyogenes
                                                                                                                                                                                                                                                                                                                                                                                 Streptococcus pyogenes strain B514 BVH-P1 mature protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54;
                                                                                                                                                                      SHIRE
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                                                                                                        AAD29299
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                                                                                                                                           Hamel J,
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                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                       BIOCHEM INC
                         74pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               634
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                                                                                                                                             Brodeur
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Pred. No. 0.11;
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more particularly an antigen
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RESULT 26
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Best Local S
Matches 61
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                                                                                                                                                                                                                                                                                                                                                               BVH-P1 gene; streptococcal infection; pharyngitis; erysipelas; impetigo; scarlet fever; bacteraemia; necrotising fascitis; toxic shock; vaccine; immune response; anti-inflammatory; immunisation; antibacterial.
                                                                                                                                                                                                                                                                                                                                Streptococcus
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                             Martin D,
                                                                                             06-JUL-2000; 2000US-216465P
                                                                                                                              06-JUL-2001; 2001WO-CA01001.
                                                                                                                                                                                               WO200204495-A2.
                                                                                                                                                                                                                                                 Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAE18360 standard; Protein; 382 AA
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                                                              (SHIR-) SHIRE BIOCHEM INC.
                                                                                                                                                                17-JAN-2002.
                                                                                                                                                                                                                                                                                 Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEEVSSAAPAQAPAEKEETSAPAAQKAVADTTSVATSNGLSYA--PNHAYNPMNAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TATVAG---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NDVSTESSSESQKQPEVPQEAVPTPKAAETTEVEPKTDIS----EDPTSANRPVPNESA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           is Streptococcus pyogenes strain B514 BVH-P1 mature protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----PPVVQQ--PAPVAPPVTEAPFATGSSGVMQFRYPVGATNPVVRRFG 215
                           Hamel J,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                              pyogenes B514
                                                                                                                                                                                                                                                                                                                                                                                                                                 pyogenes strain B514 BVH-P1
                                                                                                                                                                                                                                              /label= Signal_peptide
26..382
                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                            note= "Mature_BVH_P1_protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7.2%;
                               Brodeur
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21;
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Pred. No. 0.056;
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Dacterial pathogen. The polypeptides and polynucleotides encoding them are useful for diagnosing, preventing or treating streptococcal infection, such as pharyngitis, erysipelas, impetigo, scarlet fever, invasive diseases (bacteraemia, necrotising fascitis, toxic shock), and for eliciting an immune response. The polypeptides may also be used as immunogens for producing antibodies for the diagnosis and treatment of Streptococcus infection, or for passive immunisation. DNAs encoding polypeptides may also be used to design DNA probes for detecting the presente of Streptococcus in biological samples suspected of containing the reapputic treatment of Streptococcal infection in an individual susceptible to or infected with streptococcal infection. The present susceptible to or infected with streptococcal infection. The present sequence is Streptococcus pyogenes strain B514 BVH-P1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Cellulase, proteinase, truncated, Cel B5, Cel B4/5, Cel E1, Cel E1/2; Cel 1/2/3, Cel 6, Cel E3/B5, laundry detergent; stain-removing; cotton-containing fabric; stonewashing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New Streptococcus pyogenes antigen useful for diagnosing, preventing treating streptococcal infection, e.g. pharyngitis, erysipelas and impetigo, scarlet fever, and invasive diseases
                                                                                                                                                                                                                                                                                                                                                                                    Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY13492 standard; Protein; 1426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 21; Fig 8; 74pp; English.
                                                                                                    19-SEP-1997;
                                                                                                                                                                      15-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Truncated cellulases Cel B4/5 and
                                  (CLRN ) CLARIANT FINANCE BVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          218 SEEVSSAAPAQAPAEKEETSAPAAQKAVADTTSVATSNGLSYA--PNHAYNPMNAG 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               122 VRERSISSGVNTAHTPS----PVAVQSSRPPVQQHP----AVQKPTPPVVVVKKPTPT- 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   73 YQVKQGDTVSKIAQRYGLNWR---EIGHINNLNSSY--TIYT-----GQWLTLWSGDLK 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NDVSTESSSESQKQPEVPQEAVPTPKAAETTEVEPKTDIS-----EDPTSANRPVPNESA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TATVAG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TVQAPASSPASVSHVPSSEPLPQASATSQPTVPMAPSATPLASAKPDSSVTASSELTSST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YTVKYGDTLSTIAEAMGIDVHVLGDINHIANIDLIFPDTILTANYNQHGQATTL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                382 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7.2%; Score 120; DB 23; Length 382;
Llarity 25.8%; Pred. No. 0.061;
Conservative 21; Mismatches 78; Indels 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry
                                                                                                        97US-0932571.
                                                                                                                                                                      98EP-0810919.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----PPVVQQ--PAPVAPPVTEAPFATGSSGVMQFRYPVGATNPVVRRFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----STVTSNGMWFSGRDGDLINASNAG 245
                                  UTJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         õ
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                                                                                                                                                                                                                                                       The invention relates to a recombinant cellulase active protein free of CC proteinases of mative thermophilic and alkalinophilic origin, comprising CC the truncated sequences Cel B5, Cel B4/5, Cel E1/2/3, Cel 1/2/3, CC Cel 6 or Cel E3/B5, or a stability region from one of the defined full-CC length sequences, or functional equivalents. Cel B4/5 extends from amino CC acid A1011 to P1424 or K1425 or N1426, and Cel B4/5 extends from amino CC acid K635 to N1426 in the sequence shown in ANY13492; Cel E1 extends from maino acid Y39 to D481, Cel E1/2 extends from Y39 to G635, Cel E1/2/3 extends from Y39 to G812, Cel E6 extends from amino acid C123) to CK1751 and the stability region extends from amino acid E402 to G635 in CC K1751 and the stability region extends from amino acid E402 to G635 in CC K1751 and the stability region extends from amino acid E402 to G635 in CC K1751 and the stability of E3/B5 is shown in ANY13494. The new cenzymes are useful in laundry detergent compositions to prevent or CC remove staining, backstaining or graying, for use on cellulosic CC corpreventing redeposition of colorant during stonewashing, and for processing of textiles where cellulose breakdown is required. The new CC truncated enzymes show reduced redeposition of dye compared to using CC non-truncated cellulase compositions.
                                                                                                                                                                                       Query Match
Best Local
                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Anderson P, Bergquist PL, Day
Gibbs MD, Morgan H, Williams
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New truncated cellulase proteins, useful producing 'stonewashed' denim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-315403/27.
N-PSDB; AAX55661.
                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 7; Page 34-37; 65pp; English.
  920
                                          102 NSSYTIYTGQWLTLWSGDLKVRERSISSGVNTAH--TPSPVAVQSSRP-PVQQHPAVQKP
                                                                                   868
                                                                                                                           51
                                                                                                                                                                 59;
                                                                                                                                                                    n 7.2%;
Similarity 25.3%;
59; Conservative 1
                                                                                   SGAGVLAAGQSTKEIRLSIQKGSGSYNQSNDYSIRS----ANSYIENEKVTGYIDG-
                                                                                                                           SGSGGLAIGS-----QVITDSQGVPNRYQVKQGDTVSKIAQRYGLNWREIGHINNL 101
-----AIVWG-----REPSRGTKPAGVVTPTPAPTPTSTPTPTPTPTPTP
                                                                                                                                                                                                                                                       1426 AA;
                                                                                                                                                               Score 119.5; pred. No. 0.3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Daniels ams DP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RM,
                                                                                                                                                                                    .37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   in detergents and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Farrington
                                                                                                                                                                                                            DB 20;
                                                                                                                                                                    88;
                                                                                                                                                                    Indels
                                                                                                                                                                                                            Length 1426;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            £
                                                                                                                                                                      69;
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RESULT 28
AAAE16323
ID AAE16
AX AAE16
AX AAE16
XX 26-MA
XX ACTIV
XX ACTIV
XX ACTIV
XX CE1B5
XX Unide
XX Unide
XX Tegio
FT Regio
                                                                                      Active cellulase protein; alkalinophilic; textile processing; detergent additive; stonewashed appearance; cotton-containing CelB5; thermophilic; commercial detergent; celB gene.
 Domain
                          Region
                                                                Unidentified
                                                                                                                                            Active
                                                                                                                                                                      26-MAR-2002
                                                                                                                                                                                                                       AAE16323 standard; Protein; 1426 AA.
                                                                                                                                            cellulase
                                                                                                                                                                    (first entry)
Location/Qualifiers
635..1426
/note= "B4/5 protein"
999..1000
                                                                                                                                          protein,
                                                                                                                                            CelB.
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proteinase; denim;

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1022 193 962 159

GNKIVDKDGKPVWLTG--VNWFGFNT---GTNVFDGVWSCNLKSALAEIANRG 1069 GSSGVMQFRYPVGATNPVVRRFGTATVAGSTVTSNGMWFSGRDGDLINASNAG 245 TPPVVVVKKPTPTPPVVQQPAPVAPP-----VTEAP-------FAT 192

961 158 919

TPTVTVTPTSTPTPVSSSTPTPTATPTPTSTTTPAPTATPTPTPSVTDDTNDDWLFAQ

bacteria; fermentation;

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RESULT 29
AAR85287
ID AAR85
XX
AC AAR85
AC AAR85
DT 02-AE
XX
DE Lysir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to a cellulase active protein, which is substantially free of proteinases of native thermophilic and alkalinophilic origin, where the cellulase active protein consists of the CelB5 amino acid sequence. The cellulase active protein is useful for treating cellulosic materials including cotton-containing fabrics, as detergent additives. The cellulase active protein is also useful for improving the feel and/or appearance of cotton-containing fabrics, for removing surface fibers from cotton-containing knits or for imparting stonewashed appearance to cotton-containing denims. The present proteins are stable under condition of alkaline pH and elevated temperatures, thus suitable for textile processing and in commercial detergents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and
                    Lysin carboxy terminal repeat region.
                                                        02-APR-1996
                                                                                           AAR85287;
                                                                                                                          AAR85287 standard; Protein; 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Column 55-64; 61pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New cellulase active protein, useful in textile processing or commercial detergents, e.g. for improving the feel or appearance of cotton-containing fabrics, is stable under conditions of alkaline p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-081780/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Farrington GK, Ande
Morgan H, Williams
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US6294366-B1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CLRN ) CLARIANT FINANCE BVI LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                  1022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         elevated temperatures
                                                                                                                                                                                                                                                                                      962
                                                                                                                                                                                                                                                   193
                                                                                                                                                                                                                                                                                                                      159
                                                                                                                                                                                                                                                                                                                                                                                            102
                                                                                                                                                                                                                                                                                                                                                                                                                               868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                     TPPVVVVKKPTPTPPVVQQPAPVAPP-----VTEAP----
                                                                                                                                                                                                                                                                                                                                                                                        NSSYTIYTGQWLTLWSGDLKVRERSISSGVNTAH--TPSPVAVQSSRP-PVQQHPAVQKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SGSGGLAIGS-----QVITDSQGVPNRYQVKQGDTVSKIAQRYGLNWREIGHINNL 101
                                                                                                                                                                                                                GNKIVDKDGKPVWLTG--VNWFGFNT---GTNVFDGVWSCNLKSALAEIANRG
                                                                                                                                                                                                                                                 GSSGVMQFRYPVGATNPVVRRFGTATVAGSTVTSNGMWFSGRDGDLINASNAG
                                                                                                                                                                                                                                                                                    TPTVTVTPTSTPTPVSSSTPTPTATPTPTPSITITPÄPTATPTPTPSVTDDTNDDWLPÄQ
                                                                                                                                                                                                                                                                                                                                                                                                                             SGAGVLAAGQSTKEIRLSIQKGSGSYNQSNDYSIRS-----ANSYIENEKVTGYIDG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1426 AA;
                                                                                                                                                                                                                                                                                                                                                       ------AIVWG-----REPSRGTKPAGVVTPTPAPTPTSTPTPTPTPTPTPTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97US-0932571.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98US-0136574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Anderson P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "Linker domain" 1001..1424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     is CelB protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "B/5 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 119.5; 1
Pred. No. 0.37
17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bergquist
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ָס
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                                                                                                     ----FAT 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gibbs MD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1426;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69;
                                                                                                                                                                                                                1069
                                                                                                                                                                                                                                                   245
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 RESULT 30
AAY95030
ID AAY95
XX
AC AAY95
XX
DT 19-JU
XX
DE Human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       autolysin from a food grade Gram positive bacteria, can be used in a process for the lysis of a culture of lactic acid bacteria. The process can be used in the manufacture of products containing cultures of lactic acid bacteria e.g. cheese, where the culture is lysed following the completion of fermentation. The enhanced induction of the autolysin is performed some hours after the fermentation is finished. No extra lysin needs to be added and the lysin does not need to be isolated or encapsulated. The time of lysis can be precisely controlled. See AAR85285 for the complete
Human clone vb22_1 ORF2, SEQ ID NO:130.
                                                                       AAY95030;
                                                                                                        AAY95030
                                    19-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lysis of a culture of lactic acid bacteria in, e.g. cheese production - by in situ prodn. of an auto:lysin, regulated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    In situ production of a homologous autolysin or a heterologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 57-58; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Buist G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lactococcus lactis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lysin; autolysis; culture; lactic acid cheese; foodstuffs; induction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          inducible promoter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (UNIL ) QUEST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
                                                                                                                                                                                              194
                                                                                                                                                                                                                                                                   147
                                                                                                                                                                                                                                                                                                    206
                                                                                                                                                                                                                                                                                                                                                                          151
                                                                                                                                                                                                                                                                                                                                       68
                                                                                                                                                                                                                                                                                                                                                                                                           42
                                                                                                                                                                                                                                                                                                                                                                                                                                          91 NWREIGHINNLNSSYTIYTGOWLTLWSGDLKVRERSISSGVNTAHTPSPVAVQSSRPPVQ 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31 AGCASKPTYNSTSGSGSHRTSGSGGLAIGSQVITDSQGVPNRYQVKQGDTVSKIAQRYGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63; Conser
                                                                                                        standard;
                                                                                                                                                                                              ASIKAWNHL-----SSDTILIGQ 211
                                                                                                                                                                                                                                                                                                                                     VTPA--KPTSQTTVKVKSGDTLWALSVKYKTSIAQLKSWNHLSSDTIYIGQNLIVSQSAA
                                                                                                                                                                                                                                                                                                                                                                        QHPAVQKPTPPVVVVKKPTPT--PPVVQQPAPVAPPVTEAPFATGSSGVMQ---FRYPVG 205
                                                                                                                                                                                                                                                                                                                                                                                                         SVAQIQSANNLKST-IIYIGQKLVLTGS----ASSTNSGGSNNS------ASTTPTTS
                                                                                                                                                                                                                               GFVSSYIHIKDAQVKTGDTVRTGQ
                                                                                                                                                                                                                                                                                                    ATNPVVRRFGTATVAGSTVTSNGMWFSGRDGDLINASNAGTVIQADHNMDGASIVIQHTN 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SGGSTTTITNNNSGTNSSSTT------YTVKSGDTLWGISQRYGI 41
                                                                                                                                                                                                                                                                   ASNP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kok J, Ledeboer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         216 AA;
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                                  (first entry)
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                                                                                                        Protein;
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                                                                                                                                                                                                                                                                   -STGSGŚTATNŃSNSTŚSNSNASIHKVVKGDTLWGLSQKSGSPI-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7.1%;
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The invention relates to 40 human secreted proteins (AAY94981-Y95020), CC and cDNA sequences encoding them (AAA21423-A23462). The secreted CC proteins of the invention include those that are thought to be only CC partially secreted, i.e., transmembrane proteins. The proteins of the CI invention may exhibit one or more activities selected from the following: CC cytokine activity; cell proliferation, differentiation; immune CC modulation, haematopoiesis regulation, tissue growth activity; haemostatic clambition activity. The proteins may be administered to patients as CC vaccines, and the nucleotides may be used as part of a gene therapy credime. Diseases or conditions that may be treated using the proteins or conclectides of the invention include autoimmune diseases; genetic CC disorders, haemophilia; cardiovascular diseases; cancer; bacterial, CC fungal and viral infections, especially HIV, multiple sclerosis; culcers, osteoprosis, osteoparthritis, periodontal diseases, burns, CC ulcrs, osteoprosis, osteoarthritis, periodontal diseases and amyotrophic classes, parkinson's disease, Huntington's disease and amyotrophic lateral sclerosis (ALS). Proteins with activin/inhibin activity may can be used for treating wounds, burns, CC lateral sclerosis (ALS). Proteins with activin/inhibin activity may conditionally be used in chromosome mapping, and as source of the covantion may be used in chromosome mapping, and as a source of the covantion may be used in chromosome mapping, and as a source of the cDNA clones of the invention.
                                                                                     Matches
                                                                                                    Query Match
Best Local :
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25-NOV-1998;
23-DEC-1998;
23-DEC-1998;
23-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24-AUG-1998;
24-AUG-1998;
09-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; secreted protein; cancer; tumour; cardiovascular disorder; blood disorder; haemophilia; autoimmune disease; diabetes; inflammati infection; fungal; bacterial; viral; HIV, allergy; arthritis; neurodegenerative disease; asthma; contraceptive; open reading frame;
                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 350-351; 357pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200011015-A1
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                                                132 NTAHTPSPV---AVQSSRPPVQQHPAVQKPTPPVVVVK---KPTPTPPVVQQPAPVAPPV 185
                                                                                   l Similarity
36; Conser
                 STVPAPSPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPA---PAPAAPPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or transmembrane proteins and for treating neurodegenerative
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98US-0097659.
98US-0099618.
98US-0102092.
98US-010978.
98US-0113646.
98US-0113646.
99US-0379246.
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                                                                                                 7.1%;
39.6%;
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e disorders, autoimmune
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                                                                                                                    Length 284;
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RESULT 31
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Best Local Similarity
Matches 65; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Identifying modulators of actin polymerization, potentially useful for treating tumor metastasis and parasitic infection, using proteins that contain Ena/VASp binding sites -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 13; Pages 105-107; 109pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Saccharomyces cerevisiae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Actin polymerisation; Ena/VASP; vasodilator-stimulated phosphoprotein; metastatic cancer; parasitic infection; cytotoxic; Las17.
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(CURI-) INST CURIE.
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                                                                                                      389
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QPAVPLPQNTQAPSQATNVPVAPPPPPASLGQSQIPQSAPSAPIPPTLPSTTSAAPPPPP
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                                                DLKY-----RERSISSGVNTAHTPSPVAVQSSRPPVQQHPAVQKPTPPVVVVKKPTPTP
                                                                                                                                     -VPNRYQVKQGDTVSKIAQRYGLNWRBIGHINNLNSS-----YTTYTGQWLTLWSG
                                                                                                                                                                                                             PMRTTTEGSGVRLPAPPPPPRRGPAPPPPPHRHVTSNTLNSAGGNSLLPQATGRRGPAPP
                                                                                                   PPPRASRPTPNVTMQQNPQQYNNSNRPFGYQTNSNMSSPPPPPVTTFNTLTPQ-MTAATG
                                                                                                                                                                                                                                                                 PTYNSTSGSG------SHRTSGSGGLAIGSQVITDSQG-----
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                                                                                                                                                                                                                                                                                                                    7.1%; Score 118; DB 22; 1
23.0%; Pred. No. 0.17;
ative 34; Mismatches 104;
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                                                                                                          Best Loc
Matches
                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                             the WASP (Wiskott-Aldrich Syndrome protein) family of proteins.

Peptide fragments of WASP-family proteins of eukaryotic cells are used to prepare reagents for detecting compounds that inhibit or stimulate formation of the actin cytoskeleton, and thus inhibit or stimulate cell motility. The peptides are used to detect and identify compounds which are potentially useful for treating diseases associated with dysfunction of actin polymerisation, particularly metastatic cancer and parasite infection; as cytotoxic agents for inhibiting/stimulating formation of the actin cytoskeleton and for detecting side-effects, on actin polymerisation, of pharmaceuticals. By modulating actin polymerisation, these compounds affect cell motility, embryonic development, the immune
                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 13; Fig 7; 162pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          anticancer and antiparasitic agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New fragments of WASP family proteins, useful for detecting identifying modulators of actin cytoskeleton formation, pote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-536241/59.
N-PSDB; AAH77917.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wiskott-Aldrich syndrome protein; WASP; actin cytoskeleton; Lasl cell motility; actin polymerisation; cancer; parasite infection; embryonic development; immune response; wound repair.
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                                                                                                                                                                                                                                                                               response
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                                                                                                                                          Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               present sequence represents a Las17 protein. Las17 is a member of
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                                                                                                             65;
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                                                                                                                                       Similarity
PMRTTTEGSGVRLPAPPPPPRRGPAPPPPPHRHVTSNTLNSAGGNSLLPQATGRRGPAPP
                                                         PTYNSTSGSG-----
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                                                                                                                                                                                                                           633
                                                                                                       7.1%;
llarity 23.0%;
Conservative 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAT RECH
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                                                                                                                                                                                                                        AA;
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                                                                                                                                                                                                                                                                            repair.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sykes
                                                                                                     Score 118; DB 22;
Pred. No. 0.17;
4; Mismatches 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ç
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E
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                                                   ----SHRTSGSGGLAIGSQVITDSQG-----
                                                                                                          104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    formation, potential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Golsteyn RM;
                                                                                                                                                              Length 633;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    266
                                                                                                          80;
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                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  227
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132 NTAHTPSPV---AVQSSRPPVQQHPAVQKPTPPVVVVK---KPTPTPPVVQQPAPVAPPV 185

Matches Query Match

36;

Conservative

8;

Local

Similarity

7.1%;

Score 118; DB Pred. No. 0.39; Mismatches

21; 33;

Length 1192; Indels

14;

Gaps

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                           The invention relates to human MAGI protein, which is similar to neuroendocrine-specific protein. The MAGI protein can be expressed by standard recombinant methodology. The MAGI polypeptides, polynucleotides and antibodies are useful for treating diseases, including neuropathies, spinal injury, neuronal degeneration, neuromuscular disorders, stroke and inflammatory disorders and developmental disorders, cancer, stroke and inflammatory disorders. The polynucleotide is also useful for chromosome localization and for tissue expression studies. The present sequence represents the human MAGI protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MAGI protein; neuroendocrine-specific protein; neuropathy; human; spinal injury; neuronal degeneration; neuromuscular disorder; can psychiatric disorder; developmental disorder; inflammatory disord stroke; cytostatic; cerebroprotective; neuroprotective.
                                                                                                                                                                                                                         Novel polypeptides related to neuroendocrine-specific proteins and polynucleotides useful for diagnosis of various diseases and for treatment of cancer and neurological disorders -
Sequence
                                                                                                                                                                                            Claim 2; Page 20-21; 35pp; English.
                                                                                                                                                                                                                                                                                                            WPI; 2000-182693/16.
                                                                                                                                                                                                                                                                                                                                            Michalovich D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human MAGI polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY56967 standard; Protein; 1192 AA.
                                                                                                                                                                                                                                                                                                                                                                            (SMIK ) SMITHKLINE BEECHAM PLC
                                                                                                                                                                                                                                                                                                                                                                                                                             22-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200005364-A1
                                                                                                                                                                                                                                                                                                                                                                                                            19-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GMWFSGRDGDLIN---ASNAGTVIQADHN-MDGASIVIQHTNG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P-VVQQP----APVAPPVTEAPFATGSSGVMQFRYPVGATNPVVRRFGTATVAGSTVTSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DLKV-----RERSISSGVNTAHTPSPVAVQSSRPPVQQHPAVQKPTPPVVVVKKPTPTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PPPRASRPTPNVTMQQNPQQYNNSNRPFGYQTNSNMSSPPPPPVTTFNTLTPQ-MTAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -VPNRYQVKQGDTVSKIAQRYGLNWREIGHINNLNSS-----YTIYTGQWLTLWSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QPAVPLPQNTQAPSQATNVPVAPPPPPASLGQSQIPQSAPSAPIPPTLPSTTSAAPPPPP
1192 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                           98GB-0016024.
99GB-0016898.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          99WO-GB02360.
                                                                                                                                                                                                                                                                                                                                            Prinjha
                                                                                                                                                                                                                                                                                                                                            RK.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -GGSFAETT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        543
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문 Ś 망

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RESULT 34
AAU04591
Novel Nogo receptor protein useful for identifying modulator of Nogo protein or Nogo receptor protein, which is useful for treating central
                                                                  WPI; 2001-442138/47
N-PSDB; AAS09453.
                                                                                                                 Strittmatter SM;
                                                                                                                                                                          12-JAN-2000; 2000US-0175707.
26-MAY-2000; 2000US-0207366.
29-SEP-2000; 2000US-0236378.
                                                                                                                                                (UYYA ) UNIV YALE.
                                                                                                                                                                                                                                     12-JAN-2001; 2001WO-US01041
                                                                                                                                                                                                                                                                                                          WO200151520-A2
                                                                                                                                                                                                                                                                                                                                                                                           Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; Nogo receptor; axonal growth; immunogen; antibody; nogo protein; cranial trauma; cerebral trauma; spinal cord injury; stroke; demyelinating disease; multiple sclerosis; monophasis demyelination; encephalomyelitis; multifocal leukoencephalopathy; panencephalitis; Marchiafava-Bignami disease; pontine myelinolysis; adrenoleukodystrophy; Pelizaeus-Merzbacher disease; Spongy degeneration; Alexander's disease; Canavan's disease; metachromatic leukodystrophy; viral infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human Nogo protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-SEP-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU04591;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAU04591 standard; Protein; 1192 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               T-EAPFATGSSGVMQ---FRYPVGATNPVVR 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TPAAPKRRĠŚŚGSVDETLFALP-AASEPVIR 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "Receptor binding inhibitory peptide.
sequence is specifically claimed"
                                                                                                                                                                                                                                                                                                                                                                                           /label= Pep4
/note= "Receptor binding
sequence is specifically
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label= Pep2
/note= "Receptor binding inhibitory peptide.
sequence is specifically claimed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= pep1
/note= "Receptor binding
sequence is specifically
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'label= Lumenal_extracellular domain 'note= "This sequence is specifically claimed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
1054..1119
/label= Lumenal ext
                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Receptor binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .1088
                                                                                                                                                                                                                                                                                                                                                                                             inhibitory peptide. claimed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                            inhibitory claimed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       inhibitory peptide. This claimed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     peptide.
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RESULT 35
AAB82349
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Best Local S
Matches 36
                  New polypeptide designated NOGO-C is a splice variant of the human NOGO gene and may be useful in the treatment of neural disorders including Alzheimer's and Parkinson's diseases
     Disclosure; Page 26-27;
                                                                                                                                                  Michalovich D,
                                                                                                                                                                                                         15-NOV-1999; 99GB-0026995.
24-JAN-2000; 2000GB-0001550.
                                                                                                                                                                                                                                                      14-NOV-2000; 2000WO-GB04345
                                                                                                                                                                            (SMIK ) SMITHKLINE BEECHAM PLC
                                                                                                                                                                                                                                                                                                                                                                                        NOGO-A; human; chromosome 2p21; neuropathy; spinal injury; brain injury; stroke; neuropal degeneration; Alzheimer's disease; Parkinson's disease; neuromuscular disorder; psychiatric disorder; developmental disorder; neuroprotective; neotropic; neuroleptic; antiparkinsonian; cerebroprotective; neuroleptic; diagnosis;
                                                                                                                                                                                                                                                                                                25-MAY-2001
                                                                                                                                                                                                                                                                                                                           WO200136631-A1
                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human NOGO-A protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-JUL-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB82349;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB82349 standard; Protein; 1192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The sequence is the human Nogo protein, a 250kDa myelin-associated axon growth inhibitor. The invention relates to the use of the nogo receptor, nogo protein, their nucleic acids, vectors expressing them and antibodies growth. The agent is useful for treating a central nervous system disorder which is a result of treating a central nervous system injury, stroke or a demyelinating disease selected from multiple sclerosis, monophasis demyelination, encephalomyelitis, multifocal pontine myelinolysis, adrennoleukodystrophy, Pelizaaus-Merzbacher disease, Spongy degeneration, Alexander's disease, Canavan's disease, metachromatic leukodystrophy, viral infection and Krabbe's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; Page 101-104; 109pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nervous system disorders
                                                                                                  2001-343822/36.
DB; AAF90324.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     172 TPAAPKRRGSSGSVDETLFALP-AASEPVIR 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    186 T-EAPFATGSSGVMQ---FRYPVGATNPVVR 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            115 STVPAPSPLSAAAVSPSKLPEDDEPPARPPPPPPPPASVSPQAEPVWTPPA---PAPAAPPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         132 NTAHTESBY----AVQSSREPVQQHPAVQKETEPVVVVK---KETETEPVVQQPAPVAEPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7.1%;
Similarity 39.6%;
%%; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1192 AA;
                                                                                                                                                Prinjha
 25pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 118; DB
Pred. No. 0.39;
8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ą
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DB 4-0.39; 33;

Length 1192; Indels

14;

Gaps

6

185 171

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RESULT 36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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Best Local
The invention relates to novel human secreted polypeptides. The polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to aberrant expression or
                                                                                                                                                                                                                                                                                                                                                                                                        Tang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; vaccination; gene therapy; nutritional supplement; stem cell proliferation; haematopoiesis; nerve tissue regeneration; immune suppression; immune stimulation; anti-inflammatory; leukaemia
                                                                                                                                                                                                                        Claim 20;
                                                                                                                                                                                                                                                                                               Nucleic acids encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-APR-2000;
26-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-APR-2001; 2001WO-US08656.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-OCT-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-DEC-2001
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                                                                                                                                                                                                                                                                       vaccination,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 132 NTAHTESEV---AVQSSREEVQQHEAVQKETEEVVVVK---KETETEEVVQQEAEVAEEV 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .36;
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and therapy -
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This invention describes a swine hepatitis E virus (HEV) and its natural mutants which are capable of cross-reacting with antibodies reactive with a human HEV strain or natural mutants. The HEV and the proteins can be used in vaccines for immunising against HEV infection. The swine HEV can be used in humans to prevent possible infection by human HEV. The swine HEV can also be used as a therapeutic treatment for infection by other strains of HEV. The swine HEV can also be used for the production of antibodies which can be used in therapy, detection and diagnosis. The products can also be used for determining the susceptibility of cells or organs to infection with swine HEV. The swine HEV is particularly useful for the development of agents for the prevention, treatment and detection

a human

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RESULT 37
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the nucleic acids encoding the polypeptides and cells genetically engineered to express them are also useful for producing the proteins. The proteins are useful in genetic vaccination, testing and therapy, and can be used as nutritional supplements. They may be used to increase stem cell proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon and/or nerve tissue growth or regeneration; immune suppression and/or stimulation, as anti-inflammatory agents; and in treatment of leukaemias. AAU29510-AAU33304 represent the amino acid sequences of novel human secreted proteins of the invention.
                                                                                                                                                                  Example 1; Fig 6D-J; 70pp; English.
                                                                                                                                                                                                     New isolated swine hepatitis E virus - used to develop products the diagnosis, prevention and treatment of hepatitis E virus
                                                                                                                                                                                                                                                                                                                          18-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                            28-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                      WO9904029-A2
                                                                                                                                                                                                                                                                                                                                                                                                                              Hepatitis E virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Swine hepatitis E virus; HEV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Swine HEV ORF 1 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW93408 standard; Protein; 1708 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           physiological interactions of the polypeptide. Vectors comprising
                                                                                                                                                                                                                                                                                                                                                   17-JUL-1998;
                                                                                                                                                                                                                                                                                                 (USSH ) US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           156 STVPAPSPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPA---PAPAAPPS 212
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detection; diagnosis; prevention.
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Best Local S
Matches 79
                                      New Streptococcus pyogenes antigen useful for diagnosing, preventing treating streptococcal infection, e.g. pharyngitis, erysipelas and impetigo, scarlet fever, and invasive diseases -
                                                                                                                                                                                        WPI; 2002-171701/22.
N-PSDB; AAD29298.
                                                                                                                                                                                                                                                                                    Martin
                                                                                                                                                                                                                                                                                                                                  (SHIR-) SHIRE BIOCHEM INC.
                                                                                                                                                                                                                                                                                                                                                                                              06-JUL-2000; 2000US-216465P
                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-JUL-2001; 2001WO-CA01001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptococcus pyogenes SPY57.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BWH-P1 gene; streptococcal infection; pharyngitis; erysipelas; iscarlet fever; bacteraemia, necrotising fascitis; toxic shock; vimmune response; anti-inflammatory; immunisation; antibacterial.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptococcus pyogenes strain SPY57 BVH-P1 mature protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAE18363 standard; Protein; 364 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     849 FIMREGLAAYTLTPRPIIHAVAPDYRVEQN 878
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       135 HTPSPVAVQSSRPPVQQHPAVQKPTPPV----- 162
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vaccine;
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RESULT 39
ABP25889
ID ABP25
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CC are useful for diagnosing, preventing or treating streptococcal for are useful for diagnosing, preventing or treating streptococcal infection, such as pharyngitis, erysipelas, impetigo, scarlet fever, CC for eliciting an immune response. The polypeptides may also be used as CC streptococcus infection, or for passive inmunisation. DNAs encoding the CC streptococcus infection, or for passive inmunisation. DNAs encoding to CC polypeptides may also be used to design DNA probes for detecting the CC polypeptides of Streptococcus in biological sampless suspected of containing the CC presence of Streptococcus in biological sampless suspected of containing the bacteria. The vaccine composition is useful as a prophylactic or cc used public treatment of Streptococcal infection in an individual cc sequence is Streptococcus pyogenes strain SPY57 BVH-P1 mature protein.
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Best Local Similarity 23...
56; Conservative
Streptococcus pyogenes.
                          Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae; group A streptococcus; Streptococcus pyogenes; antibacterial; antiinflammatory; infection; vaccine; meningitis; gene therapy.
                                                                                                                               Streptococcus polypeptide SEQ ID
                                                                                                                                                                            02-JUL-2002 (first entry)
                                                                                                                                                                                                                                    ABP25889;
                                                                                                                                                                                                                                                               ABP25889 standard; Protein; 389 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      143 STNDVSTELSSESQXQPEVPQEAVPTPKAAETTEVEPKTDIS-----EAPTSANRPVPNE 197
                                                                                                                                                                                                                                                                                                                                                                                                      214 FGTATVAG--------STVTSNGMWFSGRDGDLINASNAG 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 167 -----KPTPTPPVVQQPAPVAPPVTEAPFATGSSGVMQFRYPVGATNPVVRR 213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        364 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7.0%; Score 117.5; DB 23.5%; Pred. No. 0.094; ative 22; Mismatches
                                                                                                                               NO 954.
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WO200234771-A2.

02-MAY-2002.

29-OCT-2001; 2001WO-GB04789

27-OCT-2000; 2000GB-0026333. 24-NOV-2000; 2000GB-0028727. 07-MAR-2001; 2001GB-0005640.

(CHIR-) CHIRON SPA. (GENO-) INST GENOMIC RES.

Telford J, Tettelin H; Masignani V, Margarit Ros YI, Grandi ڻ و Fraser

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RESULT 40
AAE18359
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Best Local S
Matches 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptococcus bacteria, particularly S. agalactiae and S. pyrgenes. Nucleic acids encoding (I) are used to detect Streptococcus in a biological sample. (I) is used to determine whether a compound binds to (I). A composition comprising (I) or a nucleic acid encoding (I), may be used as a vaccine or diagnostic composition. The disease caused by streptococcus that is prevented or treated may be meningitis. Nucleic acid encoding (I) may be used to recombinantly produce (I) and may be used in gene therapy. Antibodies to (I) are used for affinity chromatography, immunoassays, and distinguishing/identifying
                                                                                                                                                                        BVH-P1 gene; streptococcal infection; pharyngitis; erysipelas; impetigo scarlet fever; bacteraemia; necrotising fascitis; toxic shock; vaccine; immune response; anti-inflammatory; immunisation; antibacterial.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a protein (ABP25413-ABP30895) from group B streptcocccus/GBS (Streptcocccus agalactiae) or group A streptcocccus/GAS (Streptcocccus progenes) or group A streptcocccus/GAS (Streptcocccus progenes) comprising one of 5483 sequences (S1), given in the specification. The proteins have antibacterial and antiinflammatory activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and antibodies that bind (I) are used in the manufacture of medicaments for
                                                                                                                                          Streptococcus
                                                                                                                                                                                                                                                   Streptococcus
                                                                                                                                                                                                                                                                                       07-MAY-2002
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N-PSDB; ABN66520.
WO200204495-A2
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                                                                                        Peptide
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                                                                                                                                                                                                                                                                                                                                                          standard; Protein; 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FGTATVAG--
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                                                                                                                                        pyogenes SPY57
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A
                                                                 /label= Signal_peptide
                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7.0%; Score 117.5;
23.5%; Pred. No. 0.1;
                               "Mature_BVH_P1_protein"
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Cobacterial pathogen. The polypeptides and polynucleotides encoding them are useful for diagnosing, preventing or treating streptococcal infection, such as pharyngitis, erysipelas, impetigo, scarlet fever, invasive diseases (bacteraemia, necrotising fascitis, toxic shock), and for eliciting an immune response. The polypeptides may also be used as immunogens for producing antibodies for the diagnosis and treatment of Streptococcus infection, or for passive inmmunisation. DNAs encoding polypeptides may also be used to design DNA probes for detecting the polypeptides may also be used to design DNA probes for detecting the presence of Streptococcus in biological samples suspected of containing the bacteria. The vaccine composition is useful as a prophylactic or therapeutic treatment of Streptococcal infection in an individual susceptible to or infected with streptococcal in fection. The present
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptococcus pyogenes antigen useful for diagnosing, preventiating streptococcal infection, e.g. pharyngitis, erysipelas and etigo, scarlet fever, and invasive diseases
                                                                            168
                                                                                                                  167
                                                                                                                                                        108
                                                                                                                                                                                          127 ISSGVNTAHTPS----PVAVQSSRPPVQQHPAV---QKPTPPVVVVK--------
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SASEEVSSAAPAQAPAEKEETSAPAAQKAVADTTSVATSNGLSYA - - PNHAYNPMNAG
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                                                                                                                                                                                                                                                      YQVKQGDTVSKIAQRYGLNWREIGHINNLNSSYTIYTGQWLTL-----WSGDLKVRERS 126
                                                                            STNDVSTELSSESQKQPEVPQEAVPTPKAAETTEVEPKTDIS-----EAPTSANRPVPNE 222
                                                                                                                                                                                                                                  YTVKYGDTLSTIAEAMGIDVHVLGDINHIANIDLIFPDTILTANYNQHGQATNLTV-QAP 107
                                                                                                                                                                                                                                                                                                                                                                                                                            is Streptococcus pyogenes strain SPY57 BVH-P1 protein.
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                                                                                                                                                                                                                                                                                                            Conservative
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Pred. No. 0.1;
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                                      STVTSNGMWFSGRDGDLINASNAG 245
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Result
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        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1. /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

2. /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

3. /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

4. /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

5. /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

6. /cgn2_6/ptodata/1/iaa/backfIles1.pep:*
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US-08-456-670B-40
US-08-127-499A-26
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US-08-737-716-2
US-08-737-716-2
US-08-737-716-2
US-08-737-716-4
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US-09-136-574A-44
US-09-136-574A-44
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Sequence 11, Appl
Sequence 14, Appli
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APPLICANT: Potter, Andrew A.

APPLICANT: Rioux, Clement

APPLICANT: Rioux, Clement

APPLICANT: Schryvers, Anthony B.

TITLE OF INVENTION: CLONING AND EXPRESSION OF HAEMOPHILUS SOMNUS

TITLE OF INVENTION: TRANSFERRIN-BINDING PROTEINS

FILE REFERENCE: 9000-0049.20

CURRENT APPLICATION NUMBER: US/09/405,728

CURRENT FILING DATE: 1999-09-24

EARLIER APPLICATION NUMBER: US 09/267,749

EARLIER APPLICATION NUMBER: US 09/267,749

EARLIER PILING DATE: 1999-03-10

NUMBER OF SEQ ID NOS: 5

SOFTMARE: Patentin Ver. 2.0

SEQ ID NO 5

LENGTH: 345
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   RESULT 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT ; ORGANISM: Haemophilus somnus US-09-405-728-5
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Sequence 6, App	Sequence 5, App	•	Ø	,	2	Sequence 7, App	Sequence 7, App	Sequence 7, App	<u>ب</u>	•	Sequence. 4, Appl	•	•	e 2,	•	•	Sequence 2, App	
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|20 YKVRKGDTWFLIAYISGMDIKELATLNNMSEPYHLSIGQVLKIANNIPDSNMIPTQTINE 179
                                                                                                                                                                                                                                                                                                                                                                                                                            l Similarity
63; Conserv
IRYKGQSVDPMRYL 342
                                                                                                                                                                                         FATGSSGVMQFRYPVGATNPVVRREGTATVAGSTVTSNGMWFSGRDGDLINASNAGTVIQ 249
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                                     ISRNGVYVDPLTVL 321
                                                                                AGDALRGYGNLIIIKHNDSYLSAYAHNESILVKDQQEVKAGQQIAKMGSSGTNTIKLHFE
                                                                                                                      ADHNMDGAS--- IVIQHTNGFVSSYIHIKDAQVKTGDTVRTGQRIASMKNQPSGAALFEFR
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Pred. No. 1.5e-11;
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Best'Local Similarity 21.3
Matches 83; Conservative
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INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 478 amino acids
                                                                                                                                                                                                                                                              MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Listeria monocytogenes
STRAIN: EGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: HAMLET-KING, DIANA
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: MERCK 1694D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456,670B
FILING DATE: 01-UNN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4239567.4
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION UNDER: US 08/412,227
PRILING DATE: 27-MAR-1995
PRIOR APPLICATION UNDER: US 08/075,248
APPLICATION INDEER: US 08/075,248
PRIOR APPLICATION 11-UN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                               LENGTH: 478 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
160 TTQQAAPVAETKTEVKQTTQATTPAPKVAETKETPVIDQNATTHAVKSGDTIWALSVKYG 219
                                                                          102 İITSİKGĞ--TKVTVETTESNĞWİKITYNDĞKTGFVNGKYLTDKAVSTPVAPTQEVKKET 159
                                              66 --SQGVP--
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5. 5932415
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
1: 2200 CLARENDON BLVD., SUITE 1400
ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VIRGINIA
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PAWELZIK, MARTINA
LINXWEILER, WINFRIED
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                                                                                                                                                         9.1%; Score 151.5; DB 2;
21.3%; Pred. No. 5.7e-06;
zive 46; Mismatches 117;
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                                     -----NRYQVKQGDTVSKIAQRYG 89
                                                                                                                                                     Indels 143; Gaps
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159	102 IITSIKGGTKVTVETTESNGWHKITYNDGKTGFVNGKYLTDKAVSTFVAPTQEVKKET	DЬ
65	25 ITTCILAGCASKPTYNSTSGSGSHRTSGSGGLAIGSQVITD	8
14;	Query Match 8.8%; Score 146.5; DB 1; Length 484; Best Local Similarity 20.6%; Pred. No. 1.7e-05; Matches 81; Conservative 46; Mismatches 121; Indels 145; Gaps	
	SEQUENCE CHARACTERISTICS: LENGTH: 484 amino acids TYPE: amino acid STRANDEDNESS: TOPOLOGY: unknown -08-127-499A-26	us
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	768	
	Patentin Release #1. LICATION DATA:	
	TYPE: F1	~, ~, ~, ~
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	CURRESPONDENCE ADDRESS: ADDRESSEE: Foley & Lardner STREET: 3000 K Street, N.W., Suite 500	·, ·, ·,
	TION: HOMOLOGOUS ANTIGENIC SEQUENCES ENCES: 40	·. ·.
	APPLICANT: VAN ALSTYNE, Diane APPLICANT: SHARWA, Lawrence Rajendra TITLE OF INVENTION: ANTIRODIES WHICH BIND MENINGITIS RELATED	
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1 253	194 SSGVMQFRYPVGATNPVVRRFGTATVAGSTVTSNGMWFSGRDGDLIN	γŞ
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RESULT 4
US-08-482-847-26
     Query Match
Best Local Similarity 20.6
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                               TELEX: 904136
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
404 amino acidi
                                                                                                                                                                                                                                               NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 51:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
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TELEPAX: 904136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0
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                                                                                                                           STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                                                                                            LENGTH: 484 amino acids
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                                                                                                                                           amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SHARMA, Lawrence Rajendra
VENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR
VENTION: BACTERIAL AND VIRAL MENINGITIS CAUSING AC
VENTION: CNS CARRIER, ANTIBODIES THERETO, AND USES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
                                                                                                                                                                                                                                (202) 672-5399
                                                                                                          unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Foley & Lardner
                8.8%; Score 146.5; DB 1; 20.6%; Pred. No. 1.7e-05; tive 46; Mismatches 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----FFDYGSGİSHVĞIYV 451
                                                                                                                                                                                               26:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Version #1.30
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                                                   Length 484;
                  Indels 145;
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                  Gaps
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US-08-737-716-2
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                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION UNMBER: PCT/NL
FILING DATE: 12-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION UNMBER: EP 942
FILING DATE: 12-MAY-1994
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/08737716 Patent No. 5955258
 Query Match
                                                                                                                                                                                                                                                                                                             COUNTRY: U.S.A.
ZII: 2005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatable
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 437 amino acid
                                                     MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                     TYPE: am TOPOLOGY:
                                                                                                                                                                                                                                                                 FILING DATE: 23
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Washington
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                                                                                  : 437 amino acids
amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LNWREIGHINNLNSSYTIYTGQWLTLWSGDLKVRERSISSGVNTAHTPSPVAVQSSRPPV 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --SQGVP-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -EAPAAEKQAAPVVKENTNTNTATTEKKETATQ---QQTAPKAPTEAAKPAPAPSTNTNA 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IITSIKGG--TKVTVETTESNGWHKITYNDGKTGFVNGKYLTDKAVSTPVAPTQEVKKET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Adrianus Marinus LEDEBOER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gerard VENEMA
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                                                                                                                                                                                                                                                                      umber: US/08/737,716
22-APR-1997
N: ^^-
                                                   protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Process for the lysis of a culture of lactic acid bacteria by means of a lysin, and uses
7.8%;
                                                                                                                                                                            EP 94201353.3
                                                                                                                                                                                                                              PCT/NL95/00170
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Score 130.5;
DB
<u>ي</u>
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Length 437;
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resulting

Best Local Similarity 24.1%; p. Matches 69; Conservative 39;

Pred. No. 0.00046; 19; Mismatches 119;

Indels

59; Gaps

12;

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Matches

36; Conservative

21; Mismatches

40;

Indels

17;

Gaps

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В Ś

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APPLICATION DATA:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP 94201353.3

FILING DATE: 12-MAY-1994

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

LENGTH: 666 amino acids

TYPE: amino acids

TYPE: amino acids
                                                                                    US-08-737-716-14
                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 6
US-08-737-716-14
                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/737,716
FILING DATE: 22-APR-1997
                                                                             ORGANISM: Enterococcus n
IMMEDIATE SOURCE:
CLONE: Fig.5a (E. hirae)
                                                                                                                                                  MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                        APPLICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNBER: PCT/NL95/00170
TYNG DATE: 12-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: VOL. .....
APPLICANT: Adrianus Marinus LEDEBOER
TITLE OF INVENTION: Process for the lysis of a culture of lactic
TITLE OF INVENTION: acid bacteria by means of a lysin, and uses of the resulting
NUMBER OF SEQUENCES: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    399 KGDTLWGLSQKSGSPI-----ASIKAWNHL-----SSDTILIGO 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       244 AGTVIQADHNMDGASIVIQHTNGEVSSYIHIKDAQVKTGDTVRTGQ 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        346 WNHLSSDTIYIGONLIVSQSAAASNP-----STGSGSTATNNSNSTSSNSNASIHKVV 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           187 EAPFATGSSGVMQ----FRYPVGATNPVVRRFGTATVAGSTVTSNGMWFSGRDGDLINASN 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               296 GGSNNS-----ASTTPITSVTPA--KPISQTTVKVKSGDTLWALSVKYKTSIAQLKS 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                129 SGVNTAHTESEVAVQSSRPEVQQHPAVQKPTEPVVVVKKPTET--PEVVQQDAPVAEPVT 186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             184 TAALIGRYATDÞSYGASLNRIISQYNLTRFDGASSAGNTNSGG---STTTÍTNNNSGTNS 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RY: U.S.A.
20005-3918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       72 ---RYQVKOGDTVSKIAQRYGLNWREIGHINNLNSSYTIYTGQWLTLWSGDLKVRERSIS 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26 TTCILAGCASKPTYNST------SGSGSHRTSGSGGLAIGSQVITDSQGVPN- 71
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D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FORMATION:
                                                                                                                              Enterococcus hirae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: Pillsbury Madison & Sutro, L.L.P. 1100 New York Avenue, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Application US/08737716
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           Score 123.5; DB 2;
Pred. No. 0.0038;
                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: TO ANY COUNTRY: COUNTRY: 10201

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
APPLICATION DATA:
APPLICATION NUMBER: US/08/456,670B
FILING DATE: 01-JUN-1995
CLASSIFICATION -435
PRIOR APPLICATION NUMBER: US 08/412,227
APPLICATION NUMBER: US 08/412,227
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/075,248
PTITNG DATE: 11-JUN-1903
                                                                                                            TELEX: 64191
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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US-08-456-670B-39
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                        MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                   NAME: HAMLET-KING, DIANA REGISTRATION NUMBER: 33,302 REFERENCE/DOCKET NUMBER: MEITELECOMMUNICATION INFORMATION: TELEPHONE: 703-243-6333
                                                                                                                                                                                                                                                                                FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: DE 4219111.4
FILING DATE: 11-JUN-1992
NAME: UNIVERSITION:
                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 08/075,248
FILING DATE: 11-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER
APPLICATION NUMBER
                                                                  LENGTH: 232 amino acids TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                    TELEPHONE: 703-243-6410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE
                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C. STREET: 2200 CLARENDON BLVD., SUITE 1400 CITY: ARLINGTON STATE: VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        353 HGISMNQLIEWNNIKNNF-VYPGOOLVVSKGSSSA--SGSTSNTSTGNTSSNTA 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        304 AGSSTTNTGNNASSGNTSGNTNTSGSTGQATGA-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31 AGCASKPŢYŅSTSG----SGSHRŢSGSGGLAIGSQVITDSQGVPNRYQVKQGDŢVSKĻAQR 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HOFMANN, GOTTFRIED
BUBERT, ANDREAS
GOEBEL, WERNER
KOHLER, STEFAN
Listeria monocytogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pplication US/08456670B
                                       peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SCHUBERT, F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ION: PROCESSES AND AGENTS FOR DETECTING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHRISTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MARTINA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PETER
                                                                                                                                39:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EGFRIED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WINFRIED
                                                                                                                                                                                                                      MERCK 1694D1
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961 158 919 101

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RESULT 8
US-09-136-574A-43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 43, Application US/09136574A Patent No. 6294366 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                  INFORMATION FOR SEQ ID NO: 43:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Williams, Diane P.
TITLE OF INVENTION: Compositions and Methods for
Treating Cellulose Containing Fabrics Using
Cellulase Enzyme Compositions
                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 08/932,571
FILING DATE: September 19, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
                                                                                                                                                                                                                                                                                                                                            FILING DATE: 19-Aug-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/136,574A
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6294366e
SEQUENCE DESCRIPTION: SEQ ID NO: 43:
                                                                                                                                                                                     REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: 1997US001/CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Farrington, Graham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 191 -EAPAAEKQAAPVVKENTNTNTATTEKKETATQ---QQTAPKAP 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      150 QQHPAVQKPTPPVV------VVKKPTPTPPVVQQPAPVAP 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25 ITTCILAGCASKPTYNSTSGSGSHRTSGSGGLA--IGSQVITD------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             53;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VSVQDIMSWNNLSSS-SIYVGQKLAI---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTQQAAPVAETKTEVKQTTQATTPAPKVAETKETPVIDQNATTHAVKSGDTIWALSVKYG 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --SQGVP----NRYQVKQGDTVSKIAQRYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IITSIKGG--TKVTVETTESNGWHKITYNDGKTGFVNGKYLTDKAVSTPVAPTQEVKKET 90
                                                                             LENGTH: 1426 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: Spring House Corporate Center; P.O. Box 457
                                                                                                                                                                        TELEFAX: 215-540-5818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
                                                                                                                                                        TELEX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Howson and Howson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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Daniels, Roy
Morgan, Hugh W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gibbs, Moreland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PΑ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         underson,
                                                                                                                                                      <Unknown>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 121.5; DB Pred. No. 0.0013;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ~
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----KQTANTATPKAEVKT----
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                                                                                                                                                    ; MOLECULE TYPE: protein US-08-737-716-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-737-716-4
                                                                       Query Match
Best Local Similarity
Matches 63; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Girbe BUIST
                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: EP 94201353.3
                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/
FILING DATE: 12-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 20005-3918
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Adrianus Marinus LEDEBOER
TITLE OF INVENTION: Process for the 19sis of a culture of lactic
TITLE OF INVENTION: acid bacteria by means of a lysin, and uses of the resulting
TITLE OF INVENTION: lysed culture.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
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                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/737,716 FILING DATE: 22-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE:
                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                           LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               [TY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             159 TPPVVVVKKPTPTPPVVQQPAPVAPP------VTEAP------FAT 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         102 NSSYTIYTGQWLTLWSGDLKVRERSISSGVNTAH--TPSFVAVQSSRP-PVQQHPAVQKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                868 SGAGVLAAGQSTKEIRLSIQKGSGSYNQSNDYSIRS-----ANSYIENEKVTGYIDG-
                               31 AGCASKPTYNSTSGSGSHRTSGSGGLAIGSQVITDSQGVPNRYQVKQGDTVSKIAQRYGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51 SGSGGLAIGS------QVITDSQGVPNRYQVKQGDTVSKIAQRYGLNWREIGHINNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59;
   3 SGGSTTTITNNNSGTNSSSTT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                     amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Application US/08737716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GSSGVMQFRYPVGATNPVVRRFGTATVAGSTVTSNGMWFSGRDGDLINASNAG 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GNKIVDKDGKPVWLTG--VNWFGFNT---GTNVFDGVWSCNLKSALAEIANRG 1069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TPTVTVTPTSTPTPVSSSTPTPTATPTPTPSITITPAPTATPTPTPSVTDDTNDDWLFAQ 1021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----AIVWG-----REPSRGTKPAGVVTPTPAPTPTSTPTPIPTPTPTPTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: Pillsbury Madison & Sutro, L.L.P. 1100 New York Avenue, N.W.
                                                                                                                                                                                                                             216 amino acids
                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Jan KOK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gerard VENEMA
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                                                                                                                                                                                                                                                                                    12-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7.2%;
                                                                       7.1%; Score 118; DB 2; 1
23.9%; Pred. No. 0.0024;
1tive 35; Mismatches 106;
                                                                                                                                                                                                                                                                                                                                                              PCT/NL95/00170
                                                                                                                                                                                                                                                                     4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 119.5; DB Pred. No. 0.027;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         88;
                                                                                                              Length 216;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1426;
                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
   YTVKSGDTLWGISQRYGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69;
                                                                           60;
                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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41

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STAPHYLOCOCCUS

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APPLICANT: MENG, XIANG-JIN-
APPLICANT: Emerson, Suzanne U.
APPLICANT: DENCROIN, SUZANNE U.
APPLICANT: DENCROIN, ROBERTH H.
TITLE OF INVENTION: A SWINE HEPATITIS E VIRUS ANI
FILLE REFERENCE: 20264267US1
CURRENT APPLICATION NUMBER: US/09/462,606
CURRENT FILING DATE: 2000-06-12
PRIOR APPLICATION NUMBER: US 60/053069
PRIOR FILING DATE: 1997-07-18
PRIOR FILING DATE: 1997-07-18
PRIOR FILING DATE: 1998-07-17
NUMBER OF SEQ ID NOS: 65
SOFTWARE: PATENTING UNS: 65
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 2
TENUTION 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 10
US-09-462-606-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Hepatitis E virus
-09-462-606-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            equence 2, Application US/09462606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
                                                                                          810
                                                                                                                                                                        770
                                                                                                                                                                                                               163
       849 FIMREGLAAYTLTPRPIIHAVAPDYRVEQN 878
                                                                                                                                                                                                                                                       714
                                                                                                                                                                                                                                                                                      135 HTPSPVAVQSSRPPVQQHPAVQKPTPPV---------
                                                                                                                                                                                                                                                                                                                                   668 LWLHPEGLLGIFPPFSPGHIWEPANPFCGEGTLYTRTWST------SGFSSD 713
                                                                                                                                                                                                                                                                                                                                                                                                               608 LTYELTPAĞLQVRISSNĞLDCTATFPPĞGAPSAAPGEVAAFCSALYRYNRFTQRHSLTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                548 LTATVELTASPDRLECRTVLGNKTFRTTVVDGAHLEANGPEQYVLSFDASRQSMGAGSHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        58 I-----GSQVITDSQGVPNRYQVKQGDTVS------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       89 VTPA--KPTSQTTVKVKSGDTLWALSVKYKTSIAQLKSWNHLSSDTIYIGQNLIVSQSAA 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1708
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MTVTIAINSQNQKPIKRLGLIFGVITTCILAGC---ASKPTYNSTSGSGSHRTSGSGGLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 h 7.1%;
Similarity 20.3%;
79; Conservative 4.
                                                                                                                  TVTSNGMWFSGRDGDLINASNAGTVIQADHNMDGASIVIQHTNGFVSSYIHIKDAQVKTG 282
                                                                                                                                                                                                     VVVKKPTPTPPVVQQPAPVAPPVTEAPFATGSSGVMQFRYPVGATNPVVRRFGTATVAGS 222
                                                                                                                                                                                                                                                  FSPP----EAAAPVLAAAPGLPHPTPPVSDIWVLPPPSKESQVDAASVPPAPEPAGLPSS 769
                                             DTVRTGQRIASMKNQP-SGAALFEFRISRN 311
                                                                                                                                                                    IVLTLPPPLPPVRKPPTP--PP----SRTRRLLYTYPDGA------KVYAGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATNPVVRREGTATVAGSTVTSNGMWESGRDGDLINASNAGTVIQADHNMDGASIVIQHTN 265
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                                                                                                                                                                                                                                                                                                                                                                         -----EIGHI----NNLNSSYTIYTGQWLTLWSGDLKVRERSISSGVNTA 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -STGSGSTATNNSNSTSSNSNASIHKVVKGDTLWGLSQKSGSPI--
                                                                                     -LVNASNPG-----HRPGGG---LCH----AFYQRFPEAFYPTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Score 118; DB 4; Length 1708;
; Pred. No. 0.048;
44; Mismatches 129; Indels 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 211
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Patent No. 6380370

GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al

ITILE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAP

TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

PILE REFERENCE: GTC-007

CURRENT APPLICATION NUMBER: US/09/134,001C

CURRENT FILING DATE: 1998-08-13

PRIOR APPLICATION NUMBER: US 60/064,964

PRIOR APPLICATION NUMBER: US 60/055,779

PRIOR APPLICATION NUMBER: US 60/055,779

PRIOR APPLICATION NUMBER: US 60/055,779

LENGTH: 330

TYDE: DET

LENGTH: 330
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US-09-136-574A-44
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US-09-134-001C-4002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 44, Application US/09136574A Patent No. 6294366 GENERAL INFORMATION:
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Best Local
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TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/136,574A
FILING DATE: 19-Aug-1998
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/932,571
FILING DATE: September 19, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Center,
CITY: Spring House
STATE: PA
COLUMN 170
                                                                                                                                                                                                                          ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     75 VKQGDTVSKIAQRYGLNWREIGHINNLNSSYTIYTGQWLTLWSGDLKVRERSISSG 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54 IAKLKSLNGLTSNLIFPNQVLK-----VSGSSSRATSTNSGTV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15 KRIGLIFGVITTCILAGCASKPTYNSTSGSGSHRTSGSGGLAIGSQVITDSQGVPNRYQ 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36;
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                                                                                                                                                                                                                                                                                      COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6.6%; Score 111; DB 4; Length 330; Pred. No. 0.02; Conservative 17; Mismatches 41; Indels
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Anderson, Paige
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US-09-189-035-5
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US-09-136-574A-44
                               Best Loc
Matches
                                                                                                                                                                                       NUMBER OF SEQ ID NOS:
SOFTWARE: PERL Program
SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                   Sequence 5, Application US/09189035 Patent No. 6020165 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                               Query Match
                                                                                                                                                                                                                                 APPLICANT: Yue, Henry
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl J.
APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: CYTOKINE SIGNAL REGULATORS
FILE REFERENCE: pF-0638 US
CURRENT APPLICATION NUMBER: US/09/189,035
CURRENT FILING DATE: 1998-11-10
                                                                                               OTHER INFORMATION: g2245671
-09-189-035-5
                                                                                                                           LENGTH: 480
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE: -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ITELEX: «Unknown»
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 1751 amino acids
                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1365
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: 215-540-9200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             205 GATNPVVRREGTATVAGSTVTSNGMWFSGRDGDLINASNAGT------VIQ 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              250 ADHNMDGASIVIQH-----TNGFVSSYIHIKDAQVKTGD-TVRTGQ-----RIASMKNQP 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       102 NSSYTIYTGQWLTLWSGDLKVRERSISSGVNTAH--TPSPVAVQSSRPPVQQHPAVQKPT 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51 SGSGGLAIGS-----
                               53; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74;
9 SQNQKPIKRLGLIFGVITTCILAGCASKPTYNSTSGSGSHRTSGSGGLAIGSQVITDSQG 68
                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DGALSLQPDVNDNYVYMD 1382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NDKNVPAAVVSKFHEQSIKQNAYSAITLQMVGYVAKDGNGTVSESETAPSPRWAEVKFKK 1364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PPVVVVKKPTPTPPVVQQPAPVAPPVTE-----APFATGSSGVMQFRYPV 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SGAALFEFRISRNGVYVD 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GVVHP-ARRLG-----GNRLTGYN-WEN-----NMSNAGSDWYHSSDDYMCYIMGITG 1304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----AIVWG-----REPSRGTKPAGGVTPTPAPTPTSTP-----TPT 1208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PTTT----PTPTPTVTVTPTP-TPAVTPDVKISIDTSRGRTKISPYIYGANQDIQ----- 1258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 215-540-5818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 31,215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DESCRIPTION: SEQ ID NO:
                            6.6%; Score 109.5; DB 3; 22.8%; Pred. No. 0.048; tive 19; Mismatches 79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6.6%; Score 110.5; DI 23.3%; Pred. No. 0.25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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                                                            Length 480;
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                              Indels
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                              81;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 480
                                                                            APPLICANT:
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US-09-136-574A-47
; Sequence 47, Applicati
; Patent No. 6294366
; GENERAL INFORMATION:
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US-09-382-086-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/382,086
CURRENT FILING DATE: 1999-08-24
EARLIER APPLICATION NUMBER: 09/189,035
EARLIER FILING DATE: 1998-11-10
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PERL Program
SEQ ID NO 5
ERL PROGRAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 5, Application US/09382086
Patent No. 6201106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Yue, Henry
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl J.
APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: CYTOKINE SIGNAL REGULATORS
FILE REFERENCE: PF-0638 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Homo sapiens
FEATURE: -
                                                                                                                                                                                                                                                                                                                                                                                                                                                        129 SGVNTAHTPSPVAVQSSRPPVQQHP----AVQKPTPPVV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                164 VVKKPTPTPP-----VVQQPAPVAPPVTEAPFATGSSGVMQFRYPVGATNP 209
                                                                                                                                                                                                                                                                                                              361 IADSPTPPPPPPPDDIPMFDDSPPPPPPPPPVDYEDEEAAVVQYNDPYADGDP
                                                                                                                                                                                                                                                                                                                                                           164 VVKKPTPTPP-----VVQQPAPVAPPVTEAPFATGSSGVMQFRYPVGATNP 209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  231 SLNORPRTHSG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 361 IADSPTPPPPPPDDIPMFDDSPPPPPPPPVDYEDEEAAVVQYNDPYADGDP 412
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69 VPNRYQVKQGDTVSKIAQRYGLNWREIGHINNLNSSYTIYTGQWLTLWSGDLKVRERSIS 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9 SQNQKPIKRLGLIFGVITTCILAGCASKPTYNSTSGSGSHRTSGSGGLAIGSQVITDSQG 68
                                                                                                                                                                                                                                                                                                                                                                                                         SG-GYRRTPSVTAQFSAQPHVNGGPLYSQNSISIAPPPPPMPQLTPQIPLTGFVARVQEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SGVNTAHTPSPVAVQSSRPPVQQHP-----AVQKPTPPVV------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -PPTIGPAPG---SAPGSQYGTMTRQISRHNSTTS-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SG-GYRRTPSVTAQFSAQPHVNGGPLYSQNSISIAPPPPPPPPPQLTPQIPLTGFVARVQEN 360
                                                                                                                                                                                             Application US/09136574A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
Bergquist, Peter
Daniels, Roy
Morgan, Hugh W.
                                                                         Anderson, Paige
Gibbs, Moreland
                                                                                                                   Farrington,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6.6%; Score 109.5; DB 22.8%; Pred. No. 0.048; vative 19; Mismatches
                                                 Peter
                                                                                                                        Graham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----SSGGSGSRENSGSSSIGIPIAVPTPS--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 480;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----STS 301
                                                                                                                                                                                                                                                                                                              412
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                                                                                                                                                                                                                                                                                                                                                                                                            360
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NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Center, P.O. Box 457
CITY: Spring House
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TITLE OF INVENTION: Compositions and Methods for
Treating Cellulose Containing Fabrics Using
Cellulase Enzyme Compositions
                                                                                                                                                                                                                                                                                                                                                                                                 132 NTAHTESEVAVQSSREEVQQHEAVQKETEEVVVVKKETETEEVVQQEAEVAEEVTEAE-- 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34 ASKPTYN----STSGSGSHR-----TSGSGGLAIGSQVITDSQGVPNRYQVKQGDTVSK
                                                                                                                                                                                                                                                                TDDTNDDWLFAQGNKIVDKDGKPVWLTG---VNWFGFNT----GTNVFDGVWSCNLKSALAE
                                                                                                                                                                                                                                                                                                         -----FATGSSGVMQFRYPVGATNPVVRRFGTATVAGSTVTSNGMWFSGRDGDLIN 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IAQRYGLN-----WREIGHINNL--NSSYTIYTGQWLTLWSGDLKVRERSISSGV 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ASNVTFNFVKLSSGVSGADYYLEVGFSSGAG------QLQPGKDTGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                     IQVRFNKNDWSNYNQADDWSWLQSMTNYGENAKVTLYV-DGVLVWG-----QEPGGAV 157
                                                                                                                                                                                                                                                                                                                                                        -----PTPTAT----PTPTPSITITPAPTATP-TPTPSV 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 616;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels 83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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US-09-328-599A-1
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                                                                                                                                    Sequence 1, Application US/09328599A Patent No. 6432679
                   GENERAL INFORMATION:
APPLICANT: MOND, Jan
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELLEFAX: 212-869-8864
TELLE: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 907 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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Best Local &
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MEDIUM TYPE: Diskette
COMPUTER: LBM COmpatible
OBERATING SYSTEM: DOS
SOFTWARE: FASTSQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/783,77
FILING DATE: 15-JAN-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, LBUTE A.
REGISTRATION UMBER: 30,742
REGISTRATION UMBER: 7682-03
TELECOMMUNICATION INFORMATION:
TELEPONE: 212-899-9999
TELECOMMUNICATION INFORMATION:
TELEPONE: 212-899-9999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: unknown MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
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ZIP: 10036,
                                                                                                                                                                                                                                                                                                                                                                           581 SAVTTPTPNATSPTLGK-TSPTSAVTTPTPNATGPTVGETSPQANATN------HTLG 631
                                                                                                                                                                                                                                                                                                                                                                                                                    198 MQFRYPV-GATNPVVRRFGTATVAGSTVTSNGMWFS-GRDGDLINASNAGTVIQADHNMD 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               149 VQQHPAVQKPTP----PVVVVKKPTP--TPPVVQQPAPVAPPVTEAPFATG-----SSGV 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 470 --TADVISPTPAGITSGASPVTPSPSPWDNGTESKAPDMTSSTSPVTTPTPNATSPT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            430 TSPTLNTTGFADPNTTTG------LPSSTHVPTNLTAPASTGPTVS------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93 REIGHINNLNSSYTIYTGQWLT----LWSGDLKVRERSISSGVNTAHTPSPVAVQSSRPP 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35 SKPTYNSTSGSGSHRTSGSGGLAIGSQVITDSQGVPNRY--QVKQGDTVSKIAQRYGLNW 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ch 6.5%; Score 109; DB 3; Length 907; l Similarity 23.2%; Pred. No. 0.13; 166; Conservative 34; Mismatches 122; Indels (
                                                                                                                                                                                                                                                                                                                            GASIVIQHTNGFVSSYIHIKDAQVKTGDTVRTGQRIASMKNQPS 299
                                                                                                                                                                                                                                                                                GTS-----PTPVVTSQPKNATSAVTTGQHNITSSSTSSMSLRPS 670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----PAVTTPTPNATSPTPAVTTPTPNATSPTLGKTSPTSAVTTPTPNATSPTLGKTSPT
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           James J. and Lees, Andrew
N: Enhancement of B Cell Activation by
N: Co-Ligation of Receptors for Antigen
N: Using EBV gp350/220 or EBV gp350/220
Using
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19
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                and Complement C3d
Peptide Adjuvants
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 47:
US-09-136-574A-47

LENGTH: 616 amino acids
TYPE: amino acid
TYPE: smino acid
STRANDEDNESS: single

TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:

TELEPHONE: 215-540-9200 TELEFAX: 215-540-5818

COMPUTER: IBM COMPACTION
CORRENT APPLICATION SYSTEM: DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/136,574A
FILING DATE: 19-Aug-1998
CLASSIFICATION DATA:
APPLICATION UNDER: US 08/932,571
APPLICATION UNDER: US 08/932,571
APPLICATION UNDER: 19, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Bak, MATY E.
REGISTRATION NUMBER: 13,215
REGISTRATION NUMBER: 1997US001/CIP
TELEGRANDIO INFORMATION:

ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette

CITY: Spr STATE: PA

USA

Query Match Best Local Matches

ch 6.6%; Score 109.5; DB I Similarity 23.7%; Pred. No. 0.068; S8; Conservative 24; Mismatches

DB 4; 80;

84 65

TPTSTPTPVSSST-----

Sequence 2, Application US/08783774
Patent No. 6054130
GENERAL INFORMATION:
APPLICANT: Spacete, Richard
APPLICANT: Jackman, Winthrop

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                                                                                                                                                                                                                                  Sequence 19, Application PC/TUS9504611A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
TOPOLOGY: lin
MOLECULE TYPE:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                         NTHATTAL OF INVENTION: Non Splicing Warfer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Rel CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 1300
                                                                                                                          STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Fordis, Jean B.
REGISTRATION NUMBER: 32,984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Dunner, L.L.P.
STREET: 1300 I Street, N.W., Suite 700
                                                                                                                                                DDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ENGTH:
                                                                                                                                                                                                                                                                                                                                                                             256 GASIVIOHTNGFVSSYIHIKDAQVKTGDTVRTGQRIASMKNQPS 299
                                                                                                                                                                                                                                                                                                                                                                                                              581 SAVTTPTPNATSPTLGK-TSPTSAVTTPTPNATGPTVGETSPQANATN------
                                                                                                                                                                                                                                                                                                                                                                                                                                                  198 MQFRYPV-GATNPVVRRFGTATVAGSTVTSNGMWFS-GRDGDLINASNAGTVIQADHNMD 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      149 VQQHPAVQKPTP----PVVVVKKPTP--TPPVVQQPAPVAPPVTEAPFATG-----SSGV 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          470 --TADVTSPTPAGTTSGASPVTPSPSPWDNGTESKAPDMTSSTSPVTTPTPNATSPT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35 SKPTYNSTSGSGSHRTSGSGGLAIGSQVITDSQGVPNRY--QVKQGDTVSKIAQRYGLNW 92
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                                                                                         Palo Alto
California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TSPTLNTTGFADPNTTTG------LPSSTHVPTNLTAPASTGPTVS------
                                                                                                                                                                                                                                                                                                                                            GTS----PTPVVTSQPKNATSAVTTGQHNITSSSTSSMSLRPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----PAVTTPTPNATSPTPAVTTPTPNATSPTLGKTSPTSAVTTPTPNATSPTLGKTSPT 580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DC
                                                                                                                            B: Cooley Godward Castro Huddleson & Tatum
5 Palo Alto Square
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                                                                          USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6.5%;
ilarity 23.2%;
Conservative 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IBM PC compatible SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                               Non Splicing Variants
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US/09/328,599A
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                                                                                                                                                                                                                   Winthrop,
                                                                                                                                                                                                of.
                                                                                                                                                                                               gp350/220
                                                                                                                                                                                                                                                                                                                                            670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62;
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US-09-308-375-2
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                                                                                                                                                                                                                                                                                                            US-09-308-375-2
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                                             CURRENT APPLICATION NUMBER: US/09/308,375
CURRENT FILING DATE: 1999-05-14
EARLIER APPLICATION NUMBER: EP9719636.4
EARLIER FILING DATE: 1997-09-15
NUMBER OF SEQ ID NOS: 3
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 2285
                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                      Sequence 2, Application US/09308375 Patent No. 6300117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
         LENGTH: 2285
TYPE: PRT
ORGANISM: Bacillius subtilis
                                                                                                                                                                                                   FILE REFERENCE: GC394-PCT
                                                                                                                                                                                                               APPLICANT: Genencor International, Inc.
TITLE OF INVENTION: Proteases From Gram-Positive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: AV
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Luann Cserr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                    632
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        581 SAVTTPTPNATSPTLGK-TSPTSAVTTPTPNATGPTVGETSPQANATN---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   149 VQQHPAVQKPTP----PVVVVKKPTP--TPPVVQQPAPVAPPVTEAPFATG-----SSGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93 REIGHINNLNSSYTIYTGQWLT----LWSGDLKVRERSISSGVNTAHTPSPVAVQSSRPP 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             35 SKPTYNSTSGSGSHRTSGSGGLAIGSQVITDSQGVPNRY--QVKQGDTVSKIAQRYGLNW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MQFRYPV-GATNPVVRRFGTATVAGSTVTSNGMWFS-GRDGDLINASNAGTVIQADHNMD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---TADVTSPTPAGTTSGASPVTPSPSPWDNGTESKAPDMTSSTSPVTTPTPNATSPT---
                                                                                                                                                                                                                                                                                                                                                                                  GTS----PTPVVTSQPKNATSAVTTGQHNITSSSTSSMSLRPS
                                                                                                                                                                                                                                                                                                                                                                                                                  GASIVIQHTNGFVSSYIHIKDAQVKTGDTVRTGQRIASMKNQPS 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----PAVTTPTPNATSPTPAVTTPTPNATSPTLGKTSPTSAVTTPTPNATSPTLGKTSPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         380816 CooleyPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             415-843-5163
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In Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AVIR-003/00US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 109; DB Pred. No. 0.13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --LPSSTHVPTNLTAPASTGPTVS---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 907;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                  670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62;
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Query Match Best Local Similarity

6.5%;

Score 108.5; D Pred. No. 0.56;

DB 4;

Matches

63; Conservative

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1605 GYSKTAGNWTVIKQDDGTVAKYMHMINTPSVKAGQSVKAGQTIGKVGSTGNSTGNHLHLQ 1664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         191 ATGSSGVMQFRYPVGATNPYVRRFGTATVAGSTVTSNGMWFSGRDGDLINASNAGTVIQA 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DHNMD-GASIYIQHTNGFYSSYIH-IKDAQYKTGDTYRTGQRIASMKNQPSGAA-LFEFR 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YTNNSA---FR-----VSSKYGQQESGLRSSPHKGTDFAAKAGTAIKSLQSGKVQIA 1604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VNTAHTPSPVAVQSSRPPVQQHPAVQKPTPTVVVVVRPTPTPVQQPAPVAPPVTEAFF 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SGVGAMGLMÓLMPATAKSLG-VNNAYDÞYONVMGGTKYLAÓOLEKFGGNVEKALAAYNAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QGDTVSKIAQRYGLNWREIGHINNLNSSY-----TIYTGQWLTLWSGDLKVRERSISSG 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   THEISEN, MICHAEL
HARLAND, RICHAED J.
RIOUX, CLEMENT R.
VENTION: VACCINES FOR HAEMOPHILUS SOMNUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51; Mismatches 149; Indels
  Score 108;
                                                                                                                                                                                                                                            9000-0019.20
  DB 3;
Length 265;
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                                                                                                                                                                        Matches
                                                                                                                                                                                         Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/03/

APPLICATION NUMBER: US 08/03/

EILING DATE: 29-MAR-1993

ATTORNEY/AGENT INFORMATION:

NAME: ROBING, ROBERTA L.

REGISTRATION NUMBER: 33,208

REGERENCE/DOCKET NUMBER: 9000

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 22.0%; py Matches 39; Conservative 35;
                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (415) 327-32
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-619-812-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIF: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/619,812
FILING DATE: 15-MAR-1996
                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 279 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 UMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DDRESSEE:
                                       130 GVNTAHTESPVAVQSSRPVQQHPAVQKPTPPVVVVKKPTPTPPVVQQPAPVAPPVTEAP 189
                                                                               180 SEVTONTVNE-TWNANKPTNEOMKPVATPTHSTMPINK---TPPATSNIAWIWP-----
                                                                                                                     73 YQVKQGDTVSKIAQRYGLNWREIGHINNLNSSYTIYTGQWLTLWSG---DLKVRERSISS 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   216 -----TNGKIIQFSSADGG----NKGIDISGSRGQAVNAAAAWT 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        190 FATGSSGVMQFRYPVGATNPVVRRFGTATVAGSTVTSNGMWFSGRDGDLINASNAGT 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                166 SEVTONTVNE-TWNANKPTNEOMKPVATDTHSTMPINK---TPPATSNIAWIWP----- 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      130 GVNTAHTESEVAVQSSRPEVQQHEAYQKETEEVVVVVKKETETEEVVVQQEAEVAPEVTEAE 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           106 YKVRKGDIMFLIAYISGMDIKELATLNNWSEPYHLSIGQVLKIANNIPDSNMIPTQTINE 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 73 YQVKQGDTVSKIAQRYGLNWREIGHINNLNSSYTIYTGQWLTLWSG---DLKVRERSISS 129
                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                 TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PALO ALTO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       635 BRYANT STREET
                                                                                                                                                               6.5%; Score 108; DB 3; Length 279; Conservative 35; Mismatches 69; Indels
                                                                                                                                                                                                                                                                                                                                                                                    (415)
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THEISEN, MICHAEL
HARLAND, RICHARD J.
RIOUX, CLEMENT R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REED & ROBINS
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5; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34;
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RESULT 20 US-08-619-812-9

, Application US/08619812 6100066

OTTER, ANDREW A.

1665 IEQNGKTIDP 1674

308 ISRNGVYVDP 317

ORRESPONDENCE ADDRESS

INVENTION

T: 635 BRYANT STREET
PALO ALTO
CATTO

CALIFORNIA

UNITED STATES OF AMERICA

Query Match

6.5%;

TYPE: am

TYPE:

protein

LENGTH:

REFERENCE/DOCKET NUMBER: 900
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-899
TELEPAX: (415) 327-3231
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:

APPLICATION NUMBER: US 0 FILING DATE: 29-MAR-1993 ATTORNEY/AGENT INFORMATION:

US 08/038,719

APPLICATION NUMBER: FILING DATE: 15-MAI CLASSIFICATION: 435

15-MAR-1996

US/08/619,812

NAME: ROBINS, ROBERTA L.
REGISTRATION NUMBER: 33,208

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US-08-737-716-13
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Sequence 13, App
                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 66; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                          IMMEDIATE SOURCE:
CLONE: Fig.5a (S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 671 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/NL95/00170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/737,716
FILING DATE: 22-APR-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE: 12-MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: U.S.A. ZIP: 20005-3918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Pillsbury Madison & Sutro, L.L.P. STREET: 1100 New York Avenue, N.W.
 226
                                                                       166
                                                                                                             429
                                                                                                                                                                                     369
                                                                                                                                                                                                                                                            311 ATDPSYNAKLNNVITAYNLTQYDTPSSGGN--TGGGTVNPGTGGSNNQSGTNTYYTVKSG
                                                                                                                                              106 TIYTGQWLTLWSGDLKVRERSISSGVNTAHTPSPVAVQSSRPPVQQHPAVQKPTPPVVVV
                                                                                                                                                                                                                         79
                                                                                                                                                                                                                                                                                                 34 ASKPTYNS-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
SNG---MWFSGRDGDLINASNAGTVIQADHNMDGASIVIQHTNGFVSSYIHIKDAQVKTGD 283
                                                                       KKPTPTPPVVQQPAPVAPPVTEAPFATGSSGVMQFRYPVGATNPVVRRFGTATVAGSTVT 225
                                                                                                                                                                                     DTLNKIAAQYGVSVANLRSWNGISGDLIFVGQKLIVKKGASGNTGGSGNGGSNNNQSGTN 428
                                                                                                                                                                                                                     DTVSKIAQRYGL-----NWREI-----
                                                                                                           TYY-----TVKSGD-TLNKIAAQYGVTVANLRSWNGISGDLIFVGQK------LIV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Application US/08737716
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VENTION: Process for the lysis of a culture of lactic
VENTION: acid bacteria by means of a lysin, and uses or
                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptococcus faecalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-MAY-1994
                                                                                                                                                                                                                                                                                                                                                     6.4%; Score 107.5; DI 20.8%; Pred. No. 0.12;
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                                                                                                                                                                                                                                                                                                                                                                                                                              faecalis)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -TNGKIIQGFSSADGG----NKGIDISGSRGQAVNAAAAWT
                                                                                                                                                                                                                                                                                                                                     43;
                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                               TSGSGSHRTSGSGGLAIGSQVITDSQGVPNRYQVKQG
                                                                                                                                                                                                                                                                                                                                                                    DB 2;
                                                                                                                                                                                                                                                                                                                                   77;
                                                                                                                                                                                                                                                                                                                                                                        Length 671;
                                                                                                                                                                                                                                                                                                                                   Indels 131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and uses of the resulting
                                                                                                                                                                                                                       -GHINNLNSSY 105
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                                  US-09-556-706B-2
                                                     RESULT 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 2
Sequence 2, Application US/09556706B Patent No. 6458364
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EARLIER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Bjornvad, Mads E.
APPLICANT: Hatakeyama, Mariko
APPLICANT: Schulein, Martin
APPLICANT: Nielsen, Jack B.
TITLE OF INVENTION: Endo-Beta-1,
TITLE OF INVENTION: Saccharothrix
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EARLIER APPLICATION NUMBER: 60/053,506
EARLIER FILING DATE: 1997-07-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EARLIER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/109,841
CURRENT FILING DATE: 1998-07-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: 5195.200-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EARLIER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH:
                                                                                                                                                                                 267
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                                                                                                                                            279 VKTGDTVRTGQRIASMK 295
                                                                                                                                                                                                                                                                                                                                   168 EPTPEPTPEPTPEPTPEPTPEPTPEPTPEPTPEPTMPPVQAG------QFHVDTT
                                                                                                                                                                                                                                                                                                                                                                                                             121 FN---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 0812/97
FILING DATE: 1997-07-04
APPLICATION NUMBER: 0846/97
FILING DATE: 1997-07-11
                                                                                                                                                                                                                                                                                                                                                                                                                                             90 LIWREIGHINNLNSSYTIYTGQWLTLWSGDLKVRERSISSGVNTAHTPSPVAVQSSRPPV 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 VTVTNLGDPLSSWELSWTFPDGQGVQQLWNGVHSTSGSNVTVKEMSWNGSVGTNASVQVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MHPRSKRPLTTRRKVVPAVAAGTVLAGGVTALTSNIAQAAAGCRVDYAVTSQWPGGFGAA
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                                                                                                                                                                                   TSAAAAAGRTAVLVVYAIPGRDCGQHSSGGVSTSEYAQWIDTVAQGIVGNPWVVLDPDAL
                                                                                                                                                                                                                                                          NQSYRAWQAA-----
                                                                                                                                                                                                                                                                                               NPVVRRFGTATVAGSTVTSNGMWFSGRDGDLI-----NASNAGTVIQADHNMD----
                                                                                                                                                                                                                                                                                                                                                                      QQHP-AVQKPTPPVVVVKKPTPTPPVVQQPAP-VAPPVTEAPFATGSSGVMQFRYPVGAT
                                                                                                           PMLGDCDGQGDRVGFLK 343
                                                                                                                                                                                                                         -----GASIVI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41; Mismatches 137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 107; DB 4; Length 490; Pred. No. 0.084;
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                                                                                                                                                                                                                                                          -SGSDKDLLAKIALTPQAYWVGNWNEASHAQQEVRDI
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RESULT 25
US-08-155-171B-15
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PRIOR FILLING DATE: 1997-01-15
PRIOR PPLICATION NUMBER: 08/229,291
PRIOR FILLING DATE: 1994-04-18
NUMBER OF SEQ ID NOS: 19
SOPTWARE: Patentin version 3.0
SEQ ID NO 2
LENGTH: 878
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Jackman, Winthrop
TITLE OF INVENTION: NON SPLICING VARIANTS OF GP350/220
FILE REFERENCE: 7682-050-999
CURRENT APPLICATION NUMBER: US/09/556,706B
CURRENT FILING DATE: 2000-04-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Virus
                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE': Floppy
                                                                                                                                                                                                                                                                                         ORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                               UMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local 5.
APPLICATION NUMBER: US/0 FILING DATE: 19-NOV-1993
                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
RRENT APPLICATION DATA:
APPLICATION DATA:
                                                                                                                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                              LICANT: Anderson, Carl W.
LICANT: Mangel, Walter F.
LE OF INVENTION: Co-Factor Activated Recombinant
LE OF INVENTION: Adenovirus Proteinases (As Amen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               149 VQQHPAVQKPTP----PVVVVKKPTP--TPPVVQQPAPVAPPVTEAPFATGSSGVMQFRY 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          620 SPOANATNHTLGGTSPTPVVTSOPKNATSAVTTGOH-----NRPS 659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        470 --TADVTSPTPAGTTSGASPVTPSPSPWDNGTESKAPDMTSSTSPVTTPTPNATSPT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           430 TSPTLNTTGFADPNTTTG------LPSSTHVPTNLTAPASTGPTVS------
                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93 REIGHINNLNSSYTIYTGQWLT----LWSGDLKVRERSISSGVNTAHTPSPVAVQSSRPP 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               35 SKPTYNSTSGSGSHRTSGSGGLAIGSQVITDSQGVPNRY--QVKQGDTVSKIAQRYGLNW 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity 22.1
63; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PVGATNPVVRRFGTATVAGSTVTSNGMWFSGRDGDLINASNAGTVIQADHNMDGASI---
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                                                                                                                                                                                                              Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Application US/08155171B
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                                                                                                                                                                                          USA .
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22.1%; Pred. No. 0.22;
tive 29; Mismatches
                   US/08/155,171B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TSAVTTPTPN----ATSPTLGKTSPTSAVTTPTPNATGPTVGET 619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 4;
                                                                                                                                                                                                                                                                                                                                (As Amended)
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RESULT 26
US-08-435-998-15
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                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: PLOPBY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTION DATA:
APPLICATION NUMBER: US/08/435,998
FILING DATE: 05-MAY-1995
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION TOWBER: US 08/155,171
FILING DATE: 13-MAR-1993
APPLICATION TOWBER: US 07/851,217
PRICE ADDITIONAL DATA:
APPLICATION NUMBER: US 07/851,217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/545,585
FILING DATE: 29-JUN-1990
FILING DATE: 19-JUN-1990
FILING DATE: 19-JUN-1990
FILING DATE: 19-JUN-1990
FILING DATE: 19-JUN-1990
FILING DATE: 19-JUN-1990
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TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 15:
                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 1 STREET CITY: Lexington
STATE: Massachusetts
Three USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: (617) 861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Match 6.2%; Score 103.5; DB Local Similarity 24.0%; Pred No. 0.067; es 42; Conservative 27; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  122 TVSPEGRGEKRPRPDREETLVTQIDEPPSYEEALKQGLPTTRPI--APMATGVLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            157 KPTPPVVVVKKPTP------TPP----VVQQPAPVAPPVTEAPFATGSSG 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       82 SKIAQRYGL-----NWREIGHINNLNSSYTIYTGQWLTLWSGDL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 ASLAPRHÖSRÞFMGNWQDÍGTSNMSGGAFS-----WGSLWSGIKNFGSTIKNYGSKAWNS 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STGQMLRDKLKEQNFQQKVVDGLASGISGVVDLANQAVQNKINSKLDPRPPVEEPPPAVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Application US/08435998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3: Hamilton, Brook, Smith & Reynolds, P.C Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Anderson, Carl W. Mangel, Walter F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---KVRERS-----ISSGVNTAHTPSPVAVQSS-----RPPVQQ-HPAVQ
                                                                                                                                                                                                                                                                                                                Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US 07/545,585
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Activated Recombinant . s Proteinases (As Amended)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 250;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121
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Best Local Similarity 24.0
Matches 42; Conservative
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SEQUENCE CHARACTERISTICS:
LENGTH: 250 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 53701-2113
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy d.
                                                                                 INFORMATION FOR SEQ ID NO:
                                 SEQUENCE CHARACTERISTICS:
LENGTH: 214 amino acid
TYPE: amino acid
                                                                                                                                                                                                                APPLICATION NUMBER: US/08/217,327
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/812,233
FILING DATE: 19-DEC-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 1
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                  TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Polocyms
                                                                                                                                                    REFERENCE/DOCKET NUMBER:
                                                                                                                                                                  NAME: Seay, Nicholas REGISTRATION NUMBER:
                                                                                                                TELEPHONE:
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               TOPOLOGY:
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5. 5474925
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                          amino acid
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    I: John, Maliyakal E
    I: Barton, Kenneth A
    INVENTION: Immobilized Proteins in Cotton Fiber

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                                               214 amino acids
                                                                                                    608-251-9166
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                                                                                                                  608-251-5000
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                                                                                                                                                                                Nicholas J
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       39;
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US-09-120-927-2
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                                                                                                                                                                                       Matches
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Best Local
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APPLICANT: Kim, Jihyun E
APPLICANT: Beer, Steven
                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible COMPUTER: PC-DOS/MS-DOS OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                TYPE: amino acid
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LECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                               ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                           ELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         AME: Goldman, Michael
147 SDQFGQPGTGNNSASSGTSSSGGSPFNDLSGGKAPSGNSPSGNYSPVSTFSPP--
                           109 TGQWLTLWSGDLKVRERSISSGVNTAHTPSPVAVQSSRPPVQQHPAVQKPTPPVVVVKKP 168
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                                                                                                                         30 ANSALGQQPIDRQTIEQMAQLLAELLKSLLSPQSGNAATGAGGNDQTTGVGNAGGLNGRK 89
                                                            90 GTAGTTPQSDSQ---NMLSEMGNNGLDQAITPDGQGGGQIGDNPLLKAMLKLIARMMDGQ 146
                                                                                         57 -AIGSQVITDSQGVPNRYQVKQGDTVSKIAQRYGLNWREIGHINNLNSSYTI-----Y 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32 STPATPTPPA--STPPPTTQAPPTPTATPPPVSTPPPTSSPPPVTASPPPVSTPPPSSPP
                                                                                                                                                        6 AINSQNOKPIKRLGL-IFGVITTCILAGCASKPTYNSTSGSGSH-RTSG---SGGL----
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New York
RY: U.S.A.
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                                                                                                                                                                                                                                                                                                                                447 amino acids
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                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                              (716) 263-1600
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                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                           (716) 263-1304
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1051, Clinton
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                                                                                                                                                                                                                                                                                                                                                                                                                            19603/1581
                                                                                                                                                                                                    Score 102; DB 4; Length 447; Pred. No. 0.21;
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Pred. No. 0.06;
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con Square
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ITS USE
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US-08-276-213-3
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                                                                                                                                                                          Best Local
                                                                                                                                                                                              Query Match
Best Local :
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                              TOPOLOGY: lin
MOLECULE TYPE:
HYPOTHETICAL: N
                                                                                                                                                                                                                                                   ANTI-SENSE: NO
FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: O'Connor, Edna
REGISTRATION NUMBER: 29,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 80401-3393
ZOMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/276,213
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: NR
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                           ENGTH:
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                                           373 SPSPSPSASRTPTPTPTPTASPTPTLTPTATPTPTASPTPSPTAASGARCTASYQVNS
                                                                                                                315
                                                                                                                                    111 QWLTLWS-----GDLKVRERSISSGVNTAHTP-----SPVAVQSSRPPVQQHPAV 155
                                                                         156 Q-KPTPPVVVVKKPTPTPPVVQQPAPV-----APPVTEAPFATGSSGVM------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            311 -ADGIHLYGDAKIDNLHVTNVGEDAITVKPNSAG 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         268 VSSYIHI-KDAQVKTGDTVRTGQRIASMKNQPSG 300
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5. 5536655
                                                                                                                                                                          l Similarity
53; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION:
----QFRYPVGATNPVVRRFGTATVAGSTVTSNGMWFSGRDGDLINASNAGTVIQADHNM 254
                                                                                                       QW-TFWSWNPDSGDTGGILKDDWQTVDTVKDGYLAPIKSSIFDPVGASAS-PSSQPSPSV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TPTSPTSPLDFPSSPTKAAGGSTPVTDHPDPVGSAG-----IGAGNSVA--FTSAGAN 251
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    National Renewable Energy Laboratory
1617 Cole Boulevard

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                                                                                                                                                                                                                                                                                : protein
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                                                                                                                                                                    6.1%; Score 101.5; I 25.2%; Pred. No. 0.3; tive 20; Mismatches
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US-08-728-323A-2
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Best Local Similarity 24.0%; Pred. No. 0.95;
Matches 40; Conservative 12; Mismatches
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INFORMATION FOR SEQ ID NO:
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ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
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TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF SEQUENCES:
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APPLICANT:
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LENGTH: 1162 amino acids
TYPE: amino acid
TYPE: lines
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM Form
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STREET: 1185 Av
CITY: New York
STATE: New York
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                                                                                                                                                                                                                           180
                  239
                                                                                                 185 VTEAPFATGSSGVMQFRYPVGATNPVVRRFGTATVA-GSTVTSNGMW 230
                                                                                                                                                                                                                                                                                                                                                                                                                  120 VSPGTTDTHSPSPALPPTQSPESSORPPLSSPTGRPDSSTPMRPPPSQQTTPPHSPTTPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   127 ISSGVNTAHTPSPVAVQSSRPPVQQHPAVQKPT-----PPVVVVVKKP----TPT 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   478 NGQSVTARNMSYNNVIQPGQNTTFGFQASY 507
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      433 DWGNGFTVTVAVIN-----SGSVATKTWTVS--WTFGGNQTITNSWNAAV---
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ATESPIYVGSSS-----DGDTPP--RQPPTSPISIGSSSPSEGSW 276
                                                                                                                                                                                                   PEPPSKSSPDSLAPSTLRSLRKRRLSSPQGPSTLNPICQSP-PVSPPRCDFANRSVYPPW
                                                                                                                                                                                                                                                                                                          P-----PVVQQPAPVAPP------
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Bohenzky, ...
Russo, James J.
Russo, James J.
Redelman, Isidore S.
Charle, Patrick S.
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1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yuan
Yuan A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US/08/728,323A
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RESULT 31 US-09-298-568-2 ; Sequence 2, Application US/09298568 ; Patent No. 6322792

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Kaposi's sarcoma-associated herpesvirus
US-09-298-568-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4, Application US/09442100 Patent No. 6359193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 1162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: RHADINO VIRUS LANA ACTS IN TRANS ON A UNIT OF RHADINO TITLE OF INVENTION: VIRUS DNA TO MEDIATE EFFICIENT EPISOME PERSISTENCE FILE REFERENCE: 16412-10001R
CURRENT APPLICATION NUMBER: US/09/298,568
CURRENT FILING DATE: 1999-04-21
EARLIER APPLICATION NUMBER: US 60/109,422
EARLIER APPLICATION NUMBER: US 60/109,422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Kieff, Elliott D.
APPLICANT: Ballestas, Mary E.
APPLICANT: Kaye, Kenneth M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                     ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                    FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Yu, Wan
TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF LATS
TITLE OF INVENTION: GENES AND METHODS BASED THEREON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PPLICANT:
                                                                                                                                             APPLICATION NUMBER: FILING DATE:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 65
                                                                                                                                                                                                                                                                                                                                                                      STREET:
                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                    CITY: New York
                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              239 ATESPIYVGSSS-----DGDTPP--RQPPTSPISIGSSSPSEGSW 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 127 ISSGVNTAHTPSPVAVQSSRPPVQQHPAVQKPT-----PPVVVVKKP----TPT 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120 VSPGTTDTHSPSPALPETQSPESSQRPPLSSPTGRPDSSTPMRPPPSQQTTPPHSPTTPP 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PEPPSKSSPDSLAPSTLRSLRKRRLSSPQGPSTLNPICQSP-PVSPPRCDFANRSVYPPW
                                                                                                                                                                                                                                                                                                                                 New York
                                                                                                                                                                                                                                                                                                                                                                      3: Pennie & Edmonds
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                   USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zhang, Sheng
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                                                                                       08/411,111
                                                                                                                                                              US/09/442,100
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Pred. No. 0.95;
.2; Mismatches
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US-08-431-387-4
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                                                        Sequence 4,
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                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 1130 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                       Match 6.0%; Score Ivv.J, Local Similarity 24.3%; Pred. No. 1.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
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                                                                                                                                                                                                                                                                  127
                                                                                                                                                   525 QTVQPSPFPEGTASNVTVMPPVAEAP 550
                                                                                                                                                                                                                                                                                                                                                                           356 FMIHQNVVPAGTVNRQPPPPYPLTAANGQSPSALQTGGSAAPSSYTNGSIPQSMMVPNRN
                                                                                                                                                                                      164 VVKKPTPTPPVVQQPAPVAPPVTEAP 189
                                                                                                                                                                                                                                                                                                                                      74 QVKQGDTVSKIAQRYGL-----NWREIGHINNLNSSYTIYTGQWLTLWSGDLKVRERS 126
                                                                                                                                                                                                                                                                                                                                                                                                                22 FGVITTCILAGCASK---PTYNSTSGSG-SHRTSGSGGLAIGSQV----ITDSQGVPNRY 73
                                            Application US/08431387
5677163
                                                                                                                                                                                                                             FNNPLGNRASHSANSQPSATTVTAITPAPIQQPVKSMRVLKPELQTALAPTHPSWIPQPI
                                                                                                                                                                                                                                                                  ISSGVN----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PENNIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 100.5; I
Pred. No. 1.1;
                                                                                                                                                                                                                                                              TAHTPSPV--AVQSSR---PPVQQHPAVQKPT--PPVV 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 4; Length 1130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                     49;
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                                                                                                                                                                                                                             524
                                                                                                                                                                                                                                                                                                     464
                                                                                                                                                                                                                                                                                                                                                                             415
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TELEPHONE: (415) 742-7536 TELEFAX: (415) 742-7217 INFORMATION FOR SEQ ID NO: 4: COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IM PC compatible
COMPUTER: TEM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA; APPLICANT: SEQUENCE CHARACTERISTICS: LENGTH: 268 amino acid PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/07/950,856A
FILING DATE: September 24, 1992
ATTORNEY/AGENT INFORMATION: TELECOMMUNICATION INFORMATION: CORRESPONDENCE ADDRESS: TITLE OF INVENTION: NAME: Horn, Margaret A.
REGISTRATION NUMBER: 33,401
REFERENCE/DOCKET NUMBER: GC APPLICATION NUMBER: FILING DATE: STATE: STREET: 180 Kimball Way CITY: South San Francisco ADDRESSEE: Genencor International, Inc STREET: 180 Kimball Way CLASSIFICATION: ZIP: COUNTRY: OF SEQUENCES: 94080 ξ, Lad, Pushkaraj J. Schmidt, Brian USA Cleaning Compositions Containing No. 5677163el Alkaline Proteases US/08/431,387

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RESULT 35
US-08-296-791-5
; Sequence 5, Application US/08296791
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; TOPOLOGY: lir
; MOLECULE TYPE:
US-08-431-387-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 60/068,065
PRIOR PILING DATE: 1997-12-18
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FRSESEQ for Windows Version 3.0
SEQ ID NO 4
LENGTH: 750
                                                                                                                                                                                                                                                                                                                   Query Match 5.9%; Score 98.5; DB 4; Length 750; Best Local Similarity 31.5%; Pred. No. 0.96; Matches 46; Conservative 12; Mismatches 65; Indels 2
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Best Local Similarity 24.,
71; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: 220022000700
CURRENT APPLICATION NUMBER: US/09/165,239A
CURRENT FILING DATE: 1998-10-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: JOHNSON, ALEXANDER
APPLICANT: BRAIN, BURKHARD R.
TITLE OF INVENTION: POLYMUCLECTIDE SEQUENCES FROM CANDIDA
TITLE OF INVENTION: ALBICANS ENCODING POLYPEPTIDES ASSOCIATED WITH FILAMENTOUS
TITLE OF INVENTION: GROWTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-165-239A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     equence 4, Application No. 6344554
SNERAL INFORMATION:
                                                                                                                                           246
                                                                                                                                                                                660
                                                                                                                                                                                                      186 TEAPFAIGSSGVMQFRYPVGATNPVVRRFGTATVAGSTVTSNGMWFSGRDGDLINASNAG 245
                                                                                                         709
                                                                                                                                                                                                                                                       603
                                                                                                                                                                                                                                                                               128 SSGVNTAHTESPVAVQSSRPEVQQHPAVQKFTPPVVVVKKFTPTPPVVQQPAPVAP--PV 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         221 AGVAALVKSRYPSYTNNQIRORINQTATYLGSPSLYGNGLVHAGR 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           192 TGSSGVMQFRYPVGATNPVVRRFG-TATVAGS-TVTSNGMWFSGR 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              166 GVMAVAAVDQNGQPPSFSTYGPEIEISAPGVNVNSTYTGNRYVSLSGTSMA----TPHV 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                138 SPVAV----QSSRPP--VQQHPAVQKPTPPVVVVKKPTPTPVVQQPAPVAPPVTEAPFA 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  112 INNNMHIINMSLGSTSG-----SSTLELAVNRANNAGILLVGAAGNTGRQGVNYPARYS 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94 EIGHINNINSSYTIYTGQWLTLWSGDLKVR-ERSISSGV-----NT-----AHTP 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 HGTH---VAGTTA----ALNNSIGVLGVAPSADLYAVKVLDRNGSGSLASVAQ--GIEWA 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4
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                                                                                                       PAIQPSANS---
                                                                                                                                       TVIQADHIMDGASIVIQHTNGFVSSY 271
                                                                                                                                                                   SSAP-AVESSPVA----PGVETTPV-----APVAPSTTAKTSALVSTTEGTIPTTLESV 708
                                                                                                                                                                                                                                            SSPVAPGTESSPVAPESSAPATESAPATE -- SSPVAPGTETTPATPGAES-TPVAPVAPE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TVTTAINSQNQKPIKRLGLIFG-----VITTCI-----LAGCA----SKPTYNSTSG 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Application US/09165239A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TVVWGISFINTQQAHNRG-IFGNGARVAVLDTGIATHPDLRIAGGASFISSEFSYHDNNG
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linear
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                                                                                                     --SYTIASVSSF 727
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; Pred. No. 0.22;
46; Mismatches 95;
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                                                                                                                                                                                                                                                                                                                        23;
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RESULT 36
PCT-US95-10661A-5
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.

CURRENT APPLICATION LOATA:

APPLICATION UNMBER: US/08/296,791

FILLING DATE: 25-AUG-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Trecartin, Richard F.

REGISTRATION UNMBER: A-59941/RFT/RMS

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 781-1989

TELEPAX: (415) 789-3249

TELEPAX: (415) 789-3249

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 1702 amino acids

TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-296-791-5
                                                                                                                                                                        Sequence 5, Application PC/TUS9510661A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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                                                                                            APPLICANT: Washington ITITLE OF INVENTION: Ha NUMBER OF SEQUENCES: 9 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: St. Geme 1
APPLICANT: Falkow, St
TITLE OF INVENTION: F
TITLE OF INVENTION: I
NUMBER OF SEQUENCES
                            ADDRESSEE: Flehr,
STREET: 4 Embarcad
CITY: San Francisc
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Ho
                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: United States ZIP: 94111-4187
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STREET: 4 Embarcadero Center, Suite 3400
CTIY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ocal
                                                                                                                                                                                                                                                                             1047 ENS 1049
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                                                                                                                                                                                                                                                                                                                                                     999
                                                                                                                                                                                                                                                                                                                                                                           132 NTAHTPSPVAVQSSRPPVQQHPAVQKPTPPVVVVKKPTPTPPVVQQPAPVAPPVTEAPFA 191
                                                                                                                                                                                                                                                                                                                                                                                                                  953 N--ATRNNLNVSLVGNTVDLGAWKYKLRNVNGRYDLYNPE-----VEKR--NQTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    896 TVNSLSGNGSFYYLTDLSNKQGDKVVVTKSATGNFTL---QVADKTGEPTKNELTLFDAS 952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38 TYNSTSGSGSH--------RTSGSGGLAIGSQVITDSQGVPNRYQVKQGDTV 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                       82 SKIAQRYGLNWREIGH---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42;
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94111-4187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            h 5.9%; So Similarity 23.0%; Po 42; Conservative 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acids
                                                                                                                                                                                                                                                                                                                  TGS 194
                                                                                                                                                                                                                                                                                                                                                   DTTNITTPNNIQADVPSV-
                                               4 Embarcadero Center,
an Francisco
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                                                                                                                                   Washington University, et al.
"ENTION: Haemophilus Adherence and
                                                                                    Flehr,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Geme III, J
                                                                                  Hohbach,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Joseph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 98.5; DI
Pred. No. 3.1;
4; Mismatches
                                                               Test, Albritton & Herbert
er, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----INNLNSSYTIYTGQWLTLWSGDLKVRERSISSGV 131
                                                                                                                                                                                                                                                                                                                                            PSNNEEIARVETPVPP----PAPATPSETTETVA 1046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 4;
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                                                                                                                                   Penetration Protein
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PC-DOS/MS-DOS

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                                                                                                                                                                                                                                                                                                                                          Sequence 7, Applic Patent No. 6120988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 910 277299
INFORMATION FOR SEQ ID NO:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                     STREET: 350
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS
                                                                                                                                                                  ITTLE OF INVENTION: DNA
TITLE OF INVENTION: NO.
TITLE OF ARCHIENCES: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Trecartin, Richard F.
REGISTRATION NUMBER: 7P
REFERENCE/DOCKET NUMBER: FP
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 25-AUG-
                                                                                                                                                                                                                                                                                       APPLICANT:
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                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                        APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (415) 398-3249
                                                      COUNTRY: U
ZIP: 94306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                        ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                            1047 ENS 1049
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                                                                                                                                                                                                                                                                                                                         INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               82 SKIAQRYGLNWREIGH------INNLNSSYTIYTGQWLTLWSGDLKVRERSISSGV 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                38 TYNSTSGSGSH-------RTSGSGGLAIGSQVITDSQGVPNRYQVKQGDTV 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : 1702 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                        Application US/08478507
                                                                                                                   E: Dehlinger & Associates
350 Cambridge Avenue, Suite 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                    Reyes, Gregory R
Yarbough, Patrice O
Bradley, Daniel W
                                                                                                                                                                                                                                 Tam, Albert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   unknown
                                                                                                                                                                                                                                                      Krawczynski, Krzysztof Z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (415) 781-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-AUG-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5.9%;
                                                                                                                                                                                  DNA Sequences of Enterically Transmitted No. 6120988-A/No. 6120988-B Hepatitis Viral Agent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US 08/296,791
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 98.5; Di
Pred. No. 3.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62;
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                                                                                                                                                                                                                                           RESULT 38
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                                                                                                                                                                                   Sequence 7,
Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (650) 324-09 INFORMATION FOR SEQ ID NO:
              APPLICANT: Tam, Albert APPLICANT: Fry, Kirk E TITLE OF INVENTION: DNA TITLE OF INVENTION: NO. NUMBER OF SEQUENCES: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 05-AFR-100 PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 07/420,921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 11-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/208,997
                                                                                                     APPLICANT:
                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 4600-0183.22
TELECOMMUNICATION INFORMATION:
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PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 08/279,823
CORRESPONDENCE ADDRESS:
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                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                     685 GHVWESANPFCGESTLYTRTW------
                                                                                                                                                                                                                                                                                               786 ---
                                                                                                                                                                                                                                                                                                                            204 VGATNPVVRRFGTATVAGSTVTSNGMWFSGRDGDLINASNAGTVIQADHNMDG 256
                                                                                                                                                                                                                                                                                                                                                                                               151 QH---PAVQKPTPPVVVVKKPTPTPPVVQQPA----PVAPPVTEAPFATGSSGVMQFRYP
                                                                                                                                                                                                     7,
                                                                                                                                                                        INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96 GHI----NNLNSSYTIYTGQWLTLWSGDLKVRERSISSGVNTAHTPS-PVAVQSSRPPVQ 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
                                                                                                                                                                                                                                                                                                                                                             SRAATPTLAAPLPPPAPDPSPPPSAPALAEPASGATAGAPAITH---QTARHRRLLFTYP
                                                                                                                                                                                                     Application US/09128275A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4: (650)
(650) 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1693 amino acids
                                                                                                                Yarbough, Patrice O
Bradley, Daniel W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                   Krawczynski, Krzysztof Z
                                                                                                                                                    Reyes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
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                                                                                                                                                                                                                                                                                              -- DGSKVFAGSLFESTCTW-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   324-0960
                                                                                                                                                    Gregory R
              DNA Sequences of Enterically Transmitted
No. 6229005-A/No. 6229005-B Hepatitis Viral Agent
: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5.9%; Score 98; DB 3; Length 1693; 24.9%; Pred. No. 3.4; ative 14; Mismatches 62; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     324-0880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                               LVNASN--
                                                                                                                                                                                                                                                                                                                                                                                                                                    -SEVDAVSSPARPDLGFMSEPSIP
                                                                                                                                                                                                                                                                                            --VDHRPGG 815
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ADDRESSEE: Dehlinger & Associates STREET: 350 Cambridge Avenue, Suite 250 CITY: Palo Alto STATE: CA

94306

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RESULT 39
US-09-553-427-7
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MOLECULE TYPE: protein
US-09-128-275A-7
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TELEPAX: (650) 324-0960
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1693 amino acids
TYPE: amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 43; Conserva
      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Petithory, Joanne R.
REGISTRATION NUMBER: 42,995
REFERENCE/DOCKET NUMBER: 4600-0183.
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: OF PRIOR APPORT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 13-OCT-PRIOR APPLICATION NUMBER: 16-TIN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 11-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/208,997
FILING DATE: 17-JUN-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 03-AUG-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/279,823
FILING DATE: 25-JUL-1994
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APPLICATION NUMBER: US 07/681,078
APPLICATION NUMBER: 1991
FILING DATE: 05-APR-1991
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VALUE 16-JUN-1989

VIOR APPLICATION DATA:
APPLICATION UNMBER: US ~-
EILING DATE: 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CCC 7, Application US/09553427
No. 6379891
AL INFORMATION:
LICANT: Reyes, Gregory R
                                                                                                                                                                                      204 VGATNPVVRRFGTATVAGSTVTSNGMWFSGRDGDLINASNAGTVIQADHNMDG 256
                                                                                                                                                                                                                                                            151 QH----PAVQKPTPPVVVVKKPTPTPPVVQQPA----PVAPPVTEAPFATGSSGVMQFRYP 203
                                                                                                                                                                                                                                                                                                                                               96
                                                                                                                                                                                                                      SRAATPTLAAPLPPPAPDPSPPPSAPALAEPASGATAGAPAITH---QTARHRRLLFTYP
                                                                                                                                                                                                                                                                                                 GHVWESANPFCGESTLYTRTW-------SEVDAVSSPARPDLGFMSEPSIP 728
                                                                                                                                                                                                                                                                                                                                      GHI----NNLNSSYTIYTGQWLTLWSGDLKVRERSISSGVNTAHTPS-PVAVQSSRPPVQ 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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05-APR-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MBER: US 07/420,921
13-OCT-1989
                                                                                                                                                     -DGSKVFAGSLFESTCTW--
                                                                                                                                                                                                                                                                                                                                                                            5.9%; Score 98; DB 4; Length 1693; 24.9%; Pred. No. 3.4; ative 14; Mismatches 62; Indels 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Release #1.0, Version
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Best Local
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                                                                                       685 GHVWESANPFCGESTLYTRTW-----
                                              151 QH----PAVQKPTPPVVVVKKPTPTPPVVQQPA----PVAPPVTEAPFATGSSGVMQFRYP 203
             729 SRAATPTLAAPLPPPAPDPSPPPSAPALAEPASGATAGAPAITH---QTARHRRLLFTYP
                                                                                                             96 GHI----NNLNSSYTIYTGQWLTLWSGDLKVRERSISSGVNTAHTPS-PVAVQSSRPPVQ 150
                                                                                                                                                                l Similarity
43; Conser
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Sequence Patent N

SEVDAVSSPARPDLGFMSEPSIP 728

Gaps

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; TYPE: amino acid ; TOPOLOGY: linear ; MOLECULE TYPE: protein US-09-553-427-7 PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/505,888

FILING DATE: 05-APR-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/420,921

FILING DATE: 13-00T-1989

PRIOR APPLICATION NUMBER: US 07/367,486

FILING DATE: 16-UN-1989

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/367,486

FILING DATE: 16-UN-1989

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/336,672 FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/478,507
APPLICATION NUMBER: US/08/279,823
APPLICATION NUMBER: US/08/279,823
FILING DATE: 25-UUL-1994
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US/07/681,078
APPLICATION OFFEN-1991 TELEFAX: (650) 324-096
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS: TELECOMMUNICATION INFORMATION: TELEPHONE: (650) 324-0880 FILING DATE: 17-JUN-1988
ATTORNEY/AGENT INFORMATION: COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION NUMBER: US/09/553,42 NUMBER OF SECULIARIES OF STREET: 350 Cambridge Avenue, Suite PRIOR APPLICATION DATA: APPLICANT: STREET: 350 CTTY: Palo Alto APPLICANT: Fry, Kirk E
TITLE OF INVENTION: DNA Sequences of
TITLE OF INVENTION: NO. 6379891-A/No. REFERENCE/DOCKET NUMBER: REGISTRATION NUMBER: APPLICATION NUMBER: FILING DATE: 11-AP CATION NUMBER: 1693 amino acids 5.9%; Score 98; DB 4; Clarity 24.9%; Pred. No. 3.4; Conservative 14; Mismatches 6 Yarbough, Patrice Bradley, Daniel W Charles 324-0960 nski, Krzysztof Z Release #1.0, Version US 07/208,997 US/09/553,427 38,615 7: 4600-0183.22 Enterically Transmitted 6379891-B Hepatitis Viral Agent 250 62; Length 1693; Indels 54; 9,

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; SOFTWARE: PatentIn Ver. 2.0; SEQ ID NO 2; LENGTH: 2972; LENGTH: 2972; TYPE; PRT; ORGANISM: Human US-09-579-181-2
Search completed: July 8, 2003, 11:08:55 Job time : 30 secs
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US-09-579-181-2
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Patent No. 6365372

GENERAL INFORMATION:
APPLICANT: Chrivia, John
APPLICANT: Yaciuk, Peter
TITLE OF INVENTION: SNF2 Related CBP Activator Protein (SRCAP)
PILE REFERENCE: 16153-4247
CURRENT PILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 60/136,620
PRIOR APPLICATION NUMBER: 60/136,620
PRIOR PILING DATE: 1999-05-27
NUMBER OF COLUMBER: 1999-05-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 5.8%; Score 97; DB 4; Length 2972; Best Local Similarity 25.7%; Pred. No. 9.6; Matches 52; Conservative 20; Mismatches 52; Indels
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                                                                                                     1010 LTFQIQGNKLTLTGAQVRQLAV 1031
                                                                                                                                                                                                                                                                                                                                                                                                                                               137 PSPVAVQS--SRPEVQQHPAVQKPTPPVVVVKKPTPTPPVVQQPAPVAPPVTEAPFATGS 194
                                                                                                                                                       304 FEFRISRN-----GVYVDPLTV 320
                                                                                                                                                                                                         974 LSPD----
                                                                                                                                                                                                                                     248 IQADHNMDGASIVIQHTNGFVSSYIHIKDAQVKTGDTVRTGQRIASMKNQP----SGAAL 303
                                                                                                                                                                                                                                                                                                         928 SSLLKPLTVPPGYTFPPAAATTTSTTTATATTT------AVPAPTPAPQRLI 973
                                                                                                                                                                                                                                                                                                                                                                                                          890 PSPLGVLSGTSRP------PTPTLSL--KPTPPAPVRLSPAP--PP-----GS
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                                                                                                                                                                                                         -----MOARLPSGEVVSIGO-LASLAORPVANAGGSKP 1009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52; Indels 78;
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Post-processing: Minimum Match 0%
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Maximum DB seq length: 200000000
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Perfect score:
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Published Applications AA:*

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1670
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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108.5	110	110	110.5	112	112	112	117	118	118	118	118	118	125.5	127	127.5	142	182.5	209	Score
6.5	6.6	6.6	6.6	6.7	6.7	6.7	7.0	7.1	7.1	7.1	7.1	7.1	7.5	7.6	7.6	8.5	10.9	12.5	Query Match Length DB
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US-09-738-626-3548	US-09-925-301-1116	US-10-156-761-9957	US-10-101-464A-930	US-09-917-383-1	US-09-917-384-1	US-10-155-400-1	US-09-738-626-4458	US-09-972-599A-6	US-09-893-348-23	US-09-758-140-6	US-09-789-386-2	US-10-060-036-71	US-09-738-626-6241	US-09-468-147-166	US-10-156-761-14779	US-10-156-761-12234	US-10-156-761-9179	US-10-098-808-5	ID
Sequence 3548, Ap	Sequence 1116, Ap	Sequence 9957, Ap	Sequence 930, App	Sequence 1, Appli	۲	Sequence 1, Appli	Sequence 4458, Ap	Sequence 6, Appli	Sequence 23, Appl	Sequence 6, Appli	Sequence 2, Appli	Sequence 71, Appl	Sequence 6241, Ap	Sequence 166, App	Sequence 14779, A	Sequence 12234, A	Sequence 9179, Ap	Sequence 5, Appli	Description

108 6.5 877 9 US-10-245-033-90 108 6.5 877 9 US-10-245-107-90 108 6.5 877 9 US-10-245-107-90 108 6.5 877 9 US-10-245-851-90 108 6.5 877 9 US-10-245-851-90 108 6.5 877 9 US-10-245-833-90 108 6.5 877 9 US-10-238-183-90 108 6.5 877 9 US-10-238-183-90 108 6.5 877 9 US-10-238-183-90 108 6.5 877 9 US-10-238-183-90 108 6.5 877 9 US-10-245-055-90 108 6.5 877 9 US-10-245-147-90 108 6.5 877 9 US-10-245-147-90 108 6.5 877 9 US-10-245-149-90 108 6.5 877 9 US-10-245-196-90 108 6.5 877 9 US-10-245-033-90 108 6.5 877 9 US-10-245-033-90 108 6.5 877 9 US-10-245-033-90 108 6.5 877 9 US-10-245-033-90 108 6.5 877 9 US-10-245-880-90	45	44	43	42	41	40	39	. 38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	22
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	6.5	6.5	6.5	6.5	6.5	6.5	6.5	6. 5	6.5	6.5	6.5	6.5	6.5	6.5	6.5	6.5	6.5	6.5	6. 5	6.5	6.5	6.5	6.5	6.5	6. 5	0.0
9 US-10-245-103-90 9 US-10-245-117-90 9 US-10-245-117-90 9 US-10-245-851-90 9 US-10-245-833-90 9 US-10-238-183-90 9 US-10-238-183-90 9 US-10-238-183-90 9 US-10-238-183-90 9 US-10-245-055-90 9 US-10-245-055-90 9 US-10-245-147-90 9 US-10-245-129-90 9 US-10-245-130-90	877	877	877	877	877	877	877	877	877	877	877	877	877	877	877	877	877	877	877	877	877	877	877	877	877	0000
US-10-245-103-90 US-10-245-107-90 US-10-245-107-90 US-10-245-107-90 US-10-245-851-90 US-10-245-851-90 US-10-245-851-90 US-10-245-851-90 US-10-238-183-90 US-10-238-183-90 US-10-245-105-90 US-10-245-147-90 US-10-245-147-90 US-10-245-147-90 US-10-245-147-90 US-10-245-147-90 US-10-245-147-90 US-10-245-190 US-10-245-190 US-10-245-190 US-10-245-190 US-10-245-190 US-10-245-861-90 US-10-245-861-90 US-10-245-861-90 US-10-245-861-90 US-10-245-861-90 US-10-245-861-90 US-10-245-861-90 US-10-245-861-90 US-10-245-861-90 US-10-245-861-90 US-10-245-861-90 US-10-245-861-90 US-10-245-861-90 US-10-245-861-90 US-10-245-861-90 US-10-245-877-90 US-10-245-877-90	9	φ	φ	ø	ø	φ.	ø	ø	9	φ	9	ø	ø	ø	9	9	9	9	φ	9	9	φ	ø	ø	v	۲
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	, Appl	•	•	, Appl	-	, Appl		, Appl		•								, Appl	•	•	-	, Appl	-	-	-	rrddu 'a

ALIGNMENTS

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250 ADHNMDGASIVIQHTNGFVSSYIHIKDAQVKTGDTVRTGQRIASMKNQPSGAALFEFR 307	230TNGKIIQGFSSADGGNKGIDISGSRGQAVNAAAAGRVVY 268	190 FATGSSGVMQFRYPVGATNPVVRRFGTATVAGSTVTSNGWWFSGRDGDLINASNAGTVIQ 249	180 SEVTQNTVNE-TWNANKPTNEQMKPVATPTHSTMPINKTPPATSNIAWIWP 229	130 GVNTAHTESEVAVQSSREPVQQHEAVQKETEPVVVVKETETEPVVQQEAPVAEPVTEAE 189	120 YKVRKGDTMFLIAYISGMDIKELATLNNMSEPYHLSIGQVLKIANNIPDSNMIPTQTINE 179	73 YQVKQGDTVSKIAQRYGLNWREIGHINNLNSSYTIYTGQWLTLWSGDLKVRERSISS 129	atch 12.5%; Score 209; DB 9; Length 345; cal Similarity 24.8%; Pred. No. 9.6e-09; 63; Conservative 49; Mismatches 106; Indels 36; Gaps	; ORGANISM: Haemophilus somnus US-10-098-808-5	LENGTH: 345 TYPE: PRT	ເກ່	NUMBER OF SEQ ID NOS: 5 SOFTWARE: PatentIn Ver. 2.0	IER FILING	PRIOR FILING DATE: EARLIER FILING DATE: 1999-09-24	20	CURRENT FILING DATE: 2002-03-13	FILE REFERENCE: 9000-0049.20	OF INVENTION: TRANSFERRIN-BINDING PROTEINS	TITLE OF INVENTION: CLONING AND EXPRESSION OF HAEMOPHILUS SOMNUS		APPLICANT: Potter, Andrew A.	Publication No. US20030007981A1	US-10-098-808-5 ; Sequence 5, Application US/10098808	1
7	8	9	9	9	9	ý	6,																

RESULT 2 US-10-156-761-9179

Publication No. US20 GENERAL INFORMATION:

9179, Application US/10156761 ion No. US20030119018A1

APPLICANT: OMURA

SATOSHI

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IRYKGQSVDPMRYL 342 ISRNGVYVDPLTVL 321 269

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APPLICANT: IKEDA, HARUO
APPLICANT: IGHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHEBA, TADAYOSHI
APPLICANT: SHATORI, YOSHIYUKI
APPLICANT: HATTORI, WOVEL POLYNUCLEOTIDES
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
TILIR REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT APPLICATION NUMBER: UP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-08-02
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
LENGTH: 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      102 SAIGGDPTLIHPGLKLTIGAKSASSAATQSS-----TATKPATGVKSAT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    126 SISSGVNT-----AHTPSPVAVQSSRPPVQQHPAVQKPTPPVVVVKKPTPTPPV 174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             73 -----YQVKQGDTVSKIAQRYGLNWREIGHINNLNSSYTIYTGQWLTLWSGDLKVRER 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      46 GSHR-----TSGSGGLAI-----GSQVITDSQGVPNR-----
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                                                                                                                                                                                                                                                                                                                                                                                               -----RDGDLINASNAGTVIQAD-HNMDGASIVIQHTNGFVSSYIHIKDAQVKTGDT 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11arity 24.3%; Score 182.5; DB 9; Length 301; Pred. No. 9.8e-07; Conservative 35; Mismatches 107; Indels 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----TGGWKKLYSDN----R
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PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER: OF SEQ ID NOS: 15109
SEQ ID NO 12234
LENGTH: 203
TYPE: PRT
ORGANISM: Streptomyces avermitilis
US-10-156-761-12234
                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 240-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: UF 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-08-02
PRIOR FILING DATE: 2001-08-02
NUMBER: OF SEQ ID NOS: 15109
SEQ ID NO 14779
LENGTH: 397
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APPLICANT: OMURA,
APPLICANT: IKEDA,
APPLICANT: ISHIKU
APPLICANT: HORIKU
APPLICANT: HORIKU
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US-10-156-761-14779
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Best Local
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Publication No. US20030119018A1
GENERAL INFORMATION:
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APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
DETOR ADDITORTON
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  252 ASSDR
                                                                                                                                                                                  141 SGSATHTADRSTKRTVRDVKPQTTPQSQAGTAEMYTVLHGDTLSGIADSRHVRGGWEQLY 200
                                                                                         201 AANRGTIGADPDL-----ILPGORLHLRA---KATTRTDDASTST-HKSSTSSSKSSTEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            143 AHLSRIDVRIGQVVATGQHIALSGNTGNSSGPHLHFEIRTTPNYGSGIDFVAFLR 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             226 SNGMW---FSGRD-----GDLINASNAGTVIQADHN-----MDGASIVIQHTNGFVSSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  272 IHIKDAQVKTGDTVRTGQRIASMKN--QFSGAAL-FEFRISRN-GVYVDPLTVLK 322
                                                                                                                                    89 GLNWREIGHINNLNSSYTIYTGQWLTLWSGDLKVRERSISSGVNTAHTPSPVAVQSSRPP 148
                                                                                                                                                                                                                             43 SGSGSHRTSGSGGLAIGS---QVITDSQ-GVPNRYQVKQGDTVSKIA-----QRY 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        83
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                                                                                                                                                                                                                                                                        h 7.6%; Score 127.5; DB 9; Similarity 26.5%; Pred. No. 0.029; 79; Conservative 23; Mismatches 131;
                                        VQQHPAVQKPTPPVVVVKKPTPTPPVVQQPAPVAPPVTEAPFATGSSGVMQFRYPVGATN 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGGMWAHKHSGQDFAVPSGTEVLAAHGGTVVKAGGNGAGDGPAYGNAIVIKHGNGTYSQY
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HORIKAWA, HIROSHI
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-TEKATTSHSLV---APVNAGTGTQYHAAGSS--WSKGYHTGVDF 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15; Mismatches
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Query Match Best Local S Matches 83

Similarity

83;

; ORGANISM: Streptomyces avermitilis US-10-156-761-9179

RESULT 3
US-10-156-761-12234
IS-10-156-761-12234
IS-guence 12234, Application US/10156761
Publication No. US20030119018A1
GENERAL INFORMATION:

APPLICANT: OMURA, SATOSHI APPLICANT: IKEDA, HARUO APPLICANT: ISHIKAWA, JUN APPLICANT: HORIKAWA, HIROSHI

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LENGTH: 1708
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Best Local 9
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EARLIER APPLICATION NUMBER: US 09/173,141
EARLIER FILING DATE: 1998-10-15
EARLIER APPLICATION NUMBER: US 60/061,199
EARLIER FILING DATE: 1997-10-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: 6232.US.P1
CURRENT APPLICATION NUMBER: US/09/468,147A
CURRENT FILING DATE: 1999-12-21
EARLIER APPLICATION NUMBER: US 09/173,141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Erker, James C.
APPLICANT: Desai, Suresh M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: FastSEQ for Windows Version 3.0
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APPLICANT: Mushahwar, I. K.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT ORGANISM: Hepatitis FEATURE:
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                                                                                                                                                                                                                                                                                          574 TTVVDGAHLEANGPEEYVLSFDASRQSMGAGSHSLTYELTPAGLQVKISSNGLDCTATFP 633
                                                200 FRYPVGATNPVVRRFGTATVAGSTVTSNGMWFSGRDGDLINASNAGTVIQADHNMDGASI 259
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                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                      FCGEGTLYTRTWSTSGFSSDFSPPEAAAPASAAAPGLPYPT-----PPVSDIWVLPPPS
                                                                                                                                                                                      LNSSYTIYTGQWLTL-WSGDLKVRERSISSGVNTAHTPSPVAVQSSRPPV-----
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                                                                                                                  -QQH-----PAVQKP---TPPVVVVKKPTPTPPVVQQPAPVAPPVTEAPFATGSSGVMQ 199
                                                                                                                                                                                                                                                                                                                           TCILAGC---ASKPTYNSTSGSGSHRTSGSGGLAI-----GSQVITDSQGVPNRYQVK 76
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Pred. No. 0.19
37; Mismatches
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position 811
position 1553
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                                                                                                                APPLICANT: Benson, Darin R.
APPLICANT: Kalos, Michael D.
APPLICANT: Lodes, Michael J.
APPLICANT: Persing, David H.
APPLICANT: Hepler, William T.
APPLICANT: Jiang, Yuqiu
                                                                                                                                                                                                                                       Sequence 71, Application US/10060036 Publication No. US20030073144A1
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                                                                                                                                                                                                                         GENERAL INFORMATION:
            CURRENT APPLICATION NUMBER: US/10/060,036
CURRENT FILING DATE: 2002-01-30
NUMBER OF SEQ ID NOS: 4560
                                                               TITLE OF INVENTION: COMPOSITIONS AND METHODS TITLE OF INVENTION: AND DIAGNOSIS OF PANCREA FILE REFERENCE: 210121.566
 SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
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FastSEQ for Windows Version 4.0
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Query Match
Best Local Similarity
Matches 52; Conserve
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SEQ ID NO 6241
LENGTH: 205
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: JP 00/280988 PRIOR FILING DATE: 2000-08-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 7059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 2000-04-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT FILING DATE: 2000-12-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES FILE REFERENCE: 249-125 CURRENT APPLICATION NUMBER: US/09/738,626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: NAKAGAWA, SATOSHI
161 AAGQEIAGMGSQGFSTGSHLHFEIHPDGVTPVDP 194
                                      286 RTGORIASMKNOP-SGAALFEFRISRNGVY-VDP 317
                                                                                101 NGIDIANSIGTPIYAVMAGTVISSGPASGYGQWIRIQHDDGSISIYGHMEYLYVSVGERV
                                                                                                                         227 NGMWFSGRDGDLINASNAGTVIQADHNMD-GASIVIQHTNGFVSSYIHIKDAQVKTGDTV
                                                                                                                                                                                                                179 APVAPPVTEAPFATGSSGVMQFRYPVG--ATNPVVRRFGTATVAGSTVTS------
                                                                                                                                                                        41 ATMAPASAQTDYAGLSSGVADTVAEAAGVATTAVAPAATVARPANGTFTSGFGPRWGTFH
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OCHIAI, KEIKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OZAKI, AKIO
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TATEISHI, NAOKO
                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                           Score 125.5; DB 9;
Pred. No. 0.018;
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                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                   Length
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NUMBER OF SEQ ID NOS: 6
SOFTWARE: FASTSEQ for Win
SEQ ID NO 2
SEQ ID NO 2
LENGTH: 1192
TYPE: PRT
ORGANISM: HOMO SAPIENS
US-09-789-386-2
                                                                                                                                                                                                                                                                                                                 RESULT 9
US-09-758-140-6
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US-09-789-386-2
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                                                                                                                                                                                                                                         Sequence 6, Application US/09758140 Patent No. US20020012965A1 GENERAL INFORMATION:
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LENGTH: 1192
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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Best Local Similarity
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Patent No. US20020010324A1
GENERAL INFORMATION:
APPLICANT: Strittmatter, Stephen M.

IITLE OF INVENTION: No. US20020012965A10 Receptor-Mediated Blockade of Axonal Growth
FILE REFERENCE: 44574-5073-US
CURRENT APPLICATION NUMBER: US/09/758,140
CURRENT FILING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: US 60/175,707
PRIOR PILING DATE: 2000-01-12
PRIOR PILING DATE: 2000-01-12
PRIOR PILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 60/207,366
PRIOR APPLICATION NUMBER: US 60/207,366
PRIOR APPLICATION NUMBER: US 60/207,366
PRIOR APPLICATION NUMBER: US 60/207,366
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PRIOR FILING DATE: 1999-07-22
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT FILING DATE: 2001-02-21
PRIOR APPLICATION NUMBER: U.K. 9916898.1
PRIOR FILING DATE: 1999-07-19
PRIOR APPLICATION NUMBER: U.K. 9816024.5
PRIOR FILING DATE: 1998-07-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/789,386
CURRENT FILING DATE: 2001-02-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: MICHALOVICH, DAVID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
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36; Conserv
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Larity 39.6%; Pred. No. 0.62; Indels 14
Conservative 8; Mismatches 33; Indels 14
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ilarity 39.6%;
Conservative
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Pred. No. 0.62;
8; Mismatches 33; Indels 1:
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Sequence 23, 755

Sequence 23, 755

Patent No. US20100724ysn.

GENERAL INFORMATION:

APPLICANT: EISEMBACH-SCHWARTZ, Michal

APPLICANT: EISEMBACH-SCHWARTZ, Michal

APPLICANT: COHEM, Irun R.

APPLICANT: MOSONEGO, Alon

APPLICANT: MOSONEGO, Alon

APPLICANT: MOSONEGO, Alon

APPLICANT: MOSONEGO, Alon

APPLICANT: MOSONEGO, Alon

APPLICANT: MOSLEM, Gila

CURRENT APPLICATION NUMBER: US/09/893,348

CURRENT APPLICATION NUMBER: US/09/893,348

CURRENT APPLICATION NUMBER: US/09/893,348

CURRENT APPLICATION NUMBER: US/09/893,348

CURRENT APPLICATION NUMBER: US/09/893,348

PRIOR APPLICATION NUMBER: US/09/893,348

PRIOR APPLICATION NUMBER: US/09/893,348

PRIOR FILING DATE: 1998-05-19

PRIOR APPLICATION NUMBER: US/09/893,348

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PRIOR APPLICATION UMBER: US/09/893,348

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PRIOR APPLICATION UMBER: US/09/893,348

PRIOR APPLICATION UMBER: US/09/893,348

PRIOR APPLICATION UMB
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US-09-972-599A-6
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Best Local Similarity 39.6%;
Matches 36; Conservative
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SOFTWARE: Patentin Ver.
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TYPE: PR
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Sequence 6, Application US/09972599A Patent No. US20020077295A1 GENERAL INFORMATION:

APPLICANT: STRITTMATTER, STEPHEN M.
TITLE OF INVENTION: NOGO-RECEPTOR-MEDIATED BLOCKADE OF AXONAL GROWTH
FILE REFERENCE: C077 CIP US

CURRENT APPLICATION NUMBER: US/09/972,599A

CURRENT FILING DATE:

2001-10-06

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                                                                                                                                                                        SOFTWARE: PatentIn ver.
SEQ ID NO 4458
LENGTH: 237
TYPE: PRT
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LENGTH: 1192
                                                                     Matches
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                                                                                                      Query Match
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                                                                                                                                         ORGANISM: Corynebacterium glutamicum 09-738-626-4458
                                                                                                                                                                                                                                            PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: JF 00/280988
PRIOR FILING DATE: 2000-08-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: NAKAGAWA, SATOSHI
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TLE OF INVENTION: NOVEL POLYNUCLEOTIDES
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APPLICATION NUMBER: 09/758,140
FILING DATE: 2001-01-12
APPLICATION NUMBER: 60/236,378
FILING DATE: 2000-09-29
                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: JP 00/159162 FILING DATE: 2000-04-07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 2000-05-26
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                                                                                                                                                                                                                                                                                                                                    FILING DATE: 1999-12-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           172 TPAAPKRRGSSGSVDETLFALP-AASEPVIR 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   115 STVPAPŚPLSAAAVSPŚKLPEDDEPPARPPPPPPPASVSPQAEPVWTPPA---PAPAAPPS 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  132 NTAHTPSPV---AVQSSRPPVQQHPAVQKPTPPVVVK---KPTPTPPVVQQPAPVAPPV 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              186 T-EAPFATGSSGVMQ---FRYPVGATNPVVR 212
 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7.1%;
1 Similarity 39.6%;
36; Conservative
                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PatentIn Ver. 2.1
                                QNQKPIKRLGLIFGVITTCILAGCASKPTYNSTSGSGSHRTSGSGGLAIGSQVITDSQGV 69
 QTTSPVTKGGVAFVAVAT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKIHIRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HAYASHI, MIKIRO
OCHIAI, KEIKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MIZOGUCHI, HIROSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                           IKEDA, MASATO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEIKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000-01-12
                                                                                    7.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8;
                                                                 Score 117; DB 9; Length 237; Pred. No. 0.1; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 118; DB 10;
Pred. No. 0.62;
8; Mismatches 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33;
 -GAVSTAGAGG-AVAAQ--ASNQPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                   108;
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                                                                 Gaps
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51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/155,400
CURRENT FILING DATE: 2002-10-22
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/10155400 Publication No. US20030108988A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: ADMEY, WILLIAM S.
APPLICANT: VINZANT, TODD B.
APPLICANT: HIMMEL, MICHAEL E.
TITLE OF INVENTION: THERWAL TOLERANT AVICELASE FROM ACIDOTHERMUS
TITLE OF INVENTION: CELLULOLYTICUS
FILE REFERENCE: NREL 01-36A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: DING, SHI-YOU APPLICANT: ADNEY, WILLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT ORGANISM: Acidothermus cellulolyticus
                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: MOD_RES
LOCATION: (957)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ENGTH:
                                                                                                                                                                                                                                                                                                                                                 Local
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                                                                                                                                                                                                 737
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          187
911 R-YWFT-RDG-----GSSTLV---YNCDWAAI 932
                                                                                                                              121 KVRERSISSGVNTAHTPSPVAVQSSRPPVQQHPAVQKPTPPVVVVKKPTP---TPPVVQQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          127
                                                                                                                                                                                                                             80 T----VSKIAQRYGLNWRE--IGHINNLNSSYTIYTGQWLTLWSGDL------
                                                                                                                                                                                                                                                                                                 34 ASKPTYNSTSGSGSHR----
                                                                                                                                                                                                                                                                                                                                1 Similarity 67; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PNRYQVKQGDTVSKIAQRYG---LNWREIGHINNLNSSYTIYTGQWLTLWSGDLKVRERS
                               NGMWFSGRDGDLINASNAGTVIQADHNMDGASI 259
                                                                                             APVAPPVTE---APFATGSSGVMQFRYPVGATNP------
                                                                                                                                                                                                TTWVLINDDQHQYG-NWGQAITGDHANLRRVYIGTNGRGIVY--GDIGGAPSGSPSPSVS
                                                                                                                                                                                                                                                                 ASSGLYHSTNGGSSWSAITGVSSAVNVGFGKSAPGSSYPAVFVVGTIGGVTGAYRSDDCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HFEVYPAGGGA-VDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -FEFRISRNGVYVDP 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VIDAGPASGFGNWVRLQHEDGTITVYGHMETVEVTVGQTVKAGERIAGMGSRGFSTGSHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VIQADHNMD-GASIVIQHTNGFVSSYIHIKDAQVKTGDTVRTGQRIASMKNQ--PSGAAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EGSYTSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EAPFATGSSGVMQFRYPVGATNPVVRRFGTATVAGSTVTSNGMWFSGRDGDLINASNAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ISSGVNTAHTPSPVAVQSSRPPVQQHPAVQKPTPPVVVVKKPTPTPPVVQQPAPVAPPVT 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EVNFELTANDTTDLVAGSSAPQILSIAEFKPVVNL--
                                                                SPSSSPSSPSPTPSSSPVSGGVKVQYKNNDSAPGDNQIKPGLQVVNTGSSSVDLSTVTV
                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                               6.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---TIQYNADRIQADLDARGPS--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       226
                                                                                                                                                                                                                                                                                                                                38; Mismatches 104;
                                                                                                                                                                                                                                                                                                 -----TSGSGGLAIGSQ-----VITDSQGVPNRYQVKQGD
                                                                                                                                                                                                                                                                                                                                               Score 112; DB 9;
Pred. No. 1.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --- NHNGVDIANAIGTPILAAMDGT
                                                                                                                                                                                                                                                                                                                                                                 Length 957;
                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                             -VVRRFGTATVAGSTVTS
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                                                                                                                                                                                                                                                                                                                                 64;
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                                                                910
                                                                                                                              850
                                                                                                                                                               178
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Sequence 1, Application US/09917383

Publication No. US20030104522A1

GENERAL INFORMATION:

APPLICANT: DING, SHI-YOU

APPLICANT: ADNEY, WILLIAM S.

APPLICANT: ADNEY, WILLIAM S.

APPLICANT: HIMMEL, MICHAEL R.

APPLICANT: HIMMEL, MICHAEL E.

APPLICANT: HIMMEL, MICHAEL E.

APPLICANT: HIMMEL, MICHAEL E.

APPLICANT: HIMMEL, MICHAEL E.

APPLICANT: HIMMEL, MICHAEL E.

APPLICANT: HIMMEL, MICHAEL E.

APPLICANT: HIMMEL, MICHAEL E.

APPLICANT: HIMMEL, MICHAEL E.

APPLICANT: HIMMEL, MICHAEL E.

APPLICANT: HIMMEL, MICHAEL E.

APPLICANT: HIMMEL, MICHAEL E.

APPLICANT: HIMMEL, MICHAEL E.

APPLICANT: APPLICATION NUMBER: US/09/917,383

CURRENT APPLICATION NUMBER: US/09/917,383

CURRENT APPLICATION NUMBER: US/09/917,383

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SOFTWARE: PATENTIN Ver. 2.1

SEQ ID NO 1

LENGTH: 1228

TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Segment of OTHER INFORMATION: Guxa
US-09-917-384-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 15
US-09-917-383-1
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Best Local
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Publication No. US20030096342A1
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APPLICANT: DING, SHI YOU

APPLICANT: ADNEY, WILLIAM S.

APPLICANT: VINZANT, TODD B.

APPLICANT: DECKER, STEPHEN R.

APPLICANT: HIMMEL, MICHAEL E.

APPLICANT: HIMMEL, MICHAEL E.

APPLICANT: HIMMEL, MICHAEL B.

APPLICANT: HIMMEL, MICHAEL B.

APPLICANT: HIMMEL, MICHAEL B.

APPLICANT: HIMMEL, MICHAEL B.

APPLICANT: HIMMEL, MICHAEL B.

CELLULASE FROM ACIDOTHERMUS

FILLE REFERENCE: 40170.61901

CURRENT APPLICATION NUMBER: US/09/917,384

CURRENT FILLNG DATE: 2001-07-28
FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Segment of
                                                                  ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              992 SRGGVQPFGSQTATGVTVAGHTWNVWQGQQTS-----WKIISYVLTPGATSISNLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51 SGSGGLAIGSQVITDSQGVPNRYQVKQGDTVSKIAQRYGLNWREIGH------INNLN 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity 24.3
65; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYVVNSDWGSGFTATVTVTNTGSRATNGWTVAWSFGGNQTVTNYWNTAL-----TQSGA 1187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PPVQQHPAVQKPTPPVVVVKKPTPTPPVVQQPAPVAPPVTEAPFATGSSGVMQFRYPVGA 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TNPVVRRFGTATVAGSTVTSNG------MWFSGRDGDLINASNAGTVIQADHNMDGA 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P-----SŚŚĠV-----ACRA 1133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----VIQ----HTNGFVSSY 271
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 112; DB Pred. No. 1.9; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                        FROM ACIDOTHERMUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1228;
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RESULT 16
US-10-101-464A-930
US-10-101-464A-930
j Sequence 930, Applicat
j Publication No. US200;
j GENERAL INFORMATION:
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CURRENT APPLICATION NUMBER: US/10/101,464A

CURRENT FILING DATE: 2002-03-18

FRIOR APPLICATION NUMBER: 09/704,302

PRIOR PILING DATE: 2000-11-01

PRIOR APPLICATION NUMBER: 09/228,986

PRIOR FILING DATE: 1999-01-12

PRIOR APPLICATION NUMBER: 60/162,866

PRIOR FILING DATE: 1999-11-01

PRIOR APPLICATION NUMBER: PCT/US00/00724

PRIOR APPLICATION NUMBER: PCT/US00/00724

PRIOR APPLICATION NUMBER: 900-01-11

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US-09-917-383-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 21.5
Matches 52; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 6.7%;
Best Local Similarity 24.3%;
Matches 65; Conservative 2
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APPLICANT: Nieuwenhuizen, Nicolaas
APPLICANT: Higgins, Colleen M.
TITLE OF INVENTION: Compositions Isolated from Plant Ce
TITLE OF INVENTION: and Their Use in the Modification
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1102
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                                                                 140 VAVQSSRPPVQQHPAVQKPTPPVVVVKKPTPTPPVVQQPAPVAPPVTBAPFATGSSGVMQ 199
                                                                                                                                                     187 NLSSITKKFGSDLQNFKSLNGMNSTLTAYT----
                                                                                                                                                                                                                                                                                                                    139 ANPTLNPTD------LQIGVQVIFPIRCKCPSQAQVKNGTKMLITYTVQPVDTH 186
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                                                                                                                                                                                                             81 -VSKIAQRYGLNWREIGHINNLNSSYTIYTGQWLTLWSGDLKVRERSISSGVNTAHTPSP 139
                                                                                                                                                                                                                                                                                                                                                                                          51 SGSGGLAIGSQVITDSQGVPNRYQVKQGDTVSKIAQRYGLNWREIGH------INNLN 102
VLVPVSQRPVLSQPVSSSPPPP---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6.6%; Score 110.5; DB 9; Length 312; 21.5%; Pred. No. 0.47; ative 20; Mismatches 51; Indels 119;
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L-amino acids

Gaps

89

144

SIS

240 163 181

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Sequence 1116, Application US/09925301

Patent No. US200220052308A1

GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Ant FILE REFERENCE: PA106
CURRENT APPLICATION NUMBER: US/09/925,301
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05882
PRIOR APPLICATION NUMBER: BO/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1694
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US-10-156-761-9957
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PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 9957
LENGTH: 258
TYPE: PRT
ORGANISM: Streptomyces avermitilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity Matches 55; Conserv
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CURRENT FILING DATE: 2002-05-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: JP 2001-204089 PRIOR FILING DATE: 2001-05-30
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OFTWARE: PatentIn Ver.
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PPLICANT: HATTORI, MASAHIRA
ITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                            215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       131 VNTAHTPSPVAVQSSRPPVQQHPAVQKPTPPVVVVKKPTPTPPVVQQPAPVAPPVTEAPF 190
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                                                                                                                                                                                                                                                                                                                                                                                            QQIGISGATGNTTGPHLHFEARTTAEYGSDIDPVAYLR 252
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                                                                                                                                                                                                                                                                                                                                                                                                                                     QR--IASMKNQPSGAAL-FEFRISRN-GVYVDPLTVLK 322
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HORIKAWA, HIROSHI
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                                                                                                                                                                                             Antibodies
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                  ; ORGANISM: Corynebacterium glutamicum US-09-738-626-3548
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                                                                        PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: Patentin ver. 3.0
SEQ ID NO 3548
LENGTH: 474
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Publication No. US20020197605A1
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Best Local
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OTHER INFORMATION: X
NAME/KEY: SITE
LOCATION: (29)
OTHER INFORMATION: X
NAME/KEY: SITE
                                                                                                                                                                                                               PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: NAKAGAWA, SATOSHI
                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES FILE REFERENCE: 249-125
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
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ORGANISM: Homo sapiens
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           182 SG-GYRRTPSVTAQFSAQPHVNGGPLYSQNSISIAPPPPPMPQLTPQIPLTGFVARVQEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        110 SLNQRPRTHSG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 IADSPTPPPPPPPDDIPMFDDSPPPPPPPPVDYEDEEAAVVQYNDPYADGDP 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                164 VVKKETETEE-----VVQQEAEVAEEVTEAEFATGSSGVMQFRYEVGATNE 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 145 -PSPPTIGPAAPGSAPGSQYGTMTRQISRHNSTTS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          69 VPNRYQVKQGDTVSKIAQRYGLNWREIGHINNLNSSYTIYTGQWLTLWSGDLKVRERSIS 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9 SQNQKPIKRIGLIFGVITTCILAGCASKPTYNSTSGSGSHRTSGSGGLAIGSQVITDSQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                              HAYASHI, MIKIRO
OCHIAI, KEIKO
YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKIHIRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SGVNTAHTPSPVAVQSSRPPVQQHP----AVQKPTPPVV---
                                                                                                                                                                                                                                                                                                                                                                                        IKEDA, MASATO
OZAKI, AKIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MIZOGUCHI, HIROSHI
ANDO, SEIKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Xaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 110;
Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   naturally occurring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 10; Length 360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 L ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SSGGSGSRENSGSSSIGIPIAVPT----
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Sequence 2. Application US/09932183A
Fatent No. US20020127641A1
GENERAL INFORMATION
REPLICAMT: Estell, David A.
TITLE OF INVENTION: Proteases From Gram-Positive Organisms
FILE REFERENCE: GC394C1-US
CURRENT APPLICATION NUMBER: US/09/932,183A
CURRENT FILING DATE: 2001-08-17
PRIOR APPLICATION NUMBER: PCT/US98/18828
PRIOR APPLICATION NUMBER: PCT/US98/18828
PRIOR FILING DATE: 1999-09-18
PRIOR APPLICATION NUMBER: E99719636.4
PRIOR APPLICATION NUMBER: E99719636.4
PRIOR FILING DATE: 1997-09-15
VOTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 2285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT ; ORGANISM: Bacillius subtilis US-09-932-183A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 20
US-09-932-183A-2
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Best Local
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Best Local :
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                                                                                                                                 1515
                                   1556 YTNNSA---FR-
                                                                                                                                                                                                                                      1456
                                                                                                                                                                                                                                                                                                                                 1398 YGIVTSTTSSGGTPSSTGGSYSGKYSSYINSAASKYNVDPALIAAVIQQESGF--NAKAR 1455
                                                                                  191
                                                                                                                                                                                   131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         318 GEIPDDAALGQSSIGQRDVQMNVLQAAVMAGTVSNGGVRMEPYLV 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             258 GQTCAGGGTTTLLTAFQLSCNTAFVETGIDVGADALRASAEDFGVGQTYSLGLDNVPGGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  218 IFKIITTAAA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              213 RFGTATVAGSTVTSNGMWFSGRDGDLINASNAGTVIQADHNMDGASIVIQHTNGFVSSY- 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                101 LN-SSYTIYTGQWLTLWSGDLKVRERSISSGVNTAHTPSPVAVQSSRPPVQQH-----P 153
                                                                                                                                                                                                                                                                                                                                                                                   22 FGVITTCILAGCASKPTYNSTSGSGSHRTSGSGGL----AIGSQVITDSQGVPNRYQVK 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity 20.3 63; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity 20.3
                                                                         ATGSSGVMQFRYPVGATNPVVRRFGTATVAGSTVTSNGMWFSGRDGDLINASNAGTVIQA 250
                                                                                                                           -----PGNVIKYGGIPPFKETONYVKKIMANYSKSLSSATSSI------ASY 1555
                                                                                                                                                                           VNTAHTPSPVAVQSSRPPVQQHPAVQKPTPPVVVVKKPTPTPPVVQQPAPVAPPVTEAPF 190
                                                                                                                                                                                                                                SGVGAMGLMQLMPATAKSLG-VNNAYDPYQNVMGGTKYLAQQLEKFGGNVEKALAAYNAG
                                                                                                                                                                                                                                                                               QGDTVSKIAQRYGLNWREIGHINNLNSSY-----TIYTGQWLTLWSGDLKVRERSISSG 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AVOKETEPVV-VVKKETETEPVVQQPAPVAPPVTEAFFATGSSGVMQFRYPVGATNEVVR 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KSTPRGQISTGGQVLAESSQDDQGFYQRSYITNPTAYAPVVGYLSDVYGAAGLELGYNSI 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALRPSTGEVLAMASSPSYDPNQIVDPATAEDAWAE----YTSTEGAPLLNHATQESLPPGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LNGSDSSLFTSQWLDVISG-----SPTHGANIELTLDPNAQQTAYEQLSQSGYEGAVV 160
                                                                                                                                                                                                                                                                                                                                                                                                                            6.5%; Score 108.5; DB 10; Length 2285;
20.3%; Pred. No. 7.6;
7ative 51; Mismatches 149; Indels 47; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----LENGYSADSTVTAE----AAVTLPGTNTTLTNYG 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Score 108.5; DB 9; ; Pred. No. 1.1; 49; Mismatches 123;
                             VSSKYGQQESGLRSSPHKGTDFAAKAGTAIKSLQSGKVQIA 1604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----AALFEFRISRNGVYVDPLTV 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 474;
                                                                                                                                                                                                                                1514
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NUMBER OF SEQ ID N
SEQ ID NO 90
LENGTH: 877
TYPE: PT
OCGANISM: Homo Sa:
US-10-245-103-90
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US-10-245-103-90
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                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: PS-630R1C112

CURRENT APPLICATION NUMBER: US/10/245,103

CURRENT FILING DATE: 2002-09-17

PRIOR APPLICATION NUMBER: 10/19942

PRIOR FILING DATE: 2002-07-18

PRIOR PILING DATE: 2002-07-18

PRIOR PILING DATE: 60/059114

PRIOR APPLICATION NUMBER: 60/065014

PRIOR FILING DATE: 1997-09-17

PRIOR PILING DATE: 1997-10-24

PRIOR PILING DATE: 1997-10-24

PRIOR APPLICATION NUMBER: 60/065027

PRIOR APPLICATION NUMBER: 60/065027

PRIOR PILING DATE: 1997-11-10

PRIOR PILING DATE: 1997-11-10

PRIOR PILING DATE: 1997-11-10

PRIOR PILING DATE: 1997-11-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/086478
PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR PILING DATE: 1998-06-02
PRIOR PILING DATE: 1998-06-02
PRIOR PILING DATE: 1998-06-02
PRIOR PILING DATE: 1998-06-02
PRIOR PILING DATE: 1998-06-02
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PRIOR APPLICATION NUMBER: 60/090689
PRIOR FILING DATE: 1998-06-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 60/090557
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1665 İEQNGKTIDP 1674
                                                                            501
                                                                                                                                                                           446 GAPDICVAGRCLS-PGCDGILGSG-RRPDGCGVCGGDDSTCRLVSGN--LTD-RGGPLGY
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                                                                                                                                                                                                                          23 GVITTCILAGCASKPTYNSTSGSGSHRTSGSG------GLAIGSQVITDSQGVPNRY 73
                                                                                                                                                                                                                                                                                  64;
----TLWSGDLKVRERSISSGVNT-AHTPSPVAV----QSSRPPVQQHPAVQKPTPPVVV 164
                                                                                                                        Q----VKQGDTVSKIAQRYGLNWREIGHINNLNSSY-----TIYTGQWL-----
                                                                      QKILWIPAGALRLQIAQL------RPSSNYLALRGPGGRSIINGNWAVDPPGSY 548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ISRNGVYVDP 317
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Grimaldi, J. Christopher
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Stephan, Jean-Phillippe Watanbe, Colin Wood, William
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                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                            6.5%; Score 108; DB 9; Length 877; 24.4%; Pred. No. 2.6; tive 28; Mismatches 94; Indels
                                                                                                                                                                                                                                                                         28;
                                                                                                                                                                                                                                                                               76;
                                                                                                                                                                                                                                                                            Gaps
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LENGTH: 877
TYPE: PRT
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Best Local (
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                                                                                                                                            Matches
                                                                                                                                                                                                                 ORGANISM: Homo Sapien
-10-245-107-90
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CURRENT APPLICATION NUMBER: US/10/245,107
CURRENT FILING DATE: 2002-09-16
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APPLICATION NUMBER: 60/079689
FILING DATE: 1998-03-27
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APPLICATION NUMBER: 60/059114
FILING DATE: 1997-09-17
                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 60/090557 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090689
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FILING DATE: 1998-06-18
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501 QKILWIPAGALRLQIAQL-------RPSSNYLALRGPGGRSIINGNWAVDPPGSY 548
                                                                     446 GAPDICVAGRCLS
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                                 74 Q----TIYTGQWL-----
                                                                                                     23 GVITTCILAGCASKPTYNSTSGSGSHRTSGSG-----GLAIGSQVITDSQGVPNRY 73
                                                                                                                                          64; Conservative
                                                                                                                                                         Similarity
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                                                                     -PGCDGILGSG-RRPDGCGVCGGDDSTCRLVSGN--LTD-RGGPLGY
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; Pred. No. 2.6;
28; Mismatches 94
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                                                                                                                                                                          Length 877;
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US-10-245-143-90
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US-10-245-143-90
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                                                                                                                               Matches
                                                                                                                                                Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/245,143
CURRENT FILING DATE: 2002-09-16
PRIOR APPLICATION NUMBER: 10/197942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3630R1C90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 60/059114
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/063046
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                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 60/090689
FILING DATE: 1998-06-25
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                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 60/089801
FILING DATE: 1998-06-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 1998-03-27
                                                      446 GAPDICVAGRCLS-PGCDGILGSG-RRPDGCGVCGGDDSTCRLVSGN--LTD-RGGPLGY 500
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74 Q----VKQGDTVSKIAQRYGLNWREIGHINNLNSSY------TIYTGQWL------
                                                                                                                                                                                                                                                                                                                                                                                                                                                      LING DATE: 1998-06-02
                                                                                                                                                Similarity
                                                                                          GVITTCILAGCASKPTYNSTSGSGSHRTSGSG--
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                                                                                                                                                Score 108;
Pred. No. 2
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TITLE OF INVENTION: SCRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3503R1C98
CURRENT APPLICATION NUMBER: US/10/245,771
CURRENT FILING DATE: 2002-09-16
PRIOR APPLICATION NUMBER: 10/197942
PRIOR FILING DATE: 2002-07-18
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059114
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/063046
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/065027
PRIOR APPLICATION NUMBER: 60/07669
PRIOR FILING DATE: 1998-03-27
PRIOR FILING DATE: 1998-03-27
PRIOR FILING DATE: 1998-03-27
PRIOR FILING DATE: 1998-05-22
PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/086478
PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/080607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/080607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/080601
PRIOR FILING DATE: 1998-06-02
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/080601
PRIOR FILING DATE: 1998-06-02
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/080601
PRIOR FILING DATE: 1998-06-02
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/080601
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US-10-245-771-90
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                                                                                                                                                                                Query Match
Best Local
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                                 446 GAPDICVAGRCLS-PGCDGILGSG-RRPDGCGVCGGDDSTCRLVSGN--LTD-RGGPLGY 500
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                                                                                 23 GVITTCILAGCASKPTYNSTSGSGSHRTSGSG------GLAIGSQVITDSQGVPNRY 73
                                                                                                                                          h 6.5%; Score 108; DB Similarity 24.4%; Pred. No. 2.6; 64; Conservative 28; Mismatches
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Stephan, Jean-Phillippe
Watanbe, Colin
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Grimaldi, J. Christopher
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to. US20030068781A1
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CURRENT APPLICATION NUMBER: US/10/245,851
CURRENT FILING DATE: 2002-09-16
PRIOR APPLICATION NUMBER: 10/19942
PRIOR APPLICATION NUMBER: 0/19942
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR PILING DATE: 1997-10-14
PRIOR FILING DATE: 1997-10-24
PRIOR PILING DATE: 1997-10-10
PRIOR APPLICATION NUMBER: 60/065027
PRIOR PILING DATE: 1997-11-10
PRIOR APPLICATION NUMBER: 60/066027
PRIOR PILING DATE: 1998-01-27
PRIOR PILING DATE: 1998-01-27
PRIOR PILING DATE: 1998-05-29
PRIOR PILING DATE: 1998-05-29
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                                                                                                                                                                                                    ORGANISM: Homo Sapien US-10-245-851-90
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US-10-245-851-90
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                                                                                        Matches
                                                                                 Query Match
Query Match
Best Local Similarity 24.4%; Pred. No. 2.6,
Matches 64; Conservative 28; Mismatches
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APPLICANT:
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PRIOR FILING DATE: 1998-06-25
Remaining Prior Application data re
NUMBER OF SEQ ID NOS: 116
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APPLICANT: Baton, Dan
APPLICANT: Filvaroff, F
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                                                                                                                                                                                                                                                                                            LENGTH:
                                                                                                                                                                                                                                                              ID NO 90
ENGTH: 877
YPE: PRT
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23 GVITTCILAGCASKPTYNSTSGSGSHRTSGSG------GLAIGSQVITDSQGVPNRY 73
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Smith, Victoria
Stephan, Jean-Phillippe
Watanbe, Colin
Wood, William
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Grimaldi, J. Christopher
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                                                                                                                                    Length 877;
                                                                                 Indels
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RESULT 26
US-10-245-883-90
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                                                                                                ; ORGANISM: Homo Sapien
US-10-245-883-90
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Publication No.
Query Match
Best Local Similarity 24.4
Conservative
                                                                                                                                                                         Remaining Prior I
NUMBER OF SEQ ID
SEQ ID NO 90
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APPLICANT:
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CURRENT APPLICATION NUMBER: US/10/245,883
CURRENT FILING DATE: 2002-09-16
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                                                                                                                                     LENGTH: 87
TYPE: PRT
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OR FILING DATE: 1997-09-17
OR APPLICATION NUMBER: 60/063046
OR FILING DATE: 1997-10-24
OR APPLICATION NUMBER: 60/065027
OR FILING DATE: 1997-11-10
                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 60/079689 FILING DATE: 1998-03-27 APPLICATION NUMBER: 60/086478
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                                                                                                                                                                                                                                      APPLICATION NUMBER: 60/090689
FILING DATE: 1998-06-25
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                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 60/090557
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                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 1998-05-22
                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 60/089801
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Godmaldi, J. Christopher
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Watanbe, Colin
Wood, William
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                                                                                                                                                                                                Application data removed - See File Wrapper or PALM
D NOS: 116
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                                                                                                                                                                                                                                                                                                                     1998-06-18
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              6.5%; Score 108; DB 9; Length 877; 24.4%; Pred. No. 2.6; tive 28; Mismatches 94; Indels
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                76;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 60/059114
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/063046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/10/237,535
CURRENT ETLING DATE: 2002-09-06
PRIOR APPLICATION NUMBER: 10/197942
PRIOR FILING DATE: 2002-07-18
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                                                  DR FILING DATE: 1998-07-01

R APPLICATION NUMBER: 60/091978

DR FILING DATE: 1998-07-07

DR APPLICATION NUMBER: 60/099803

DR FILING DATE: 1998-09-10

DR APPLICATION NUMBER: 60/106932
                                                                                                                                                                                                                                                                         OR FILING DATE: 1998-03-27

OR APPLICATION NUMBER: 60/086478

OR FILING DATE: 1998-05-22

OR PILICATION NUMBER: 60/087607

OR FILING DATE: 1998-06-02

OR APPLICATION NUMBER: 60/089801

OR FILING DATE: 1998-06-18
                                                                                                                                                                                                            APPLICATION NUMBER: 60/090557
FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090689
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FILING DATE: 1997-11-10
                APPLICATION :
                                                                                                                                                                         APPLICATION NUMBER: 60/091358
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No. US20030073188A1
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Watanbe, Colin
Wood, William
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Grimaldi, J. Christopher
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: SECRETED AND TRANSMEM TITLE OF INVENTION: ACIDS ENCODING THE S. FILE REFERENCE: P3630R1C11
CURRENT APPLICATION NUMBER: US/10/238,183
CURRENT FILING DATE: 2002-09-09
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FILING DATE: 2002-02-20
APPLICATION NUMBER: 10/119480
FILING DATE: 2002-04-09
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Grimaldi, J. Christopher
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Filvaroff, Ellen
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Pred. No. 2
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red. No. 2.6;
Mismatches 94;
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FILING DATE: 1999-03-12
APPLICATION NUMBER: 60/123972
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APPLICATION NUMBER: 60/127372
                                                                                FILING DATE: 2000-01-20
APPLICATION NUMBER: 60/179851
FILING DATE: 2000-02-02
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APPLICATION NUMBER: 60/149327
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APPLICATION 1
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APPLICATION NUMBER: 60/146222
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APPLICATION I
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FILING DATE: 1999-06-23
APPLICATION NUMBER: 60/144732
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APPLICATION NUMBER: 60/
FILING DATE: 1999-06-22
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APPLICATION NUMBER: 60/138385
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FILING DATE: 1999-05-25
APPLICATION NUMBER: 60/135729
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FILING DATE: 1999-05-11
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FILING DATE: 1999-01-12
APPLICATION NUMBER: 60/119342
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FILING DATE: 1998-09-10
APPLICATION NUMBER: 60/106932
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APPLICATION NUMBER: 60
FILING DATE: 2000-04-11
APPLICATION NUMBER: 60

NUMBER:

60/198587 /199614

DR FILLING DATE: 2000-06-05
DR FILLING DATE: 2000-07-13
DR FILLING DATE: 2000-07-13
DR FILLING DATE: 2000-08-02
DR APPLICATION NUMBER: 60/222695
DR FILLING DATE: 2000-09-03
DR FILLING DATE: 2000-09-05
DR FILLING DATE: 2000-09-05
DR APPLICATION NUMBER: 60/230621
DR APPLICATION NUMBER: 60/235147
DR APPLICATION NUMBER: 60/235147
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DR APPLICATION NUMBER: 60/26421

FILING DATE: 2000-05-23
APPLICATION NUMBER: 60/209832 APPLICATION NUMBER: 60/206368 FILING DATE: 2000-04-25
APPLICATION NUMBER: 60/206330

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APPLICANT: Eaton, Dan
APPLICANT: Eaton, Dan
APPLICANT: Eaton, Dan
APPLICANT: Gridard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
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APPLICANT: Goddard, Audrey
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APPLICANT: Goddard, Audrey
APPLICANT: Smith, Victoria
APPLICANT: Watanbe, Colin
APPLICANT: Watanbe, Colin
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APPLICANT: Watanbe, Colin
APPLICANT: Fong, Sherman
APPLICANT: Fong, Sherman
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APPLICANT: FONG, Sherman
APPLICANT: FONG, Sherman
APPLICANT: FONG, Sherman
APPLICANTON NUMBER: US/10/238, 283
CURRENT APPLICATION NUMBER: US/10/238, 283
CURRENT APPLICATION NUMBER: 10/19742
PRIOR APPLICATION NUMBER: 60/059114
PRIOR APPLICATION NUMBER: 60/059114
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PRIOR APPLICATION NUMBER: 60/059114
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/05027
PRIOR APPLICATION NUMBER: 60/065027
PRIOR APPLICATION NUMBER: 60/079689
PRIOR APPLICATION NUMBER: 60/079689
PRIOR APPLICATION NUMBER: 60/086478
PRIOR APPLICATION NUMBER: 60/086478
PRIOR APPLICATION NUMBER: 60/086478
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US-10-238-283-90
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Matches 64
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OR FILING DATE: 1999-03-12
OR APPLICATION NUMBER: 09/380137
OR FILING DATE: 1999-08-25
OR APPLICATION NUMBER: 09/380138
OR FILING DATE: 1999-10-18
OR FILING DATE: 1999-10-18
OR APPLICATION NUMBER: 09/403297
OR FILING DATE: 1999-11-10
OR APPLICATION NUMBER: 09/802706
OR APPLICATION NUMBER: 09/802706
OR APPLICATION NUMBER: 09/802706
OR APPLICATION NUMBER: 09/872035
OR FILING DATE: 2001-03-09
OR APPLICATION NUMBER: 09/918585
OR FILING DATE: 2001-06-01
OR APPLICATION NUMBER: 09/918585
OR FILING DATE: 2001-07-30
OR APPLICATION NUMBER: 09/924419
OR APPLICATION NUMBER: 09/927796
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FILING DATE: 2001-04-04
APPLICATION NUMBER: 60/290589
FILING DATE: 2001-05-09
APPLICATION NUMBER: 09/180997
FILING DATE: 1998-11-19
APPLICATION NUMBER: 09/267213

FILING DATE: 2001-04-04
APPLICATION NUMBER: 60/282199
FILING DATE: 2001-04-04

APPLICATION NUMBER: 60/282129 FILING DATE: 2001-03-09 APPLICATION NUMBER: 60/280982

2001-04-03

APPLICATION NUMBER: FILING DATE: 2001-0

2001-02-09

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APPLICATION NUMBER:

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US-10-238-283-90
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Publication No.
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APPLICANT:
APPLICANT:
                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/238,370
CURRENT FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: 10/197942
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                                                                                                                                                                                                           TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3630R1C10
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                                                                                                                                    PRIOR FILING DATE: 2002-07-18
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                                                        APPLICATION NUMBER: 60/063046 FILING DATE: 1997-10-24
                                                                                               APPLICATION NUMBER: 60/059114 FILING DATE: 1997-09-17
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FILING DATE: 1998-06-02
APPLICATION NUMBER: 60/089801
FILING DATE: 1998-06-18
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                APPLICATION NUMBER: 60/065027
FILING DATE: 1997-11-10
APPLICATION NUMBER: 60/079689
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                                                                                                                                                                                                                                                                            Fong, Sherman
                                                                                                                                                                                                                                                                                                                                Smith, Victoria
Stephan, Jean-Phillippe
Watanbe, Colin
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                                                                                                                                                                                                                                                                                            Zhang, Zemin
                                                                                                                                                                                                                                                                                                                  Wood, William
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Pred. No. 2
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; LENGTH: 877
; TYPE: PRT
; ORGANISM: Homo S
US-10-238-370-90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 90, Application US/10245055 Publication No. US20030073192A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Remaining Prior Application
NUMBER OF SEQ ID NOS: 116
SEQ ID NO 90
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                                                 CURRENT APPLICATION NUMBER: US/10/245,055
CURRENT FILING DATE: 2002-09-16
PRIOR APPLICATION NUMBER: 10/197942
PRIOR FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/059114
PRIOR FILING DATE: 1997-09-17
                                   PRIOR APPLICATION NUMBER: 60/063046
                                                                                                                                                         TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3630R1C88
                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
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PRIOR PILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
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FILING DATE: 1997-10-24
APPLICATION NUMBER: 60/065027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 60/090557
FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090689
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----TLWSGDLKVRERSISSGVNT-AHTPSPVAV----QSSRPPVQQHPAVQKPTPPVVV 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QKILWI PAGALRLQIAQL------RPSSNYLALRGPGGRSI INGNWAVDPPGSY
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                                                                                                                                                                                                               Fong, Sherman
                                                                                                                                                                                                                                                Stephan, Jean-Phillippe Watanbe, Colin Wood, William
                                                                                                                                                                                                                                                                                                        Smith, Victoria
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Grimaldi, J. Christopher
                                                                                                                                                                                                                                                                                                                                                                                             Eaton, Dan
                                                                                                                                                                                                                                Zhang, Zemin
                                                                                                                                                                                                                                                                                                                                                                            Filvaroff, Ellen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94;
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                                                                                                                                                                                              NUCLEIC
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; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-245-055-90
APPLICANA: "TOTAL APPLICANA": POOLYPEPTIDES AND NUCLEIC REPLICANT: PONG Sherman
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
CURRENT APPLICATION NUMBER: US/10/245,147
CURRENT FILING DATE: 2002-09-16
PRIOR APPLICATION NUMBER: 10/197942
PRIOR FILING DATE: 2002-07-18
PRIOR FILING DATE: 2002-09-16
PRIOR APPLICATION NUMBER: 60/059114
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/063046
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PRIOR PILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/086478
PRIOR FILING DATE: 1998-05-22
PRIOR PELICATION NUMBER: 60/087607
PRIOR PILING DATE: 1998-06-07
PRIOR PILING DATE: 1998-06-07
PRIOR APPLICATION NUMBER: 60/089801
PRIOR PILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090689
PRIOR APPLICATION NUMBER: 60/090689
PRIOR APPLICATION NUMBER: 60/090689
PRIOR APPLICATION NUMBER: 60/090689
PRIOR APPLICATION NUMBER: 60/090689
PRIOR FILING DATE: 1998-06-25
PRIOR FILING DATE: 1998-06-25
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Best Local S
Matches 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 90, Appublication No.
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NUMBER OF SEQ ID NOS: 116
EQ ID NO 90
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Similarity 24.4%; Pred. No. 2.6;
64; Conservative 28; Mismatches 94; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PVVRRFGTATVAGSTVTSNGMW 230
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Smith, Victoria
Stephan, Jean-Phillippe
Watanbe, Colin
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Grimaldi, J. Christopher
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PRIOR FILING DATE: 1997-11-10
PRIOR FILING DATE: 1998-03-27
PRIOR FILING DATE: 1998-03-27
PRIOR FILING DATE: 1998-03-27
PRIOR FILING DATE: 1998-03-27
PRIOR PELICATION NUMBER: 60/086478
PRIOR PELICATION NUMBER: 60/087607
PRIOR APPLICATION NUMBER: 60/089901
PRIOR APPLICATION NUMBER: 60/089901
PRIOR PILING DATE: 1998-06-18
PRIOR PILING DATE: 1998-06-24
PRIOR PILING DATE: 1998-06-24
PRIOR PILING DATE: 1998-06-24
PRIOR PILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090689
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APPLICANT: Baker, Kevin
APPLICANT: Eatcon, Dan
APPLICANT: Grimandi, Ju
APPLICANT: Grimaldi, Ju
APPLICANT: Grimaldi, Ju
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US-10-245-730-90
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; ORGANISM: Homo Sapien
US-10-245-147-90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 90, Application US/10245730 Publication No. US20030073194A1 GENERAL INFORMATION:
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Best Local
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Grimaldi, J. Christopher
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APPLICANT: Gurney, Austin
APPLICANT: Smith, Victoria
APPLICANT: Scephan, Jean-Phillippe
APPLICANT: Stephan, Jean-Phillippe
APPLICANT: Watanbe, Colin
APPLICANT: Watanbe, Colin
APPLICANT: Mood, William
APPLICANT: Pong, Sherman
ITITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND
ITITLE OF INVENTION: ACIDS ENCODING THE SAME
ITITLE OF INVENTION: ACIDS ENCODING THE SAME
CURRENT APPLICATION NUMBER: US/10/245,730
CURRENT APPLICATION NUMBER: US/10/245,730
CURRENT APPLICATION NUMBER: 10/197942
PRIOR APPLICATION NUMBER: 60/059114
PRIOR APPLICATION NUMBER: 60/059114
PRIOR APPLICATION DATE: 1997-09-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  501 QKILWIPAGALRLQIAQL-------RPSSNYLALRGPGGRSIINGNWAVDPPGSY 548
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Publication No.
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                                                                                                                             APPLICANT:
 CURRENT APPLICATION NUMBER: US/10/245,739
                                      FILE REFERENCE: P3630R1C86
                                                   TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
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                                                                                                              PPLICANT:
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                                                                                                                                                                                                                                                                                             PPLICANT: Baker, Kevin
                                                                                         PPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ENGTH: 877
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Local Similarity 24.4%;
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                                                                                                                           Smith, Victoria
Stephan, Jean-Phillippe
Watanbe, Colin
Wood, William
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2002-09-1
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    See File Wrapper or PALM

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NUMBER OF SEQ ID NOS: 116
SEQ ID NO 90
LENGTH: 877
                                                                                                                                                                                                                                                                                                                      Sequence 90, Application US/10246210 Publication No. US20030073196A1
                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION
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                                           TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE TITLE OF INVENTION: ACIDS ENCODING THE SAME
                                                                                                                                                                                                                                                                                    APPLICANT: Baker, Kevin
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FILING DATE: 1998-06-18
APPLICATION NUMBER: 60/090557
FILING DATE: 1998-06-24
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Grimaldi, J. Christopher
Gurney, Austin
Smith, Victoria
                                                                                    Fong, Sherman
                                                                                                                                     Stephan, Jean-Phillippe
Watanbe, Colin
                                                                                                     Zhang, Zemin
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                                                                                                                        Wood,William
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           P3630R1C121
FION NUMBER: US/10/246,210
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2002-09-18
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Pred. No. 2.6;
28; Mismatches
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RESULT 36
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US-10-246-210-90
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PRIOR FILING DATE: 2002-07-18
PRIOR PPLICATION NUMBER: 60/059114
PRIOR PPLICATION NUMBER: 60/059114
PRIOR FILING DATE: 1997-09-17
PRIOR PRIOR PLING DATE: 1997-10-24
PRIOR PRIOR PLING DATE: 1997-10-24
PRIOR PRIOR APPLICATION NUMBER: 60/05027
PRIOR PRIOR DATE: 1997-11-10
PRIOR PPLICATION NUMBER: 60/079689
PRIOR APPLICATION NUMBER: 60/086478
PRIOR PPLICATION NUMBER: 60/086478
PRIOR PPLICATION NUMBER: 60/087607
PRIOR PILING DATE: 1998-05-22
PRIOR PILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/089801
PRIOR APPLICATION NUMBER: 60/090557
PRIOR APPLICATION NUMBER: 60/090557
PRIOR APPLICATION NUMBER: 60/090689
PRIOR PILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090689
PRIOR PILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090689
PRIOR FILING DATE: 1998-06-25
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APPLICANT:
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Best Local
TITLE OF INVENTION: SECRETED AND TRANSMEMERANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3630R1C8
                                                                                                                                                                                                                                                   APPLICANT: Baker, Kevin
APPLICANT: Eaton, Dan
APPLICANT: Filvaroff, F
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                                                                                                      Goddard, Audrey
Grinaldi, J. Christopher
Griney, Austin
Smith, Victoria
Stephan, Jean-Phillippe
Watanbe, Colin
Wood, William
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                                                                                                                                                                                                                                                      Filvaroff, Ellen
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                                                                                     Zemin
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CURRENT APPLICATION NUMBER: US/10/239,196
CURRENT FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: 10/197942
PRIOR FILING DATE: 2002-07-18
PRIOR FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/059114
PRIOR APPLICATION NUMBER: 60/063046
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/079689
PRIOR FILING DATE: 1997-11-10
PRIOR APPLICATION NUMBER: 60/086478
PRIOR APPLICATION NUMBER: 60/086478
PRIOR APPLICATION NUMBER: 60/08667
PRIOR APPLICATION NUMBER: 60/08667
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/090689
PRIOR APPLICATION NUMBER: 60/090689
PRIOR APPLICATION NUMBER: 60/090689
PRIOR APPLICATION NUMBER: 60/090689
PRIOR APPLICATION NUMBER: 60/090689
PRIOR PILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090689
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090689
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US-10-243-024-90
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; Publication No. US2003007
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
APPLICANT: Eaton, Dan
; APPLICANT: Filvaroff, El
; APPLICANT: Goddard, Audr
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; ORGANISM: Homo Sapien
US-10-239-196-90
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INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
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Smith, Victoria
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Grimaldi, J. Christopher
                                           Zhang, Zemin
Fong, Sherman
                                                                                                             Stephan, Jean-Phillippe Watanbe, Colin Wood, William
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No. US20030077741A1
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RESULT 38
US-10-243-409-90
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US-10-243-024-90
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Publication No.
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Best Local (
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                                       APPLICANT:
APPLICANT:
APPLICANT:
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                                                                                                                 APPLICANT:
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CURRENT FILING DATE: 2002-09-12
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FILING DATE: 1997-10-24
APPLICATION NUMBER: 60/065027
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APPLICATION NUMBER: 60/059114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 60/079689
                                                                                                                                                                        INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         549 RAGGTVFRYNRPPREEGKGESLSAEGPTTQPVDVYMIFQEENPGVFYQYVISSPPP---I
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Similarity 24.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                  VKKPTPTPPVVQ-QP--APVAPPVTEAPFATGSSGVMQF------RYPVGATN 208
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                                                                                                                                                                                                                                                                                                                                         PVVRRFGTATVAGSTVTSNGMW
                                                                                                                                                                                      Application US/10243409 No. US20030077742A1
                                       Gurney, Austin
Smith, Victoria
                                                                        Goddard, Audrey
Grimaldi, J. Christopher
Stephan, Jean-Phillippe
Watanbe, Colin
                                                                                                                 Filvaroff,Ellen
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GENERAL INFORMATION:

APPLICANT: Baker, Kevin

APPLICANT: APPLICANT: APPLICANT:

Goddard, Audrey Grimaldi, J. Christopher

Eaton, Dan Filvaroff, Ellen

APPLICANT:

APPLICANT:

PPLICANT:

PPLICANT:

Gurney, Austin Smith, Victoria Stephan, Jean-Phillippe Watanbe, Colin Sequence 90, Application US/10245033 Publication No. US20030078401A1

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RESULT 39
US-10-245-033-90
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US-10-243-409-90
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NUMBER OF SEQ ID NOS: 116
SEQ ID NO 90
LENGTH: 877
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Best Local Similarity
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PRIOR FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/059114
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/063046
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CURRENT FILING DATE: 2002-09-12
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
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PRIOR APPLICATION NUMBER: 60/065027
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 60/089801 FILING DATE: 1998-06-18
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Pred. No. 2.6;
28; Mismatches
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RESULT 40
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CURRENT FILING DATE: 2002-09-16
PRIOR APPLICATION NUMBER: 10/197942
PRIOR FILING DATE: 2002-07-18
PRIOR FILING DATE: 2002-07-18
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/05914
PRIOR TILING DATE: 1997-10-24
PRIOR PRILING DATE: 1997-10-24
PRIOR PRILING DATE: 1997-11-10
PRIOR APPLICATION NUMBER: 60/05627
PRIOR APPLICATION NUMBER: 60/07689
PRIOR PILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/086478
PRIOR PILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/087607
PRIOR APPLICATION NUMBER: 60/087607
PRIOR APPLICATION NUMBER: 60/089801
PRIOR PILING DATE: 1998-06-02
PRIOR PILING DATE: 1998-06-02
PRIOR PILING DATE: 1998-06-01
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PRIOR PILING DATE: 1998-06-02
                                                                                                                                                                 Sequence 90, Application Publication No. US200300 GENERAL INFORMATION:
APPLICANT: Baker, Kevin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Remaining Prior Application data removed - See
NUMBER OF SEQ ID NOS: 116
SEQ ID NO 90
LENGTH: 877
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PRIOR FILING DATE: 1998-06-25
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PPLICANT: FONG, Sherman
PPLICANT: FONG, Sherman
FITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FITLE OF INVENTION: ACIDS ENCODING THE SAME
FITLE REFERENCE: P363GRIC84
FITLE REFERENCE: P363GRIC84
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Goddard, Audrey
Grimaldi, J. Christopher
Gurney, Austin
Smith, Victoria
                                                                                                            Eaton, Dan
Filvaroff, Ellen
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to US20030077743A1
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PRIOR FILING DATE: 2002-07-18
PRIOR PELICATION NUMBER: 60/059114
PRIOR PELICATION NUMBER: 60/05914
PRIOR PELING DATE: 1997-09-17
PRIOR PELING DATE: 1997-0-24
PRIOR PELING DATE: 1997-10-24
PRIOR PELING DATE: 1997-10-24
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PRIOR PELING DATE: 1998-03-27
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PRIOR APPLICATION NUMBER: 60/09057
PRIOR APPLICATION NUMBER: 60/09057
PRIOR PILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/09057
PRIOR PILING DATE: 1998-06-24
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Matches 64; Conserv
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NUMBER OF SEQ ID NOS: 116
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LENGTH: 877
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CURRENT APPLICATION NUMBER: US/10/245,621
CURRENT FILING DATE: 2002-09-17
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Watanbe, Colin
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Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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4: pir4:*
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(c) 1993 - 2003 Compugen Ltd
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ALIGNMENTS

conserved hypothetical protein PA3623 [imported] - Pseudomonas aeruginosa C;Species: Pseudomonas aeruginosa C;Decies: Pseudomonas aeruginosa C;Date: 27-Oct.1996 #sequence_revision 13-Mar-1997 #text_change 31-Dec-2000 C;Accession: S55063; E83193

RESULT S55063

A;Molecule Type: DNA
A;Rosidues: 1-297 <TAN)
A;Cross-references: EMBL:D26134; NID:g440375; PIDN:BAA05130.1; PID:g440377
A;Cross-references: EMBL:D26134; NID:g440375; PIDN:BAA05130.1; PID:g440377
A;Cross-references: EMBL:D26134; NID:g440375; PIDN:BAA05130.1; PID:g440377
A;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Briadman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, i. Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathog A; Reference number: A82950; MUID:20437337; PMID:10984043
A;Status: preliminary
A;Molecule type: DNA
A;Status: preliminary
A;Molecule type: DNA Ś A;Gene: PA3623 C;Superfamily: lipoprotein D A;Residues: 1-297 <STO> A;Cross-references: GB:AE004782; GB:AE004091; NID:g9949772; PIDN:AAG07011.1; GSPDB:GN001: A;Experimental source: strain PAO1 R;Tanaka, K.; Takahashi, H. Gene 150, 81-85, 1994 A;Title: Cloning, analysis and expression of an rpoS homologue A;Reference number: S55062; MUID:95047554; PMID:7959068 S 밁 망 Ś 片 Ś 밁 S A; Accession: S55063 A;Status: preliminary Query Match
Best Local Similarity ;Genetics: Matches 185 239 INASNAGTVIQADHNMDGAS--IVIQHTNGFVSSYIHIKDAQVKTGDTVRTGQRIASMKN 133 TAHTESEVAVQ-SSREEVQQHPAVQKETEEVV--VVKKETETEEVVQ-----QPAEVAEE 184 69 73 YQVKQGDTVSKIAQRYGLNWREIGHINNLNSSYTIYTGQWLTLWSGDLKVRERSISSGVN 132 25 20 LIFGVITTCILAGCASKP-----TYNSTSGSGSHRTSGSGGLAIGSQVITDSQGVPNR VTEAPFATGSSGVMQ-----FRYPVGATNPVVRRFGTATVAGSTVTSNGMWFSGRDGDL LLLGAVVCSLLAACSSSPPGGVKVVDRNGSAPAARRTPVTSG-----Q STTTPPSSGATPVVAGPAVGGWAWPASGT--LIGRF----ASNGSLNKGIDIAGQLGQP -----AIOFGGRASTO--PSVAKNTPVVAAPVATKPTPVPPAVSTSVPAKPAP-APA 156 YIVRRGDTLYSIAFRFGWDWKALAARNGIAPPYTIQVGQ----Conservative 17.8%; Score 298; DB 2; 28.0%; Pred. No. 2.7e-14; tive 50; Mismatches 106 106; Indels Length 297; gene from Pseudomonas aeru 78; Gaps 107 83

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lipoprotein XF0855 [imported] - Xylella fastidiosa (strain 9a5c)
()Species: Xylella fastidiosa
()Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
(;Accession: A82754
R;Anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide R;Anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide R;Aritle: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Tetle: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:2035717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
A;Accession: A82754
A;Accession: A82754
A;Coss-references: GB:AE003925; GB:AE003849; NID:g9105758; PIDN:AAF83665.1; GSPDB
A;Experimental source: strain 9a5c
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A;Cross-refer
A;Experimenta
C;Genetics:
A;Gene: nlpD
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A;Accession: T50918
A;Status: prelimina:
A;Molecule type: DN/
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I Similarity 25.6%; Pred. No. 4.2e-12;
84; Conservative 43; Mismatches 161;
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ce: strain 9a5c
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     NID:g9105758; PIDN:AAF83665.1; GSPDB:GN00:
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A;Status: preliminary; nucleic acid sequence not shown; translation not snown A;Molecule type: DNA A;Residues: 1-259 < BLAT'>
A;Residues: 1-259 < BLAT'>
A;Cross-references: GB:AE000369; GB:U00096; NID:g2367168; PIDN:AAC75903.1; PID:g1789228; A;Experimental source: strain K-12, substrain MG1655
C;Superfamily: lipoprotein D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; I.A.; Kose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: A65070
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C;Species: Escherichia coli
C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
C;Accession: A65070
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submitted to GenBank, June 2000

A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohme J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigre Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marrino, C.L.; Marques, M.V.; Martins, E. A.Authors: Martins, E.M.F.; Matkuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; P.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A., P.G.; Nunes, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasaki, Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Za, A.Confartica, A.S.; Vettore, A.L.; Za, A.Confartica, A.S.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Za, A.Confartica, A.S.; Vettore, A.L.; Za, A.Confartica, A.S.; Vettore, A.L.; Za, A.Confartica, A.S.; Vettore, A.L.; Za, A.Confartica, A.S.; Vettore, A.L.; Za, A.Confartica, A.S.; Vettore, A.L.; Za, A.Confartica, A.S.; Vettore, A.L.; Za, A.Confartica, A.S.; Vettore, A.L.; Za, A.Confartica, A.S.; Vettore, A.L.; Za, A.Confartica, A.S.; Vettore, A.L.; Za, A.Confartica, A.C.; A.S.; Vettore, A.L.; Za, A.Confartica, A.S.; Vettore, A.L.; Za, A.Confartica, A.S.; Vettore, A.L.; Za, A.Confartica, A.S.; Vettore, A.L.; Za, A.Confartica, A.S.; Vettore, A.L.; Za, A.Confartica, A.S.; Vettore, A.L.; Za, A.Confartica, A.C.; A.S.; Vettore, A.L.; Za, A.Confartica, A.C.; A.C.; A.C.; A.C.; A.C.; A.C.; A.C.; A.C.; A.C.; A.C.; A.C.; A.C.; A.C.; A.C.; A.C.; A.C.; A.C.; A.C.; A.C.; A.C.; A.C.; A.C.; A.C.; A.C.; A.C.; A.C.; A.C.; A.C.; A.C.; A.C.; A.C.; A.C.; A.C.; A.C.; A.C.; A.C.; A.C.; A.C.; A.C.; A.C.; A.C.; A.C.; A.C.; A.C.; A.C.; A.C.; A.C.; A.C.; A.C.; A.C.; A.C.; A.C.; A.C.; A.C.; A.C.; A.C.; A.C.; A.C.; A.C.; A.C.; A.C.; A.C.; A.
16 KRLGLIFGVITTCILAGCASKPTYNSTSGSGSHRTSGSGGLAIGSQVITDSQGVPNRYQV
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                                                                                                         ; Score 238; DB 2;
; Pred. No. 4.8e-10;
46; Mismatches 103
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VIYVS-

conserved hypothetical protein PA4924 [imported] - C;Species: Pseudomonas aeruginosa C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 C;Accession: B83031

, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig,

M.J.; Br K.; Lim,

PA01,

an

opportunistic patho

#text_change

31-Dec-2000

Pseudomonas aeruginosa

(strain

PAO1)

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A;Bolecule type: DNA
A;Molecule type: DNA
A;Residues: 1-259 <HAY>
A;Cross-references: GB:BA000007; PIDN:BAB37161.1; PID:g13363210; GSPDB:GN00154
A;Cross-references: strain O157:H7, substrain RIMD 0509952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Fgasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: B91096
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                                                                                                                                                                                                                                                                          132 NTAH-TPSPVAVQSSRPPVQQHPAVQKPTPPVVVVKKPTPTPPVVQQPAPVAPPVTEAPF 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               251
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                                                                                                                                                                                                                                                                                                                                                                                                                                        78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                            RYRATAIDPLRYL 250
                                                                                                                                                    DHNMDGAS---IVIQHTNGFVSSYIHIKDAQVKTGDTVRTGQRIASMKNQPSGAALFEFRI 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RYRATAIDPLRYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DHNMDGAS--IVIQHTNGFVSSYIHIKDAQVKTGDTVRTGQRIASMKNQPSGAALFEFRI 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STADGG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NTAH-TPSPVAVQSSRPPVQQHPAVQKPTPPVVVVKKPTPTPPVVQQPAPVAPPVTBAPF 190
                                                                                         SRNGVYVDPLTVL
                                                                                                                      GNQLRGYGNLIMIKHSEDYITAYAHNDTMLVNNGQSVKAGQKIATMGSTDAASVRLHFQI
                                                                                                                                                                                      STADGG
                                                                                                                                                                                                              ATGSSGVMQFRYPVGATNPVVRRFGTATVAGSTVTSNGMWFSGRDGDLINASNAGTVIQA 250
                                                                                                                                                                                                                                               KTASVTPSSAVPKSSWPPVGQRCWLWPTTGKVIM-----
                                                                                                                                                                                                                                                                                                                                        KQGDTVSKIAQRYGLNWREIGHINNLNSSYTIYTGQWLTLWSGDLK----VRERSISSGV 131
                                                                                                                                                                                                                                                                                                                                                                       KSLGIVMLLSVGLLLAGC-----SGSKSSDTGTYSG-----SVYTV
                                                                                                                                                                                                                                                                                                                                                                                                      KRLGLIFGVITTCILAGCASKPTYNSTSGSGSHRTSGSGGLAIGSQVITDSQGVPNRYQV 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SRNGVYVDPLTVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GNQLRGYGNLIMIKHSEDYITAYAHNDTMLVNNGQSVKAGQKIATMGSTDAASVRLHFQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATGSSGVMQFRYPVGATNPVVRRFGTATVAGSTVTSNGMWFSGRDGDLINASNAGTVIQA 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KTASVTPSSAVPKSSWPPVGQRCWLWPTTGKVIM----
                                                                                                                                                                                                                                                                                                           KRGDTLYRISRTTGTSVKELARLNGISPPYTIEVGQKLKL--GGAKSSSSTRKSTAKSTT 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KRGDTLYRISRTTGTSVKELARLNGISPPYTIEVGQKLKL--GGAKSSSITRKSTAKSTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KQGDTVSKIAQRYGLNWREIGHINNLNSSYTIYTGQWLTLWSGDLK----VRERSISSGV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     14.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 238; DB 2;
Pred. No. 4.8e-10
                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----NKGIDISAPRGTPIYAAGAGKVVYV 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
                                                                                                                                                                                  -NKĠIDIŚAPRGTPÍYAAGAGKVVYV 177
                                                                                                                                                                                                                                                                                                                                                                                                                                      103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 259
                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                96;
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th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N., S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Atthors: Parry, C.
                                                                                                                                                                                         A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-250 <PAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Wadman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.F.; LOTY, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: B83031
 ঠ
                                                                                                                                                                                                                                               A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov A;Reference number: AB0502; PMID:11677608
A;Accession: AD0871
                                                                                                                                                                                                                                                                                                                                                                                                     C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change
C;Accession: AD0871
                                                                                                                                                                                                                                                                                                                                                                                                                                         probable lipoprotein (imported) - Salmonella enterica subsp. C;Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
                                                                                                                                                                         A;Cross-references: GB:AL513382;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Experimental source: strain PAO1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Residues: 1-231 <STO>
A;Cross-references: GB:AE004905; GB:AE004091; NID:g9951195;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary A;Molecule type: DNA
                                                                                                                 ;Superfamily: lipoprotein
                                                                                                                                                       ;Genetics:
                                                         Query Match
Best Local (
                                         Matches
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                                         76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     68; Conservative
                                                           Similarity
LGLIFGVITTCILAGCASKPTYNSTSGSGSHRTSGSGGLAIGSQVITDSQGVPNRYQVKQ 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EIRQNGRPLDPLSLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RISRNGVYVDPLTVL 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VRGEYRVKRGDTLYSIATRHGWNYKDLARANGIRPPYAVKVGQ-VVRFDGRKSTYVASSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FAVNNMRGYGNLVIIQHGTSYTSTYAHNSRLLVKEGQMVGKGQKIAEAGSSDADRVQLYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QADHNMDGAS--IVIQHTNGFVSSYIHIKDAQVKTGDTVRTGQRIASMKNQPSGAALFEF 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----LRGWQWPM--KGPVIRRF----SSSDKLNKGIRIAGTLGQPVQASLAGKVV 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PFATGSSGVMQFRYPVGATNPVVRRFGTATVAGSTVTSNGMWFSGRDGDLINASNAGTVI 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SSSNTR----- 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SGVNTAHTPSPVAVQSSRPPVQQHPAVQKPTPPVVVVKKPTPTPPVVQQPAPVAPPVTEA 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VPNRYQVKQGDTVSKIAQRYGLNWREIGHINNLNSSYTIYTGQWLTLWSGDLKVRERSIS 128
                                         Conservative
                                                         13.9%;
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                                       49;
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                                                                                                                                                                     PIDN:CAD02868.1; PID:g16504121; GSPDB:GN00176
                                 Score 232.5; DB 2;
Pred. No. 1.1e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 234; DB 2
Pred. No. 8e-10;
7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2;
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                                       Indels
                                                                       Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   enterica serovar Typhi
                                       87;
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RESULT 9
E75291
probable cell wall glycyl-glycine endopeptidase - Deinococcus radiodurans
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C;Superfamily:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           lipoprotein D homolog - Haemophilus influenzae (strain Rd KW20)

C;Specles: Haemophilus influenzae

C;Date: 1B-Aug-1995 #sequence_revision 1B-Aug-1995 #text_change 29-Sep-1999

C;Accession: F64087, T09410

R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.

Science 269, 496-512, 1995

Science 269, 496-512, 1995

A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.

A;Reference number: A64000; MUID:95350630; PMID:7542800
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Best Local S
Matches 76
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                                                                                                                                                                                                                                                                                         131 VNTAHTESPVAVQSSRPPVQQHPAVQKPTP------PVVVVKKPTPTPPVV 175
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                                                                                                                                                                                                                                                                                                                                                                                          Similarity 27.8
76; Conservative
                                                                                                                                                                   FSGRDGDLINASNAGTVIQADHNMDGAS--IVIQHTNGFVSSYIHIKDAQVKTGDTVRTG 288
                                                                                                                                                                                                                              QQPAPVAPPVTEAPFATGSSGVMQFRYPVGATNPVVRRFGTA--TVAGSTVT---SNGMW 230
                                                                                                                                                                                                                                                                                                                        NTYKVNKGDTMFLIAYLAGIDVKĖLAALNNLSEPYNLSLGOVLKISNCDIKTVTTTVS--
                                                                                                                                                                                                                                                                                                                                             NRYQVKQGDTVSKIAQRYGLNWREIGHINNLNSSYTIYTGQWLTLWSGDLKVRERSISSG
                                                                                QDIAKMGSSGTNTVKLHFEIRYKGKSVDPVRYL
                                                                                                                                      IŚĠSRĠQAVKAAAAĠRIVYAGNALRĠYGNLIIKHNDDFLSAYAHNDKILVADQQEVKAG
                                                                                                                                                                                               TSSTQVTSSVNNANSTPINSNVVA---PI-ASN-VVWQWPTSGNIIQGFSSTDGGNKGID 309
                                                                                                                                                                                                                                                           -----VKQPAVTASTATPVK--PAVTY-TPGANGTQIGSDGTIIGPIKSEAGTSPSVPVA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GSSGVMQFRYPVGATNPVVRRFGTATVAGSTVTSNGMWFSGRDGDLINASNAGTVIQADH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AEGG----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GDTLYRISRATGTSVKELARLNGISPPYTIEVGORIKV-RGSAKSSSSTRKTSNKTATKT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LGIAVLLCTGLLLAGC-----SSNSGSGTY--SGS-----
                                                                                                                                                                                                                                                                                                                                                                                     13.1%; Score 219.5; DB 2; 27.8%; Pred. No. 1.8e-08; tive 46; Mismatches 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----NKGIDIAGARGTPVYAAGAGKVVYVGN
                                                                                402
                                                                                                                                                                                                                                                                                                                                                                                                                   Length 405;
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A; Gene: DR2291
                                                                                      Query Match
Best Local
                                                                                                                                                    Genetics:
Gene: nlp
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Best Local S
Matches 73
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       PMIRLRRVAACTVVSLWLVGCTND---NSTSAP----ISSVGGDRSGTMLSKANTDSSGG 58
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A; Gene: nlpD
C; Superfamily: lipoprotein
                                                                                                                                                                                                                                               A;Status: preliminary
A;Molecule type; DNA
A;Residues: 1-333 <KUR>
A;Cross-references: GB:AL590842; PIDN:CAC92586.1; PID:g15981283; GSPDB:GN00175
                                                                                                                                                                                                                                                                                                                                                                                                                                                       k;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.,
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; I
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, I
Mature 413, 523-527, 2001
                                                                                                                                                                                                                                                                                                                                                                                  A;Title: Genome sequence of Yersinia pestis, the causative agent of plague A;Reference number: AB0001; MUID:21470413; PMID:11586360 A;Accession: AF0407
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C;Bate: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
C;Accession: E75291
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dc. N.; Shen, M.; Vanathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zale S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodu A;Reference number: A75250; MUID:20036896; PMID:10567266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               lipoprotein [imported] - Yersinia pestis (strain CO92)
C;Species: Yersinia pestis
C;Species: Yersinia pestis
C;Accession: AF0407
C;Accession: AF0407
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; P:
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A;Molecule type: DNA
A;Residues: 1-454 <WH]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity es 73; Conserv
14 PIKRLGLIFG-VITTCILAGCASKPTYNSTSGSGSHRTSGSGGLAIG---SQVITDSQG- 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       290 ARPSPAQPAPPRVAQATPEHHARVVVRQTSSHSLWQWPLPGYGRITSDFGWRVLDGEREK 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        176 QQPAPVAPPVTEAPFAT------GSSGVMQFRYPVGATNPVVRRFGTATVAGSTVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120 LKVRERSISSGVNTAHTPSPVAVQSSRP-PVQ---QHPAVQKPTPPVVVVKKPTPTPPVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60 SQVITDSQGVPNRYQYKQGDTVSKIAQRYGLNWREIGHINNLNSSYTIYTGQWLTLWSGD
                                                                 Similarity 25...
91; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1-454 <WHI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SNGMWFSGRDGDLINASNAGTVIQADHNMD-----GASIVIQHTNGFVSSYIHIKDAQVK 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HQGIDVAAPPGTPVIAARSGRVIQA--HLDETYGWGWTVVIQHPDGWQTRYAHLSRISVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGQLVRQGERVGAVGSTGRVTGPHL-HFGLYRNWDPHNPL
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                                                                                        13.1%;
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                                                              ; Score 218.5; DB 2;
; Pred. No. 1.7e-08;
52; Mismatches 130;
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Pred. No. 2.1e-08;
0; Mismatches 116;
                                                                                                                      Length
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                                                              87;
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                                                           Gaps
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T.; Zalewski,
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AH0855
lipoprotein NipD precursor [imported] - Salmonella enterica subsp. enterica serovar Typh C;Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 17-May-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-373 < PAR>
A; Cross-references: GB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica sero
A;Reference number: AB0502; PMID:11677608
A;Accession: AH0855
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84;
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                                                                          VIQHTNGFVSSYIHIKDAQVKTGDTVRTGQRIASMKNQPSGAALFEFRISRNGVYVDPLT 319
                                                                                                                                                                                                                                                                                                                                                                  ÓPVTEQPVQMENGRIVYNRQYGNIPKGSYTGGSTYTVKKGDTLFYIAWITGNDFRDLAQR 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SAYSGNSGKONVGKMLPSSGAVVATTAPVTAPSSSVSEPASNGGPVSGWRWPTD-----
  VL 321
                                        IIKHNDDYLSAYAHNDTMLVREQQEVKAGQKIATMGSTGTSSTRLHFEIRYKGKSVNPLR
                                                                                                                                                          YPVGATNPVVRRFGTATVAGSTVTSNGMWFSGRDGDLINASNAGTVIQADHNMDGAS--I
                                                                                                                                                                                                                                                                                                                       NNLNSSYTIYTGQWL-----TLWSGDLKVRERSISSGVNTAHTPSPVAVQSSRPPV- 149
                                                                                                                                                                                                                                                                                                                                                                                                      QVITDSQ-----GVP-----NRYQVKQGDTVSKIAQRYGLNWREIGHI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RRFGTATVAGSTVTS-----NGMWFSGRDGDLINASNAGTVIQADHNMDGAS--IVI 261
                                                                                                                      WP--TDGKVIENFG-ASEGG----NKGIDIAGSKGQAIVATADGRVVYAGNALRGYGNLI
                                                                                                                                                                                                                                           ----QQHPAVQKPT--PPVVVVKKPTPTPPVVQQPAPVAPPVTEAPFATGSSGVMQFR 201
                                                                                                                                                                                                                                                                                 NSISAPYSLNVGQTLQVGNASGTPITGGNAITQADAAQQGVVTRSAQNSTVAVASQPTIT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12.6%; Score 210; DB 2; Length 373; 23.2%; Pred. No. 8e-08; tive 56; Mismatches 138; Indels
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C;Genetics:
A;Gene: VC0533
A;Map position:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Title: DNA Sequence of both chromosomes of the cholera pathogen A; Reference number: A82035; MUID:20406833; PMID:10952301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Accession: H82311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001;
Accession: H82311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;Species: Vibrio cholerae
                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
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                                 GQRIASMKNQPSGAALFEFRISRNGVYVDP 317
                                                                     DIAGQRGQAVVATADGTVVYSGNALRGYGNLIIIKHNEHYLSAYAHNDQLLAKEGQTVQA
                                                                                                     WFSGRDGDLINASNAGTVIQADHNMDGAS--IVIQHTNGFVSSYIHIKDAQVKTGDTVRT 287
                                                                                                                                                                              VVQQPAPV----APPVTEAPFATGSSGVMQFRYPVGATNPVVRRFGTATVAGSTVTSNGM
                                                                                                                                                                                                                ASSTSASVAKAATTATVAQTVSKSSNTKNVQNGSTNSQNLTKKDPVKTVDQTKTKEYVEP
                                                                                                                                                                                                                                                                                                                           QGDTVSKIAQRYGLNWREIGHINNLNSSYTIYTGQWLTLW-----
                                                                                                                                                                                                                                                                                                                                                              RLGLL---LFCSLLFGCTA-PTPAPVSGLGKDYNKVERGSYRGSY--
                                                                                                                                                                                                                                                                                                                                                                                                RLGLIFGVITTCILAGCASKPTYNSTSGSGSHRTSGSGGLAIGSQVITDSQGVPNRYQVK 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ĭ.
GQKIATMGSSGTNSVRLHFEIRYQGKSVNP
                                                                                                                                            VGKQNVNVNVAKAKPSDEK-----IAKWLWP--TKGRVIKNFS----AGDQ-GNKGI
                                                                                                                                                                                                                                                   ---RERSISSGVNTAHTPSPVAVQSSRPPVQ-----QHPAVQKPTPPVVVVKKPTPTPP
                                                                                                                                                                                                                                                                                         KGDTLYFIAYLTDKDVNDLISYNDLAPPYTIHPGQKIKLWLPNYTPPAYGGTGGAATVAV 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 370
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     12.5%;
25.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                  48; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GB:AE003852; NID:g9654953; O1; strain N16961; biotype
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 208.5; DB 2
Pred. No. 8.1e-08;
306
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El Tor
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H.; Dragoi, :
                                                                                                                                                                                                                                                                                                                                                              ----YEVK
                                                                                                                                                                                                                                                                                                                                                                                                                                    59;
                                                                                                                                                                                                                                                                                                                           -SGDLKV--
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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I.; Sellers,
                                                                     276
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RESULT 13
AI3386

AI3386

Lipoprotein nlpD [imported] - Brucella melitensis (strain 16M)

C;Species: Brucella melitensis

C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002

C;Accession: AI3386

R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, I.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letessor, Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002

A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens: A;Reference number: AD3252; PMID:11756688

A;Accession: AI3386

A;Status: preliminary

A;Kesidues: 1-427 <KUR>
A;Cross-references: GB:AE008917; PIDN:AAL52260.1; PID:g17983047; GSPDB:GN00190

A;Experimental source: strain 16M
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 14
G81864
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A; Map position: I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;Status: preliminary
;Molecule type: DNA
;Rosidues: 1-415 cPAR>
;Coross references: GB:AL162756; GB:AL157959; NID:g7380091; PIDN:CAB84920.1;
;Experimental source: serogroup A, strain 22491
                                                                                                                                                                                                                                                                                                                                                                                          Matches
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Best Local
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Best Local
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                                                         330
                                                                                               240
                                                                                                                                       280
                                                                                                                                                                               184
                                                                                                                                                                                                                        234
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                                                                                                                                                                                                                                                                                               185 HTIVRGDTVYNISKRYHISQDDFRAWNGMTDN-TLSIGQ-----IVKVKPAGYAA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    367
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           215 VPVDQLKAANGLTSG-AIRVGQSLVI-----PSAAAGAPTQVAAITPQPANPAKAA
                                                                                                                                                                                                                                                                                                                                     73 YQVKQGDTYSKIAQRYGLNWREIGHINNLNSSYTIYTGQWLTLWSGDLKYRERSISSGVN 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90 LNWREIGHINNLNSSYTIYTGQWLTLWSGDLKVRERSISSGVNT---AHTPSPV-AVQSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30 LAGCASKPTYNSTSGSGSHRTSGSGGLAIGSQVITDSQGVPNRYQVKQGDTVSKIAQRYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     h 12.3%; Score 205; DB 2; Length 427; Similarity 26.2%; Pred. No. 2.2e-07; 79; Conservative 45; Mismatches 132; Indels
                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                     NASNAGTVIQADHNMDGAS--IVIQHTNGFVSSYIHIKDAQVKTGDTVRTGQRIASMKNQ
                PSGAALFEFRISRNGVYVDP 317
                                                 LAAADGKVVYAGSGLRGYGNLVIIQHNSSFLTAYGHNQKLLVGEGQQVKRGQQVALMGNT
                                                                                                                                     PAPQSPAASPSGTRSVGGIVWQRP--TQGKVVADFGG-
                                                                                                                                                                      PVTEAPFA----TGSSGVMQFRYFVGATNPVVRRFGTATVAGSTVTSNGMWFSGRDGDLI
                                                                                                                                                                                                              ----PKAAAVK-SRPAVP--AAVQTPV-----kPAAQPPVQSAPQPAAPAAENKAVPA
                                                                                                                                                                                                                                                       TAHTPSPVAVQSSRPPVQQHPAVQKPTPPVVVVKKPTPTPPVVQQPAPVAP-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -RGRILASFGORE---GTSVSDGIDIMVPEGTPVKAAENGVVIYAGDGLKEFGOTVLIRH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATNPVVRREGTATVAGSTVTSNGMWESGRDGDLINASNAGTVIQADHNMD--GASIVIQH 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SAPANGGAEVKPYTPPQASNK-----VIEDAE-----KDQAAAPSSTGISQMRWPV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RPPVQQHPAVQKPTPPVVVVKKPTPTPVVQQPAPVAPPVTEAPFATGSSGVMQFRYPVG
                                                                                                                                                                                                                                                                                                                                                                              12.2%; Score 203; DB 2; Length 415; ilarity 27.3%; Pred. No. 2.9e-07; Conservative 42; Mismatches 97; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels 46;
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                                                                  RESULT 16
D91078
probable lipoprotein [imported] - Escherichia coli (strain O157:H7, substrain C;Species: Escherichia coli (strain O157:H7, substrain C;Species: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 17-May-2002
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A;Molecule type: DNA
A;Rosidues: 1-379 <BLAT>
A;Residues: 1-379 <BLAT>
A;Cross references: GB:AE000358; GB:U00096; NID:g2367156; PIDN:AAC75784.1; PID:g1789099;
A;Experimental source: strain K-12, substrain MG1655
A;Experimental source: strain K-12, substrain MG1655
R;Takayanagi; Y: Tanaka, K: Takahashi, H.
Mol. Gen. Genet. 243, 525-531, 1994
Mol. Gen. Genet. 243, 525-531, 1994
A;Title: Structure of the 5' upstream region and the regulation of the xpoS gene of Esch A;Reference number: S45579, MUID:94268497, PMID:8208244
A;Reference number: S45580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Residues: 1-379 < ICH>
A;Residues: 1-379 < ICH>
A;Residues: 1-379 < ICH>
A;Cross-references: GB:L07869; NID:g433183; PIDN:AAA17875.1; PID:g433185
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.;
A; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Recession: B65055
A;Accession: B65055
A;Status: preliminary; nucleic acid sequence not shown; translation not sho
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A;Residues: 99-138,'A',140-379 <TAK>
A;Cross-references: EMBL:D17549; NID:g404097; PIDN:BAA04487.1; PID:g404099
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A;Title: A gene at 59 minutes on the Escherichia coli chromosome A;Reference number: A55522; MUID:94179096; PMID:8132457
A;Recession: B55522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            lipoprotein D precursor - Bscherichia coli (strain K-12)
C;Species: Escherichia coli
C;Date: 25-Aug-1995 #sequence revision 25-Aug-1995 #text_change 01-Mar-2002
C;Accession: B5552; B65055; S45580
R;Ichkawa, J.K., Li, C.; Fu, J.; Clarke, S.
J. Bacteriol: 176, 1630-1638, 1994
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Best Local
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   341
                                                                                                          281
                                                                                                                                                                                                                    228
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                                                                                                                                                                                                                                                                                                                           168
                                                                                                                                                                                                                                                                                                                                                                                 133
                                              286 RTGQRIASMKNQPSGAALFEFRISRNGVYVDPLTVL 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             h 12.1%;
Similarity 26.1%;
72; Conservative 4
                                                                                                    GIDIAGSKGQAIIATADGRVVYAGNALRGYGNLIIKHNDDYLSAYAHNDTMLVREQQEV
                                                                                                                                                                                                           TATTVTAPVTVPTASTTEPTVSSTSTSTPISTWRWP--TEGKVIETFG-ASEGG----NK 280
                                                                                                                                                                                                                                                                                                                     ASGTPITGGNAITQADAAEQGVVIKPAQNSTVAVASQPTITYSESSGEQSANKMLPNNKP
                                                                                                                                                                                                                                                                                                                                                                          TAHTPSPVAVQSSRPPVQQHPAVQKP--TPPVVVVKKPT-------
KAGQKIATMGSTGTSSTRLHFEIRYKGKSVNPLRYL
                                                                                                                                                      GMWFSGRDGDLINASNAGTVIQADHNMDGAS--IVIQHTNGFVSSYIHIKDAQVKTGDTV
                                                                                                                                                                                                                                                             TPPVVQQPAPVAPPVTEAPFATG---SSGVMQFRYPVGATNPVVRRFGTATVAGSTVTSN 227
                                                                                                                                                                                                                                                                                                                                                                                                                            YTVKKGDTLFYIAWITGNDFRDLAQRNNIQAPYALNVGQ---TLQVG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YQVKQGDTVSKIAQRYGLNWREIGHINNLNSSYTIYTGQWLTLWSGDLKVRERSISSGVN 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : | : : | | : | EASRTQLHFEVRQNGKPVNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Score 202.5; DB 2; pred. No. 2.8e-07; 42; Mismatches 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
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M.; Co.

RIMD

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C;Accession
R;Hayashi,
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A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7 A;Reference number: A85480; MUID:21074935; PMID:11206551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary
A;Molecule: type: DNA
A;Residus: 1-379 <HAY>
A;Residus: 1-379 <HAY>
A;Cross-references: GB:BA000007; PIDN:BAB37019.1; PID:g13363067; GSPDB:GN00154
A;Experimental source: strain O157:H7, substrain RIMD 0509952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                lipoprotein [imported] - Escherichia coli (strain O157:H7, substrain EDL933) C;Species: Escherichia coli (strain O157:H7, substrain EDL933) C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 17-May-2002 C;Accession: E85923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; I
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7
A;Reference number: A99629; MUID:21156231; PMID:11258796
                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-379 <STO>
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A;Experimental source: strain O157:H7, substrain EDL933
                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary
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Best Local S
Matches 72
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                                                                                                                                                                                                                                                                                      Superfamily: lipoprotein
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Best Local Similarity
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                                                                                                                                                                                                    2h 12.1%; Score 202.5; DB 2
Similarity 26.1%; Pred. No. 2.8e-07;
72; Conservative 42; Mismatches 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YQVKQGDTVSKIAQRYGLNWREIGHINNLNSSYTIYTGQWLTLWSGDLKVRERSISSGVN 132
                                                                                                                      YTVKKGDTLFYIAWITGNDFRDLAQRNNIQAPYALNVGQ--TLQVG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KAGOKIATMGSTGTSSTRLHFEIRYKGKSVNPLRYL 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GMWFSGRDGDLINASNAGTVIQADHNMDGAS--IVIQHTNGFVSSYIHIKDAQVKTGDTV 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TPPVVQQPAPVAPPVTEAPFATG----SSGVMQFRYPVGATNPVVRRFGTATVAGSTVTSN 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TAHTPSPVAVQSSRPPVQQHPAVQKP--TPPVVVVKKPT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YTVKKGDTLFYIAWITGNDFRDLAQRNNIQAPYALNVGQ--TLQVG------N 167
                                                                             TAHTPSPVAVQSSRPPVQQHPAVQKP--TPPVVVVKKPT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GIDIAGSKGQAIIATADGRVVYAGNALRGYGNLIIIKHNDDYLSAYAHNDTMLVREQQEV
                                           ASGTPITGGNAITQADAAEQGVVIKPAQNSTVAVASQPTITYSESSGEQSANKMLPNNKP
                                                                                                                                                               YQVKQGDTVSKIAQRYGLNWREIGHINNLNSSYTIYTGQWLTLWSGDLKVRERSISSGVN 132
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                                                                                                                                                                                                                                             DB 2;
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RESULT G87496

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R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, ri, H.; Qin, H.; Vymathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. Science 287, 1809-1815, 2000
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R
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A; Residues: 1-415 <TET>
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A;Reference number: A81000; MUID:20175755; PMID:10710307
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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Best Local
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                                                                                                                                                                                                                                                                                                    131 --VNTAHTPSP-VAVQSSRPPVQQHPAVQKPTPPVVVVKKPTPTPPVVQQPAPVAP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KAGQKIATMGSTGTSSTRLHFEIRYKGKSVNPLRYL
                                                                                                                                                                   KAVPAPAPQSPAASPSGTRSVGGIVWQRP--TQGKVVADFGG------NNKGVDIAGN
                                                                                                                                                                                                                                                            VKVKPAGYAAPKTAAVESRPAVP--AAVOTPV----KPAAOPPVQSAPQPAAPAAEN
                                                                                                                                                                                                                                                                                                                                                  HTIVRGDTVYNISKRY-----HISQDD-----FRAWNG---MTDNMLSIGQI
LMGNTDASRTQLHFEVRQNGKPVNP
                                  SMKNOPSGAALFEFRISRNGVYVDP 317
                                                                               AGOPVLAAADGKVVYAGSGLRGYGNLVIIQHNSSFLTAYGHNQKLLVGEGQQVKRGQQVA 384
                                                                                                                          DGDLINASNAGTVIQADHNMDGAS--IVIQHTNGFVSSYIHIKDAQVKTGDTVRTGQRIA 292
                                                                                                                                                                                                                ----PVTEAPFA----TGSSGVMQFRYPVGATNPVVRRFGTATVAGSTVTSNGMWFSGR 234
                                                                                                                                                                                                                                                                                                                                                                                        YQVKQGDTVSKIAQRYGLNWREIGHINNLNSSYTIYTGQWLTLWSGDLKVRERSISSG--
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                          11.9%;
27.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                      38; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 198; DB 2;
Pred. No. 6.8e-07;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      60;
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strain MCS
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J.A.,

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RESULT 20
Aprobacterium tumefaciens (strain C58, Dupont)
lipoprotein [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
lipoprotein: Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
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A,Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens A,Feference number: AB2577; PMID:11743193

A,Accession: AF2785

A,Status: preliminary
A,Molecule: UNA
A,Residues: L7537 <KUR>
A,Cross-references: GB:AE008688; PIDN:AAL42700.1; PID:g17740136; GSPDB:GN00186
A,Experimental source: strain C58 (Dupont)
C,Genetics:
A,Gene: Atu1700
A,Map position: circular chromosome
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A;Status: preliminary
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-609 <STO>
A;Cross-references: GB:AE005673; NID:g13423465; PIDN:AAK23971.1;
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Best Local S
Matches 81
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;Molecule type: DNA
;Residues: 1-537 <KUR>
;Cross-references: GB:AE008688; PIDN:AAL42700.1; PID:g17740136; GSPDB:GN00186
;Experimental source: strain C58 (Dupont)
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                                                                                                                                   PPSGG----YKVQPGDSLAKIARANGVSVAALKAANGI-SNESIRVGQTLAM------
                                                                                                                                                                                         TDSQGVPNRYQVKQGDTVSKIAQRYGLNWREIGHINNLNSSYTIYTGQWLTLWSGDLKVR
PGASTDAIKTASVPAKEA--AAAKPVE--TASIKPEPYKAPAAAATTAAPATPATASVSD
                                                             ERSISSGVNTAHTESPVAVQSSRPPVQQHPAVQKPTP---PVVVVKKPTPTPPVVQQPAP
                                                                                                                                                                                                                                                                                                                               IAINSQNQKPIKRLGLIFGVITTCILAGCASKPTYNSTSGSGSHRTSGSGGLA-IGSQVI
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                                                                                                                                                                                                                                                                                                                                                                                             11.3%; Score 188.5; DB 2; 25.1%; Pred. No. 4.6e-06; ative 64; Mismatches 131;
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23.6%; Pred. No. 1.5e-06;
tive 54; Mismatches 110;
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C;Species: Agrobacterium tumefaciens
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-2002
C;Date: 30-Sep-5001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-2002
C;Accession: H97564
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001 the plant Pathogen and Biotechnology Agent Agrobacterium tume A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tume A;Reference number: A97359; PMID:11743194
A;Accession: H97564
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A;Molecule type: DNA
A;Residues: 1-562 <KUR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;Genetics:
;Gene: AGR_C_3124
;Map position: circular chromosome
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535 MTGSAKRPQVHFEVRKDATPVNP
                                     298
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                                                                                                               NASNAGTVIQADHNMD--GASIVIQHTNGFVSSYIHIKDAQVKTGDTVRTGQRIASMKNQ 297
                                                                                                                                                                                                                                                                                                                      PPSGG----YKVQPGDSLAKIARANGVSVAALKAANGI-SNESIRVGQTLAM-----
                                 PSGAA---LFEFRISRNGVYVDP 317
                                                                           KAAENGVVIYAGNGLKQLGNTVLVRHDDGKVTVYGNAANLDVQRGQKVQRGQTIAT--SG
                                                                                                                                                                                                                                                                              ERSISSGVNTAHTPSFVAVQSSRPFVQQHPAVQKFTF---FVVVVKKFTFTFFVVQQPAF 180
                                                                                                                                                                                                                                                                                                                                                                                                                                          IAINSQNQKPIKRLGLIFGVITTCILAGCASKPTYNSTSGSGSHRTSGSGGLA-IGSQVI 63
                                                                                                                                                            IEKKADMASIAPESTGIGKYRWPVRGA---VINNFGD-NVEGS--RNDGINISVPEGTPI
                                                                                                                                                                                                VAPPVTEAPFATGSSGVMQFRYPV-GATNPVVRRFGTATVAGSTVTSNGMWFSGRDGDLI
                                                                                                                                                                                                                                        PGASTDAIKTASVPAKEA--AAAKPVE--TASIKPEPYKAPAAAATTAAPATPATASVSD 422
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ilarity 25.1%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Score 188.5; DB 2;
; Pred. No. 4.8e-06;
64; Mismatches 131;
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probable secreted peptidase - Streptomyces coelicolor C;Species: Streptomyces coelicolor C;Species: Streptomyces coelicolor C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 21-Jan-2000 C;Accession: T35413 R;Oliver, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajanc submitted to the EMBL Data Library, March 1999 A;Reference number: Z21577 A;Accession: T35413 A;Status: preliminary; translated from GB/EMBL/DDBJ

B.G.; Rajandream,

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A; Residues: 1-312 <OLI>
A; Cross-references: EMBL: ALO49485; PIDN: CAB39706.1;
A; Experimental source: strain A3(2)
C; Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      probable lipoprotein Z4203 [imported] - Escherichia coli (strain O157:H7, s C;Species: Escherichia coli (C;Species: Escherichia coli C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Dec-2001 C;Accession: F85941
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C;Superf
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A;Experimental source: strain O157:H7, substrain EDL933
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A; Residues: 1-223 <STO>
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                                                                                                                                                                                                                                                                                Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RSISSGVNTAHTPSPVAV--QSSRPPVQQHPAVQKPTPPVVVVKKPTPTPPVVQQPAPVA 182
                                    SSRPPVQQHPAVQKPTPPVVVVKKPTPTPPVVQQPAPVAPPVTEAPFATGSSGVMQFRYP 203
                                                                               GTSVKELARLNGISPPYTIEVGQKLKL--GGAKSSSSTRKSTAKSTTKTASVTPSSAVPK 102
                                                                                                                        GLNWREIGHINNLNSSYTIYTGQWLTLWSGDLK----VRERSISSGVNTAH-TPSPVAVQ 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GORI -- ASMKNOPSGAAL-FEFRISRN-GVYVDPLTVLK 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EAVGSDPSLIHPGLKLSIDGQAAKPSAPSSAQSQKPA-----QKSAEKPAEKTAAKPA 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EKNSDSRTYTVKSGDYLSKI ADEQDVD-
SSWPPVGQRCWLWPTTGKVIM----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----RDGDLINASNAGTVIQAD-HNMDGASIVIQHTNGFVSSYIHIKDAQVKTGDTVRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PPVTEAPFATGSSGVMQFRYPVGATNPVVRRFGTATVAGSTV----TSNGMWFSG----
                                                                                                                                                                     LLAGC----SGSKSSDTGTYSG-----SVYTVKRGDTLYRISRTT
                                                                                                                                                                                                              ILAGCASKPTYNSTSGSGSHRTSGSGGLAIGSQVITDSQGVPNRYQVKQGDTVSKIAQRY 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GOOVGLSGATGNVTGPHLHFEIRTTPDYGSDIDPLAFLR 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TDFVVPTGTSLKAVGAGTVVSAGWGGAYGNQVVIQLADGHYAQYAHLSSLSVSAGQSVTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GKHRRTRAMRLTRTIAVAGTGGAALALPLMGAAAANAAPAHSVSEQAVQSVPASAKKAAA 64
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                                                                                                                                                                                                                                                       10.1%; Score 169; DB 2; 24.0%; Pred. No. 3.8e-05; tive 35; Mismatches 79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10.3%;
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Pred. No. 3.8e-05;
13; Mismatches 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Escherichia coli (strain O157:H7, substrain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         B.; Glasner, J.D.; Rose, imalanta, E.; Potamousis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GSPDB: GN00070;
                                                                                                                                                                                                                                                                                                  Length 223;
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-PYSTADGG--
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         cell wall binding proteins homolog lmo2504 [imported] - Listeria monocytogenes C;Species: Listeria monocytogenes C;Species: Listeria monocytogenes C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001 C;Accession: AH1387 R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Perche, P.; pominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; J. Jones, L.M.; Karst, U. Science, L.M.; Karst, U. Science 294, 849-852, 2001 A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournarok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; A;Title: Comparative genomics of Listeria species. A;Reference number: AB1077; MUID:21537279; PMID:11679669 A;Scatus; preliminary
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A;Title: Complete genome sequence of Treponema pallidum, the syphia, Reference number: A71250; MUID:98332770; PMID:9665876
A;Rccession: A71359
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A;Residues: 1-271 <COL>
A;Residues: 1-271 <COL>
A;Cross-references: GB.AE001200; GB:AE000520; NID:g3322419;
A;Experimental source: strain Nichols
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  conserved hypothetical protein TP0155 - syphilis spirochete
C;Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 05-Nov-1999
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                                                                                                                                                                                                                                                                                                 130 GVNTAHTPSPVAVQSSRPPVQQHPAVQXPTPPVV-VVKKP------TPTP-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                         TATVAGSTVTSNGMWFSGRDGDLINASNAGTVIQADHN-MDGASIVIQHTNGFVSSYIHI
                                                                                                                                                                                                                                                         SIAAAH-----QISLERLVLLNTPSSSKESPPSVRTLVSPFYNSAARESCVPFPFSSAKQ 201
                                                                                                                                                                                                                                                                                                                                                                               YQVKQGDTVSKIAQRYGLNWREIGHINNLNSSYTIYTGQWLTLWSGD----LKVRERSISS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VGATNPVVRRFGTATVAGSTVTSNGMWFSGRDGDLINASNAGTVIQADHNMDGAS--IVI
QTVLVSAGTRVTSATKİGLLGKTGRSTGPHLHFTİYKNGSAINPTSLLR
                                       KDAQVKTGDTVRTGQRIASM-KNQPSGAALFEFRISRNGVYVDPLTVLK 322
                                                                                 SDPFTGARSFHNGLDMVSRRGTPVYSALGGIVRTVGYSAVYGNYLIVGHHAGYQTLYGHL
                                                                                                                                                                     WRENTSFDAVQPLQPA----RVLFLPGAHLSARALQEINGDLFRAPLRSRYYVSSRYGWR
                                                                                                                                                                                                             -----PVVQ--QPAPVAPPVTEAPFATGSSGVMQ-----FRYPVGATNPVVRRFG--
                                                                                                                                                                                                                                                                                                                                           YEVREGDVVGRIAQRYDISQDAIISLNKLRSTRALQVGQLLKIPSVDGILYTVKNGDTFS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 10.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                               47; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 167; DB 2;
Pred. No. 0.0001;
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F.; Berche, P.; ; Entian, K.D.; I

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 probable lipoprotein - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
C;Accession: F75467
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson,
M.; Shen, M.; Vamathevan; J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski,
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R
A;Reference number: A75250; MUID:20036896; PMID:10567266
A;Accession: F75467
                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary
A;Molecule type: DNA
A;Residuss: 1-375 < WHI>
A;Cross references: GB:AE001939;
A;Experimental source: strain R1
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Best Local
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;Cross-references: GB:NC_003210; PIDN:CAD00582.1; PID:g16411992; GSPDB:GN00177
;Experimental source: strain EGD-e
;Genetics:
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           182
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9.5%; Score 158; DB 2; I
Similarity 21.7%; Pred. No. 0.00046;
74; Conservative 36; Mismatches 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      h
Similarity · 24.8%;
56; Conservative 3:
EVRLGGDVVRGQIPVGDLGQRVQHLNLPPSISKVLQDPAREAEDAAVEQAYQRRTPQQWQ
                                                                        GDGFALRLSGEQAANVTVRFPSELGEDVRQPNEELRPLWSSGQYIVPGRVVLGKTTPVIY 181
                                                                                                                                                   GEGAATPATPAPAAPATPATPAPAAPAPAPAPATKLPTVATAANVLKLPGVTITAPKALKM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAGTVIQADHNMDGAS-----IVIQHTNGFVSSYIHIKDAQVK--TGDTVRTGQRIAS 293
                                                                                                                                                                                                                            GVAGAYTVKKGDTLYSLARGSGLTVDALMRLNGL-STPELRVGQVIKL-------P
                                                                                                                                                                                                                                                               GVPNRYQVKQGDTVSKIAQRYGLNWREIGHINNLNSSYTIYTGQWLTLWSGDLKVRERSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MGSTGQSTGQHL-HFEIHKNGIPVDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           M--KNOPSGAALFEFRISRNGVYVDP 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ASGTVVFSGFGASGSGFGGYGYVVKIDHGNGFQTLYGHMRAGSLKVVTGQQVSQGQPIGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGGQFIKPASGILTSGFSERTNPVTGKYESHKGQDIAGGGTVT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TPSPVAVQSSRPPVQQHPAVQKPTPPVVVVKKPTPTPPVVQQPAPVAPPVTEAPFATGSS 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GVMQFRYPVGA-----TNPVVRRF----GTATVAGSTVTSNGMWFSGRDGDLINAS 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AKQEAAIKAAEEKRMQEAAAASSAKSAAVVK------QPSSSSNEATE----TVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EKNDLVMALANKKDLT-----KSEQTLLASE----QGALTDEEKRLASNIAGEK
                                                                                                              ----VVQQPAPVAPPVTE----APFATGSSGVMQFRYPVGATNPVV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 33; Mismatches 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         GB:AE000513; NID:g6458563; PIDN:AAF10427.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          432
                                                                                                                                                                                                                                                                                                                                        Length 375;
                                                                                                                                                                                                                                                                                                       Indels 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 436;
                                       ------RR-----
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  241
                                     213
                                                                                                              211
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                                                                                                                                                                                         173
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probable peptidase - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change
C;Accession: T36379
R;Oliver, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell,
submitted to the EMBL Data Library, April 1999
A;Reference number: Z21573
A;Accession: T36379
A;Scatus: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-228 <OLT
A;Experimental source: Strain A3(2)
C.comption
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status; preliminary
A;Molecule type: DNA
A;Residuse: 1-437 <GLA>
A,ICOSS-:references: GB:AL592022; PIDN:CAC97874.1; PID:g16415184; GSPDB:GN00178
A;Experimental source: strain Clip11262
C;Genetics:
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C;Bate: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C;Aacession: ABI763
C;Aacession: ABI763
R;Glaser; P; Frangenl; L.; Buchrieser, C; Amend, A.; Baquero, F; Berche, P;
; Dominguez-Bernal, G; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; I
D.; Jones, L.M.; Karst, U.
D.; Jones, L.M.; Karst, U.
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Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.;
A;Authors: Kreft, J.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.;
A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AB1763
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AB1763
cell wall binding protein homolog lin2647 [imported] - Listeria innocua (strain Clip1126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              밁
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Best Local Similarity
Matches 62; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                136 TPSPVAVQSSRPPVQQHPAVQKPTPPVVVVKKPTPTPPVVQQPAPVAPPVTEAPFATGSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         255 AKQEAAIKAAEEKRMQEAAAKNAT------VAAQQPSSVTSSAGTGATDTVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    210 EKNDLVMALANKKDLT------KSEQTLLTNE-----QGALSDEQKKLASNIAGEK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76 KQGDTVSKIAQRYGLNWREIGHINNLNSSYTIYTGQWLTLWSGDLKVRERSISSGVNTAH 135
                                                                                                                                                                                                                                                                                                                                                                                                                        MGSTGQSTGQHL-HFEIHKNGIPVDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAGTVIQADHNMDGAS-----IVIQHTNGFVSSYIHIKDAQVK--TGDTVRTGQRIAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  M--KNOPSGAALFEFRISRNGVYVDP 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ASGRVVFSGFGATGSGFGGYGYVVKIDHGNGFQTLYAHMRAGSLKVVTGQQVSQGQPIGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGGQFIKPASGMLTSGFSERTNPVTGKYESHKGQDIAGGGTIT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GVMQFRYPVGA-----TNPVVRRF----GTATVAGSTVTSNGMWFSGRDGDLINAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QPFASALASGKATSSSFGQPRTYVAGGKVAYHYGTDYPARSGTAVLAINDGTVVIAGRYP 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VRGGLVVIDHGAGVVSLYFHQSKVTAKVGQQIKRGQKVGEV 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9.3%; Score 155; DB 2; Length 437; ilarity 23.3%; Pred. No. 0.00092; Conservative 35; Mismatches 103; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---GMWFSGRDGDLINASNAGTVIQAD-HN 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----VSAA
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Voss, H.; Wehland,
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Fsihi, H.
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PIDN:CAB40868.1; GSPDB:GN00070; SCOEDB:SCE94.19c

B.G.; 03-Dec-1999

Rajandream,

706 LLVQAGQQVRQGQQIAAM---

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--GSTGFSTGPHTHFEIHKTGKGAINPIAML

752

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R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, SDNA Res. 8, 205-213, 2001

A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A;Reference number: AB1807; MUID:21595285; PMID:11759840

A;Accession: AB2225
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A;Residues: 1-760 <KUR>
A;Cross-references: GB:BA000019; PIDN:BAB75052.1; PID:g17132448; GSPDB:GN00179
A;Experimental source: strain PCC 7120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Accession: AB2225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein alr3353 [imported] - Nostoc sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Gene: SCOEDB:SCE94.19c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Species: Nostoc sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
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                                    646
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                                                                                                                                                                                                                                                                                                                  406 SVPITVPTPGADSETPVDTIVPLESASAPAETQGVGGNVPIPKAFIEIQRPQQPGKRAAR 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          219 VAGSTVTSNGMW----FSGRD-----GDLINASNAGTVIQADHN------MDGASIVIQHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity 20.1
95; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                           LKVRERSISSGVNTAHTPS------
                                                                                                                                                                                                                                                                                                                                                                                                                                                          QPLTETSASTANTYEVKPGDTLAAIASRYNTSVAELVKVNNLSNPNQLKISQQLIIPS--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QVITD-SQGVPNRYQVKQGDTVSKIAQRYGLNWREIGHINNLNSSYTIYTGQWLTLWSGD 119
 AQVKTGDTVRTGQRIASMKNQPSGAALF---
                                 GWRWGRMHRGIDIAAPVGTPVFAAADGVVEKSGWNRGGYGNLVDIRHPDGSLTRYAHNSR
                                                                                                      RLNASESLGRMRGTTVSPKLPPLAAVDQYLPQAIDESVPPPSDSTTAFIWPAKGVLTSGY 645
                                                                                                                                                                                                                                              AKGDRLRSLQAEIQRLQAKYRDQQTGNTFVFVVANQNNNTAIFIFVTSFNNFAVTRFISR 525
                                                                                                                                                                                                                                                                                                                                                                                        ----AIDSSSTIAQAPAIISSNRVQYPGTPTVPNFPVDTARVNPSLPVAQPPSIANND 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LK 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LSASFAQNGGMWAHKHSGQDFAVPIGTNVVAAHGGTVVKAGGNGAGDGPAYGNAIVIKHG
                                                                                                                                         ----TSNG 228
                                                                                                                                                                          QQEIAVPIAVPTPLAPNDSNHPVKPQFRATLPVNEALNPEFLPNNAPQNPSVRRVATPPV
                                                                                                                                                                                                             ---PAPVAPPVTEAPFATGSSGVMQFR--YPVGAT---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NGFVSSYIHIKDAQVKTGDTVRTGQRIASMKN--QPSGAAL-FEFRISRN-GVYVDPLTV 320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9.1%;
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37.7%; Pred. No. 0.00055;
                                                                  ----DGDLINASNAGTVIQADHNMDGAS--IVIQHTNGFVSSYIHIKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 152; DB 2;
Pred. No. 0.0031;
1; Mismatches 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                   TPTPPVVQQ
                                                                                                                                                                                                                                                                                                                                                                                                                         ----PVAVQSSRP--PVQQHPAVQK--
-EFRISRNGV-YVDPLTVL 321
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Query Match
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Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.;
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.;
A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AG1147
                                                                                                                                                                                                                                                                                                                                    C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision
C;Accession: AG1147
                                                                                                                                                                                                                                                                                 R;Glaser, P.; Frangeul, L.; .; Dominguez-Bernal, G.; Duc
                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 31
AG1147
P60 extracellular protein, invasion associated protein Iap [imported] - Listeria monocyto
     A;Cross-references: GB:NC_003210;
                             A; Residues: 1-482 <GLA>
                                                        A; Molecule type: DNA
                                                                                A;Status: preliminary
                                                                                                                                                                                                                                                              D.; Jones, L.M.; Karst,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Gene: acmA
C;Keywords: hydrolase
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A;Cross-references: GB:AE005176; PID:g12723133; PIDN:AAK04370.1;
A;Experimental source: strain IL1403
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus A;Reference number: A86625; MUID:21235186; PMID:11337471 A;Accession: H86658
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
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                                                                                                                                                                                                                                                                                    L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8.8%; Score 146.5; DB 2; 23.6%; Pred. No. 0.0038;
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PIDN:CAC98661.1; PID:g16409958;
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     GSPDB: GN00177
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Voss, H.; Wehland,
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source:

strain

BG.

8.8%;

Score

146.5;

ВB

2

Length

482;

Qy 90 LNWREIGHINNLASSYTIYTGQWLTLWSGDLKVRERSISSGVNTAHTPSPVAQQSSRPPV 149 c) 1	Qy 25 ITTCİLAGCASKPTYNSTSGSGSHRTSGSGGLAIGSQVITD	C;Genetics: A;Gene: iap A;Gene: iap F;1-27/Domain: signal sequence #status predicted <sig> F;1-27/Domain: signal sequence #status predicted <mat> F;28-484/Product: protein 60 #status predicted <mat> Query Match Best Local Similarity 20.6%; Score 146.5; DB 2; Length 484; Best Local Similarity 20.6%; Pred. No. 0.0043; Matches 81; Conservative 46; Mismatches 121; Indels 145; Gaps 14;</mat></mat></sig>	nce number: A41487; MUID:90256283; PMID:2111287 ion: A41487 le type: DNA es: 1-484 < KOE> references: GB:X52268 ion: B41487 le type: protein es: 28-49 < KO2>	eria asso gene e_re e_re 19), 19	QY 250 ADHNMD	Qy 150 QQHPAVQKPTPPVVVVKKPTPTPPVVQQPAPVAPPVTEAPFATGSSGVMQ 199	Best Local Similarity 20.6%; Pred. No. 0.0043; Matches 81; Conservative 46; Mismatches 121; Indels 145; Gaps 14; Oy 25 ITTCILAGCASKPTYNSTSGSGSHRTSGSGGLAIGSOVITD
RESULT 34 \$76492 Ilipoprotein nlpD - Synechocystis sp. (strain PCC 6803) N'Alternate names: protein slr0993 C;Species: Synechocystis sp. A;Variety: PCC 6803	Db 323 TPSKWINTNTNTNINTNQGSTINNASASALIAEAQKHLGKAYSWGGNGFTTFDC 377 Qy 265 NGFVSSYIHIKDAQVKTGDTVRTGQRIASMKNQPSGAALFEFRISRNGVYV 315	91 NWREIGHINNIASSYTIYTGGWLTLWSGDLKVRESISSGVNTAHTSSPVAVQSSREPVQ : ::	ITTCILAGCASKPTYNSTSGSGSHRTSGSGGLAIGSQVITD	A, Molecule type: DNA A), Residues: 1-465 < GLA- A), Residues: -465 < GLA- A), Residues: -465 < GLA- A), Cross references: GB: AL592022; PIDN: CAC95823.1; PID: g16413031; GSPDB: GN00178 A), Experimental source: strain Clipi1262 C)Genetics: A; Gene: iap A; Gene: iap Query Match Best Local Similarity 21.1%; Pred. No. 0.013; Matches 75; Conservative 51; Mismatches 143; Indels 87; Gaps 14;	.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H. D.; Jones, L.M.; Karst, U. Science 294, 849-852, 2001 A.Authors: Kreft, J.; Kinh, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Title: Comparative genomics of Listeria species. A.Reference number: AB1077; MUID:21537279; PMID:11679669 A;Scatus: preliminary	RESULT 33 . AG1506 AG1506 P60 extracellular protein, invasion associated protein Iap [imported] - Listeria innocua C; Species: Listeria innocua C; Species: Listeria innocua C; Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001 C; Accession: AG1506 C; Accession: AG1506 R; Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker	Db 260 -EAPAAEKQAAPVVKENTNTNTATTEKKETATQQQTAPKAPTEAAKPAPASTUTNA 315 Qy 200 FRYPVGATNPVVRREGTATVAGSTVTSNGMWFSGRDGDLINASNAGTVIQ 249 11

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A;Experimental source: strain 9a5c
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Agripson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H. Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H. Barlones, Docena, C.; Bl-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S. submitted to GenBank, June 2000
A;Authors: Perreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm J.D.; Junqueira, W.L.; Kemper, B.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, B.E.; Laigrandado, M.A.; Madeira, M.B.,; Matsino, C.L.; Marques, M.V.; Martine, E.A.; Michors: Martine, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, B.C.; Miyaki, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; M.; Santelli, R.V.; Sawasak Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein XF0987 [imported] - Xylella fastidiosa (strain 9a5c) C;Species: Xylella fastidiosa C;Species: Xylella fastidiosa C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000 C;Accession: C82736 C;Accession: C82736 R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Nature 406, 151-157, 2000
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                                                                                                                                                                                                                                                                                                A;Molecule type: DNA
A;Residues: 1-285 <SIM>
A;Cross-references: GB:AE003937; GB:AE003849; NID:g9105920; PIDN:AAF83797.1; GSPDB:GN00:
                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Title: The genome sequence of the plant pathogen Xylella fastidiosa A;Reference number: A82515; MUID:20365717; PMID:10910347 A;Note: for a complete list of authors see reference number A59328 be
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A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C;Genetics:
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A;Accession: S76492
A;Status: nucleic acid sequence not shown; translation
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A; Residues: 1-715 <KAN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAPIGTPIMAAASGEVVFSGWNSGGFGNLVKIRHGDGSVTYYAHNNRLLVRRGEYVEQGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YOVKOGDTVSKIAORYGLNWREIGHINNLNSSYTIYTGOWLTLWSGDL-----KVRERSI 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RIASM--KNOPSGAAL-FEFRISRNGVYVDPLTVL 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YNDTIQIPVIQEVSPELPGLSTPDFPRSPGQFNGYIWPAKGVFTSGFGPRWGRMHRGIDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---QFRYPV-----GATNPVVRRF-----GTATVAGSTVTSN-----GMWFSGRD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EPVPDWQARSPQALPAKFNQPRQDLAQLQRQYSPQAQRSQFSTSVGQSQIVGAAPSPVQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---PAVQKPTPPVVVKKPTPTPPVVQQPAPVAPPVTEAPFAT--GSSGVM------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PSFVSTQPTASTIVARAQAEPEAQYQTQLRAEVTQLNQTQPIRTPMVPRSALTVARQVNN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YQVKPGDTLSQIARSHDIQPEKIQQANGLSNPDEIKAEQILVIPPPNTVAAVPEPTPPSL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Score 138.5; DB 2;
; Pred. No. 0.027;
44; Mismatches 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  711
                                                                                                                                                                                                                                                                                                                                                                                                                                                     number A59328 below
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Yamada, M.; Yasuda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      677
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A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A;Reference number: A59328
A;Contents: annotation
C;Genetics:
C;Genetics:
A;Gene: XF0987
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IKRLGLIFGVITTCILAGC--ASKPTYNSTSGSGSHRTSGSGGLAIGSQVITDSQGVPNR 72
                                                                                             TATGTPVKAPAAGVITFAAPDLYLTGGTVLLDHGAGVSSNFLHLSRIDVKVGDHVDQGQV
                                                                                                                                                                                                                                                                                                                                                                                        SRVEYSGQVLRVDDKGQVVFGVGRNNIGPLILRIQSPEGTVKQVNITVTTRQW------
                                                                                                                                                                                                                                                                                                                                                                                                                                   YQVKQGDTVSKIAQR----YGLNWREIGH-INNLNS-----SYTIYTGQWLTLWSGD 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VNRL-LALGMLVTLTLPPITYAKNKTNTQETRSEFPTNVSQGALVIGT-----VPAG
IGAVGATGRATGPHL-HWGMNWFNVRIDPLLVLE 282
                                                                                                                                                                                           ----QITDARQRNDDRSDFAQAFIWPV--QGRISGRFGSARIYNGQTAGNG--HSGMDIA 189
                                                                                                                                                                                                                                           PVAPPVTEAPFATG--SSGVMQFRYPVGATNPVVRRFGTATVAGSTVTSNGMWFSGRD--
                                             IASM--KNQPSGAALFEFRISRNGVYVDPLTVLK 322
                                                                                                                                           GDLINASNAGTVIQA--DHNMDGASIVIQHTNGFVSSYIHIKDAQVKTGDTVRTGQR 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8.2%;
                                                                                                                                                                                                                                                                                           ----PLEVVNGVPPKTVNP-----PPEIAAR-----ITREQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      49;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 136.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             No. 0.011;
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C;Accession: D64158
R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, ;
Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.;
Science 269, 496-512, 1995
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A;Reference number: A64000; MUID:95350630; PMID:7542800 hypothetical protein HI0756 - Haemophilus influenzae (strain C;Species: Haemophilus influenzae C;Date: 18-Aug-1995 #sequence ravision in the control of the A;Accession: D64158
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DAA
A;Molecule: DAA
A;Residues: 1-410 <TICR>
A;Cross-references: GB:U32760; GB:L42023; NID:g1573764; PIDN:AAC22415.1;
A;Note: best homolog was a hypothetical protein from Escherichia coli ;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 08-Oct-1999 ;Accession: D64158 Matches Query Match Best Local Similarity 188 134 AHTPSPVAVQSSRPPV-QQHPAVQKPTPPVVVVKKPTPTPPVVQQPAPVAPPVTEAPFAT 192 74 63 ; STSGLGAAKKQYSLPVSGS--ILHTFG--SIQAGEVRWKGMVIGASAGTPVKAIAAGRVI GSSGV----MOFRYPVGATNPVVRRFGTATVAGSTVTSNGMWFSGRDGDLINASNAGTVI QKKQQQALQKAQQEHQ-----STLNELNKNLALDQDKLNT-----LKANEQALRQEIQR 236 QVKQGDTVSKIAQRYGLNWREIGHINNLNSSYTIYTGQWLTLWSGDLKVRERSISSGVNT 133 AEQAAREQEKREREALAQRQKAEEKRT-----8.1%; 36; Score 135; Pred. No. 0 Mismatches DB 2; 111; Length 410 Indels -SKPYQPTVQERQLLN ᇟ 42; PID:g1573765; 248 278

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QADH-NMDGASIVIQHTNGFVSSYIHIKDAQVKTGDTVRTGQRIASMKN--QPSGAALFE

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hypothetical protein HI0409 - Haemophilus influenzae (strain Rd KW20)
(;Species: Haemophilus influenzae
(;Species: Haemophilus influenzae
C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 29-Sep-1999
C;Accession: F64151
R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage,
C;Gccayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman,
D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.
Science 269, 496-512, 1995
Science 269, 496-512, 1995
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,
A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A;Reference number: A6400; MUID:9535030; PMID:7542800
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C, Species: Pseudomonas aeruginosa
C, Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C, Accession: A83005
R; Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A, Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic A, Reference number: A82950; MUID: 20437337; PMID: 10984043
A, Accession: A83005
A, Status: preliminary
A, Status: preliminary
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, Residues: 1-428 <STO>
;Cross-references: GB:AE004926; GB:AE004091; NID:g9951424; PIDN:AAG08518.1;
;Experimental source: strain PAO1
                                                                             Cross-references: GB:U32724; GB:L42023; NID:g1573378; PIDN:AAC22068.1; PID:g1573382; Note: best homolog was a hypothetical protein from Escherichia coli Superfamily: hypothetical protein HI0409
                                                                                                                                                        Status: nucleic acid somolecule type: DNA Residues: 1-475 <TIGR>
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Best Local :
        Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             140 VAVQSSRPPVQQHPAVQKPTPPVVVVKKPTPTPPVVQQPAPVAPPVTEAPFATGSSGVMQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           200 FRYPVGATNPVVRRFGTATVAGSTVTSNGMWFSGRDGDLINASNAGTVIQADHNMDGAS-
           Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LVILDHGGGYLSLYGHNQSLLKDA--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -IVIQHTNGFVSSYIH----IKDAQVKTGDTVRTGQRIASM--KNQPSGAALFEFRISRN
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llarity 28.2%;
Conservative 28
                                                                                                                                                                                                           acid sequence not shown; translation not shown
        7.9%;
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; Pred. No. 0.02
28; Mismatches
        Pred. No. 0.
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           DB 2;
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K.; Lim,
                                                                                                                                                                                                                                                                                                              Venter,
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probable cell wall protein - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
C;Accession: E75461
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Do, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zale S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodu A;Reference number: A75250; MUID:20036896; PMID:10567266
A;Accession: E75461
A;Scatus: preliminary
A;Molecule type: DNA
A;Residues: 1-665 <WHI >
A;Residues: 1-665 <WHI >
A;Experimental source: strain R1
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RESULT 39
S71558
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Plant Mol. Biol. 31, 771-781, 1996
A;Title: Transcripts of a gene encoding a putative cell
A;Reference number: S71558; MUID:96400032; PMID:8806408
A;Accession: S71558
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A; Residues: 1-376 < GOO>
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                217 RKEVLKGEIQNSLNSSLREKGLDTRQISQLSNALQWQVSLRKLKKGTQFAILVSREYLGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      72 RYOVKOGD---TVSKIAQRYGLNWREIGHINNL-----
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                                                                 SSGVMQFRYPVGATNPVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HLSKSLVKAGQTVKKGERIALSGNTGISTGPHLHYEFHI--NGRAVNPLTV 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTATVAGSTVTSNGMWFSGRDGDLINASNAGTVIQADHNMDGAS--IVIQHTNGFVSSYI 272
                                                                                                                                                TPTPPVVTPPTPPTPPVVTPPTPAPVVTPPTPPVVTPPTPPVVTPPTPPVVTPPTPPVVT-
                                                                                                                                                                                                              TPSPVAVQSSRPPVQQHPAVQKPTPPVVVVKKPTPTPPVVQQPAPVAPPVT--EAPFATG 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HIKDAQVKTGDTVRTGQRIASMKNQ--PSGAAL-FEFRISRNGVYVDPLTV
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243
                                                                      211
                                                                                                                                                                                                                                                                                             Score 131; DB 2; Length 376; Pred. No. 0.041; Indels
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GB:AE000513; NID:g6458624; PIDN:AAF10484.1;

PID:g645862

J.D.; Dodson, T.; Zalewski,

R.J. Ma.

radiodurans

R1

Search completed: Job time : 44 secs	망	Ş	Db	Ş	ΣЪ	Ş	B	Ş	Db		Query Ma Best Loc Matches	C;Genetics: A;Gene: DR0910 A;Map position: 1
Search completed: July 8, 2003, 11:08:21 Job time : 44 secs	183 RVEQLERINGLIGDAL 198	290 RIASMKNQPSGAAL 303	140QRLNGLKGNTIAVGQVLRLTAPPTTYRVQPGDTLPKIGVKVGL 182	245 GTVIQADHNMDGASIVIQHTNGFVSSYIHIKDAQVKTGDTVRTGQ 289	110 LKPAP	185 VTEAPFATGSSGVMQFRYPVGATNPVVRRFGTATVAGSTVTSNGMFSGRDGDLINASNA 244	71TPLVKLSPAPVKLVPA	130 GVNTAHTPSPVAVQSSRPPVQQHPAVQKPTPPVVVVKKPTPTPPVVQQPAPVAPP 184	26 PQTVVVRPGQTLYRIALQNGLSVAELQRLNGLHST-TIEVGQVLRV 70	70 PNRYQVKQGDTVSKIAQRYGLNWREIGHINNLNSSYTIYTGQWLTLWSGDLKVRERSISS 129	Query Match 7.8%; Score 130.5; DB 2; Length 665; Best Local Similarity 25.0%; Pred. No. 0.092; Matches 64; Conservative 25; Mismatches 62; Indels 105; Gaps 11;	: :0910 tion: 1

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YIBP_HABIN
YEBA_HAEIN
ACMA_LACLC
PRLB_ACHLY
GUNA_CALSA
MUR2_ENTHR
LA17_YEASTI
LA17_YEASTI
LYCES
NLPD_BUCALI
NFF1_LYCES
NLPD_STERN
MOZ_HUMAN
HES1_RAT
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                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Pred. No. 8.5e-14;
0; Mismatches 106
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N-ACYL DIGLYCERIDE (PROBABLE).
; 2CDFD26FF4CBC704 CRC64;
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Best Local S
Matches 78
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SEQUENCE
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Hypothetical protein; Membrane; Lipoprotein;
Complete proteome.
                                                                                   SEQUENCE FROM N.A.

STRAINARd / KW20 / ATCC 51907;

MEDLINE=95350630, PubMed=7542800;

Relighmann R.D., Adams M.D., White O., Clayton R.A., Kirkness B.F.,

Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,

Kerlavage A.R., Sutt C.J., Tomb J.-F., Dougherty B.A., Gocayne J.D.,

McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,

Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,

Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,

Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,

Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,

Fine L.D., Fritchman J.L., Fuhrmann J.L., Gocghagen N.S.M.,

Gnehm C.L., McDonald L.A., Small K.V., Frasear C.M., Smith H.O.,

Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                       LPPB HABIN STANDARD; PRT; 405 Am. P44833; 91-NOV-1995 (Rel. 32, Created) 01-NOV-1995 (Rel. 32, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) 0uter embrane antigenic lipoprotein B precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pfam; pF01476; LysM; 1.
pfam; pF01551; Peptidase_M37; 1.
pfam; pF00157; LysM; 1.
sMART; SM00257; LysM; 1.
prosire; pS00013; pROKAR_LIPOPRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIGNAL
          "Whole-genome random sequencing and assembly of RCI.", SCIENCE 269:496-512(1995).
-I- FUNCTION: MAY BE A VIRULENCE DETERMINANT.
-I- SUBCELLULAR LOCATION: Attached to the outer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR002886; Peptidase_M37
                                                                                                                                                                                                                                                                                                                     Haemophilus influenzae.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                   Haemophilus.
NCBI_TaxID=727;
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78; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RYRATAIDPLRYL 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KTASVTPSSAVPKSSWPPVGORCWLWPTTGKVIM---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KSLGIVMLLSVGLLLAGC-----SGSKSSDTGTYSG-----SVYTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SRNGVYVDPLTVL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STADGG----
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251 HYPOTHETICAL LIPOPROTEIN YGER.
26 N-ACYL DIGLYCERIDE (POTENTIAL)
26564 MW; FCD6235D39790475 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14.3%; Score 238; D)
24.9%; Pred. No. 9.4;
:ive 46; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      321
                                                                                                                                                                                                                                                                                                                      gamma subdivision; Pasteurellaceae;
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                 membrane
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RESULT 4

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DT 15-UN

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Q56131;
Q1-NOV-1997
15-JUN-2002
15-JUN-2002
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SEQUENCE
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MEDLINE=21534947; PubMed=11677608;
Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebail Baker S., Basham D., Brooks K., Chillingworth T., Connerton P. Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J. Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagel
                                                                                                                                          SEQUENCE FRO
                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; gamma subdivision;
                                                                                                                                                                                                                                                                              Salmonella typhi
                                                                                                                                                                                                                                                                                                      Lipoprotein nlpD precursor. NLPD OR STY3050.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF01476; LysM; 1.
Pfam; PF01551; Peptidase_M37; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U32753; AAC22363.1; -. MEROPS; M37.UPW; -.
                                                                                                                                                                                                                                     Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This
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InterPro; IPR002886; Peptidase_M37.
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                                                                                                                                                                                                                TaxID=601;
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6; Mismatches
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Pred. No. 3e-
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use by non-profit institutions as content
modified and this statement is not removed. Usage by ar
entitles requires a license agreement (See http://www.isb-
or send an email to license@isb-sib.ch).
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Pfam; PF01551; Peptidase_M37; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=95220644; PubMed=7705608;
Robbe-Saule V., Coynault C., Novel F.;
"The live oral typhoid vaccine Ty21a is a rpoS m
susceptible to various environmental stresses.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Whitehead S., Barrell B.G.; "Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18.";
                                                                                                                                                                                                                                                                                                                          SIGNAL
                                                                                                                                                                                                                                                                                                                                                                SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL;
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between the Swiss Institute of Bioinformatics and the EMBL
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Quail M., Rutherford K
                                                                                                                                                                                                                                                                                                                                                    PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR002482; LysM
InterPro; IPR002886; Pept
                                                                                                                                                                                                                                                                                                                                                                                                                            MEROPS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SIMILARITY: BELONGS TO THE E.COLI NLPD / HAEMOPHILUS LPPB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SUBCELLULAR LOCATION: Attached to the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               AL627276; CAD06031.1; -.
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                                                                                                                                                                                                                                                                                                                                       membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  X81641; CAA57297.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pos mutant atters postulated by live typhoid vaccine Ty21a.";
liverobiol. Lett. 170:141-143(1999).

NCTION: MAY BE INVOLVED IN STATIONARY-PHASE SURVIVAL.
                                                                                                                                                                                                                                                                                                                                                 SM00257; Lysm;
E; PS00013; PRO
                                                                                                                                                                         84;
                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                            M37.UPW;
                                                                                         QVITDSQ------GVP-------NRYQVKQGDTVSKIAQRYGLNWREIGHI
                                                                         QPVTEQPVQMENGRIVYNRQYGNIPKGSYTGGSTYTVKKGDTLFYIAWITGNDFRDLAQR
                                                  NNLNSSYTIYTGQWL---
                                                                                                                        LAGCTSSSNPPAPVTSVDSGSSSNTNSGMLITPPPKMGATPQQAPQIQPVQRPVTQPMQT
                                                                                                                                                LAGCASK-----PTYNSTSGSGSHRTSG-----SGGL-
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-----QHPAVQKPT--PPVVVVKKPTPTPPVVQQPAPVAPPVTEAPFATGSSGVMQFR
                       NSISAPYSLNVGQTLQVGNASGTPITGGNAITQADAAQQGVVTRSAQNSTVAVASQPTIT
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205 1
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39183 MW;
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                                                                                                                                                                                     Score 210;
Pred. No. 1
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                                               ---TLWSGDLKVRERSISSGVNTAHTPSPVAVQSSRPPV-
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N-ACYL DIGLYCERIDE
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EMBL; X82129; CAA57639.1; -.
MEROPS; M37. UPW; -.
InterPro; IPR002482; Lysm.
InterPro; IPR002482; Peptidase_M37.
InterPro; IPR000437; Prok_1ipoprot.
Pfam; PP01476; Lysm; 1.
Pfam; PP01551; Peptidase_M37; 1.
SMART; SM00257; Lysm; 1.
PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
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P39700;
01-FEB-1995
16-OCT-2001
15-JUN-2002
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SIGNAL
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REPEAT
                                                                                                                                                                                                                                                                                                                                                        Krause M.W., El-Gedaily A.;
Submitted (OCT-1994) to the EMBL/GenBank/DDBJ databases.
-i- FUNCTION: MAY BE INVOLVED IN STATIONARY-PHASE SURVIVAL.
-i- SUBCELLULAR LOCATION: Attached to the inner membrane by a lipid
-i- SUBCELLULAR LOCATION: Attached to the inner membrane by a lipid
-i- SIMILARITY: BELONGS TO THE E.COLI NLPD / HAEMOPHILUS LPPB FAMILY.
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                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Paesold G., Krause M.;
"Analysis of rpoS mRNA in Salmonella dublin: identification of
multiple transcripts with growth-phase dependent variation in
transcript stability.";
J. Bacteriol. 181:1264-1268(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Salmonella dublin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=98360;
                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 284-377
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(Rel. 40, Last sequence update)
(Rel. 41, Last annotation update)
nlpD precursor.
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Lipoprotein; R
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6 377 N
6 26 N
3 250 4
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n; Repeat; Signal.
BY SIMILARITY.
LIPOPROTEIN NLPD.
N-ACYL DIGLYCERIDE (BY SIMILARITY).
4 X 7 AA APPROXIMATE REPEATS.
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RESULT 6
NLPD_SALTY
ID NLPD_S.
AC P40827
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Best Local
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P40827;

01-FHB-1995 (Rel. 31, Created

15-JUN-2002 (Rel. 41, Last and 15-JUN-2002 (Rel. 41, Last and 15-JUN-2002 (Rel. 41, Last and Lipoprotein nlpb precursor.
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REPEAT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                            STRAIN=LT2 / SGSC1412 / ATCC 700720;

MEDLINE=21534948; PubMed=11677609;

MCCLelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,

McCurtney L., Porwollik S., Ali J., Dante M., Du P., Hou S., Layman D.,

Courtney L., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,

Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,

Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,

Waterston R., Wilson R.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Salmonella typhimurium.
Bacteria; Proteobacteria;
                                                                    MEDLINE=94368857; PubMed=8086465;
Prince R.W., Fang F.C., Libby S.J.;
Prince R.W., Fang F.C., Libby S.J.;
"Cloning and sequencing of the gene encoding
factor from Salmonella typhimurium 140288.";
Biochim. Biophys. Acta 1219:198-200(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. STRAIN=LT2 / SGSC1
     SEQUENCE OF STRAIN=C52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=602;
                                                                                                                                                                                           SEQUENCE OF 280-377 FROM N.A. STRAIN=ATCC 14028S;
                                                                                                                                                                                                                                                                        Nature 413:852-856(2001).
                                                                                                                                                                                                                                                                                                       'Complete genome sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             147
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84; Conser
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ilarity 23.0%;
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39671
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Last sequence update)
Last annotation update)
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Matches 84
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CONFLICT
SEQUENCE
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REPEAT
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InterPro; IPR002886; Peptidase_M37.
InterPro; IPR000437; Prok_lipoprot.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute. The use by non-profit institutions as not removed. modified and this statement is not removed. entitles requires a license agreement (See lor send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF01551; Peptidase M37; 1.
PROSITE; PS00013; PROKAR_LIPOPROTEIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AE008833; AAL21805.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            J. Bacteriol. 176:6852-6860(1994).
-i- FUNCTION: MAY BE INVOLVED IN STATIONARY-PHASE SURVIVAL.
-i- SUBCELLULAR LOCATION: Attached to the inner membrane by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kowarz L., Coynault C., Robbe-Saule V., Norel F.; "The Salmonella typhimurium katf (rpoS) gene: cloning, sequence, and regulation of spvR and spvABCD virulence
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NPLRYL 374
                                   DPLTVL 321
                                                                      GNLIIIKHNDDYLSAYAHNDTMLVREQQEVKAGQKIATMGSTGTSSTRLHFEIRYKGKSV
                                                                                                         S--IVIQHTNGFVSSYIHIKDAQVKTGDTVRTGQRIASMKNQPSGAALFEFRISRNGVYV
                                                                                                                                                 SAWRWP--TDGKVIENFG
                                                                                                                                                                                  MOFRYPVGATNPVVRREGTATVAGSTVTSNGMWFSGRDGDLINASNAGTVIQADHNMDGA
                                                                                                                                                                                                                                                           PPV-----QQHPAVQKPT--PPVVVVKKPTPTPPVVQQPAPVAPPVTEAPFATGSSGV
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                                                                                                                                                                                                                                                                                                                                                                                                              -IGSQVITDSQ------GVP-----NRYQVKQGDTVSKIAQRYGLNWRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                   LAGCTSSSNPPAPVTSVDSGSSSNTNSGMLITPPPKMGATTQQTPQQAPQIQPVQRPVTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LAGCASK-----PTYNSTSGSGSHRTSG-----SGGLA-----
                                                                                                                                                                                                                         PTITYSEGSGEQSANKMLPNNKPAGTVVTAPVTAPTVSTTEPNASSTSTSAP
                                                                                                                                                                                                                                                                                                                                     IGHINNLNSSYTIYTGQWL-----TLWSGDLKVRERSISSGVNTAHTPSPVAVQSSR
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-; NOT_ANNOTATED_CDS
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243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              56;
                                                                                                                                               -ASEGG----NKGIDIAGSKGQAIVATADGRVVYAGNALRGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 209; DB
Pred. No. 1.5e
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LIPOPROTEIN NLPD.

N-ACYL DIGLYCERIDE (BY SIMILARITY).

4 X 7 AA APPROXIMATE REPEATS

1.
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27C29D77A145ABF0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1;
.5e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Complete
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CRC64;
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RESULT 7
NLPD_ECOLI
SIGNAL
CHAIN
LIPID
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P33648;
                                                                                       Pfam; PF01476; LysM; 1. — Pfam; PF01551; Peptidase M37; 1. SMART; SM00257; LysM; 1. — PROKAR_LIPOPRO PROSITE; PS00013; PROKAR_LIPOPRO
                                                                                                                                                                                                            EMBL;
                                                                                                                                                                                                                        EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
                                                                                                                                    EcoGene; EG12111; nlpD.
InterPro; IPR002482; LysM.
InterPro; IPR002886; Peptidase_M37
                                                                                                                                                                                                                                                          entities requires a license agreement (Some send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Ew the European Bioinformatics Institute. There are no restructe by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lipoprotein nlpD
NLPD OR B2742.
           REPEAT
                                                                                                                                                                                                                                                                                use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=94268497; PubMed=8208244;
Takayanagi Y., Tanaka K., Takahashi H
"Structure of the S' upstream region
gene of Escherichia coli.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=K12 / MG1655;
MEDLINE=97426617; PubMed=9278503;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ichikawa J.K., Li C., Fu J.C., Clarke S.;
"A gene at 59 minutes on the Escherichia coli chromosome
"Ipoprotein with unusual amino acid repeat sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Escherichia coli
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                                 DOMAIN
                                                                                                                                                                                      MEROPS;
                                                                                                                                                                                                   EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 99-379 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                         ol. Gen. Genet. 243:525-531(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteriol. 176:1630-1638(1994).
                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: BELONGS TO THE E.COLI NLPD / HAEMOPHILUS
                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: Attached to
                                                                                                                                                                                                                                                                                                                                                                  anchor (Potential)
                                                                                                                                                                                                 D17549;
                                                                                                                                                                                                          L07869; AAA17875.1; -. U29579; AAA69252.1; -. AE000358; AAC75784.1;
                                                                                                                                                                                     M37.UPW;
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                                                                              Lipoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           precursor
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40,
                                                                                        PROKAR_LIPOPROTEIN;
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26
97
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                                N-ACYL DIGLYCERIDE.
4 X 8 AA TANDEM REPEATS
                                                                            Repeat; Signal; Complete
                                             LIPOPROTEIN NLPD.
N-ACYL DIGLYCERIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        subdivision; Enterobacteriaceae;
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STATIONARY-PHASE SURVIVAL.
(APPROXIMATE)
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Best Local S
Matches 72
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REPEAT

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CONFLICT

SEQUENCE
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_HAESO
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01-NOV-1995
01-OCT-1996
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                                                                                                      STRAIN=HS25;
MEDLINE=9339280; PubMed=8478068;
Theisen M., Rioux C.R., Potter A.A.;
"Molecular cloning, nucleotide sequence, a
"Molecular an antigenic 40-kilodalton
                                                                                                                                                                                                                                                                          Haemophilus somnus.
Bacteria; Proteobacteria;
Haemophilus.
                                                                                                                                                                                                                                                                                                                                                              LPPB_HAESO
P36685;
                                                                                                                                                 CONCEPTUAL
                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                               ANCHOR.

SIMILARITY: BELONGS TO THE E.COLI NLPD / HAEMOPHILUS LPPB FAMILY.
CAUTION: THIS IS A CONCEPTUAL TRANSLATION; THREE FRAMESHIFTS HAD
TO BE INTRODUCED IN POSITIONS 264, 266 AND 328.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                       Immun. 61:1793-1798(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YQVKQGDTVSKIAQRYGLNWREIGHINNLNSSYTIYTGQWLTLWSGDLKVRERSISSGVN 132
                                                                                                                                                                                                                                                                                                                                                                                                                             KAGOKIATMGSTGTSSTRLHFEIRYKGKSVNPLRYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                RTGQRIASMKNQPSGAALFEFRISRNGVYVDPLTVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GIDIAGSKGQAIIATADGRVVYAGNALRGYGNLIIİKHNDDYLSAYAHNDTMLVREQQEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GMWFSGRDGDLINASNAGTVIQADHNMDGAS--IVIQHTNGFVSSYIHIKDAQVKTGDTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TPPVVQQPAPVAPPVTEAPFATG---SSGVMQFRYPVGATNPVVRRFGTATVAGSTVTSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ASGTP1TGGNA1TQADAAEQGVV1KPAQNSTVAVASQPT1TYSESSGEQSANKMLPNNKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TAHTPSPVAVQSSRPPVQQHPAVQKP--TPPVVVVKKPT--------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TATTVTAPVTVPTASTTEPTVSSTSTSTPISTWRWP--TEGKVIETFG-ASEGG----NK
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(Rel. 32, Last sequence upd
(Rel. 34, Last annotation u
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90

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211

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245

245

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40149 MW;
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                                                                                                                                                                                                                                                                                       gamma
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Pred. No. 4.1e-07;
2; Mismatches 113;
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A8E6A2B8456105FE CRC64;
                                                                                                                                                                                                                                                                                        subdivision;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (APPROXIMATE).
7 AA APPROXIMATE REPEATS
                                                                                                                                                                                                                                                                                                                                           update)
                                                                                                                                                                                                                                                                                                                                                                          337
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B precursor
                                                                                                                                                                                         and characterization of
n lipoprotein of Haemophilus
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                                                                                                       by · а
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RESULT ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL ACMAL
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Best Local S
Matches 61
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NON TER
SEQUENCE
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Outer men
SIMILARITY).

1. CAPALYTIC ACTIVITY: Hydrolysis of the 1,4-beta-linkages between acetyl-D-glucosamine and N-acetylmuramic acid in peptidoglycan heteropolymers of the prokaryotes cell walls.

1. DOMAIN: THE LYSM REPEATS ARE THOUGHT TO BE INVOLVED IN PEPTIDOGLYCAN BINDING.

1. SIMILARITY: BELONGS TO FAMILY 73 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                SEQUENCE FROM N.A.

STRAIN-IL1403;

MEDLINE-21235186; PubMed=11337471;

MEDLINE-21235186; PubMed=11337471;

Bolotin A., Wincker P., Mauger S., Jaillon O., Malarme K.,

Weissenbach J., Ehrlich S.D., Sorokin A.;

"The complete genome sequence of the lactic acid bacterium L.

1actis ssp. lactis IL1403.";

Genome Res. 11:731-753 (2001).

Genome Res. 11:731-753 (2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence up)
15-UNN-2002 (Rel. 41, Last annotation)
Probable N-acetylmuramidase precursor
hydrolase) (Autolysin) (Lysosyme).
ACMA OR LL0272.
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Pfam; PF01551; Peptidase_M37; 1.
SMART; SM00257; LysM; 1.
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MEROPS; M37.UI
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InterPro; IPR002886; Pept
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
Bacteria; Pirmicutes; Lactobacillales; Streptococcaceae; Lactococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACMA LACLA
Q9CIT4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=1360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  73
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337 AA;
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Pred. No. 1.4e-06;
B; Mismatches 104
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(EC 3.2.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                           P60_LISMO STANDARD;
P21171; Q03493;
01-MAY-1991 (Rel. 18, Created)
01-NOV-1995 (Rel. 32, Last seq
15-JUN-2002 (Rel. 41, Last ann
          SEQUENCE

MEDLINE=90256283; PubMed=2111287;
Koehler S., Leimeister-Machine
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                                                                                                                                                                                                                              Listeria monocytogenes
Bacteria; Firmicutes; I
                                                                                                                                                                                                                                                                                                   Protein p60 precursor IAP OR LMO0582.
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SMART; SM00047; LYZ2; 1.
SMART; SM00257; LYBM; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF01476; LysM; 3. Pfam; PF01832; Amidase_4; 1.
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InterPro; IPR000423; Flag_FlgJ.
InterPro; IPR002482; LysM.
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                                                                                                                                                                                               NCBI_TaxID=1639;
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RA Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,

Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,

Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,

A Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,

Bentian K.-D., Fshin H., Garcia-del Portillo F., Garrido P.,

Gautier L., Goobel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,

A Jones L.-M., Kaerst U., Krett J., Kuhn M., Kunst F., Kurapkat G.,

A Madueno E., Maicournam A., Mata Vicente J., Ng E., Nedjari H.,

A Madueno E., Maicournam A., Mata Vicente J., Ng E., Nedjari H.,

A Mordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,

A Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,

Varquez-Boland J.-A., Voss H., Wehland J., Cossart P.,

"Comparative genomics of Listeria species.",

Science 294:849-852(2001).

C -1-FUNCTION: THIS MAJOR EXTRACELULAR PROTEIN MAY BE INVOLVED IN THE
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               Query Match
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ListiList; LMO00582; -.
MEROPS; C40.UPW; -.
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                                                            SEQUENCE
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Pfam; PF01476; LysM; 2.
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InterPro; IPR000064;
InterPro; IPR003646;
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MEDLINE=21537279; PubMed=11679669;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Structural and functional properties different Listeria species.";
J. Bacteriol. 174:8166-8171(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE: FROM N.A., AND DISCUSSION OF STRAIN-Mackaness / Serovar 1/2a; MEDLINE=93094153; PubMed=1459966; Bubert A., Kuhn M., Goebel W., Koehler
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STRAIN=Mackaness /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       use as a specific probe for Listeria monocytogenes.", Infect. Immun. 58:1943-1950(1990).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -1- DOMAIN: LYSM REPEATS
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SM00287; SH3b;
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DISCUSSION OF SEQUENCE.

MEDLINE-93094.153; PubMede1459966;

Bubert A., Kuhn M., Goebel W., Koehler S.;

Bubert A., Kuhn M., Goebel W., Koehler S.;

"Structural and functional properties of the p60 proteins from different Listeria species.";

J. Bacteriol. 174:8166-8171(1992).

-i- FUNCTION: THIS MAJOR EXTRACELLULAR PROTEIN MAY BE INVOLVED IN THE INVASION OF MOMPROFESSIONAL PHAGOCYTIC CELLS BY LISTERIA.

-i- DOMAIN: LYSM REPEATS ARE THOUGHT TO BE INVOLVED IN PEPTIDOGLYCAN BINDING.

-i- SIMILARITY: BELONGS TO THE E.COLI NLPC / LISTERIA P60 FAMILY.

-i- SIMILARITY: CONTAINS 3 LYSM REPEATS.
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                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

MEDLINE=92384582; PubMed=1514809;

Bubert A., Koehler S., Goebel W.;

"The homologous and heterologous regions within the iap
genus- and species-specific identification of Listeria;

polymerase chain reaction.";
                            EMBL; M80350; AAA25284.1;
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InterPro; IPR003646; S43_Bac.
Pfam; PF00877; NLPC_P60; 1.
Pfam; PF00476; LysM; 3.
SMART; SM00257; LysM; 3.
SMART; SM00257; LysM; 3.
SMART; SM00287; S43b; 1.
Repeat; Signal.
DISCUSSION OF SEQUENCE.

DISCUSSION OF SEQUENCE.

MEDLINE=93094153; PubMed=1459966;

MEDLINE=93094153; PubMed=1459966;

Bubert A., Kuhn M., Goebel W., Koehler S.;

Bubert A., Kuhn M., Goebel W., Koehler S.;

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INVASION OF NONPROPESSIONAL PHAGOCYTIC CELLS BY LISTERIA.

INVASION OF NONPROPESSIONAL PHAGOCYTIC CELLS BY LISTERIA.
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MEDLINE=92384582; PubMed=1514809;
Bubert A., Koehler S., Goebel W.;
The homologous and heterologous regions within the iap gene allow genus- and species-specific identification of Listeria spp. by polymerase chain reaction.";
Appl. Environ. Microbiol. 58:2625-2632(1997)
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Bacteria; Firmicutes;
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InterPro; IPR000464; SH3 Dac.
Pfam; PF00877; NLPC P60; 1.
Pfam; PF01476; Lysm; 3.
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- SIMILARITY: (
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                                                                                                                                                                                                                                                        DTVRTGQRIASMKNQPSGAALFEF--RISRNGVYV
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                                                                                                                                                                                                                                                                                                      NTNQSSSNSSSASAIIAEAQKHLGKAYSWGGNGPTTFDCSGF-TSYVFAQSGITLPRTSG
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    25,
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PROTEIN P60.
LYSM 1.
LYSM 2.
LYSM 3.
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Pred. No. 0.0
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RESULT 14
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Best Local S
Matches 47
P60 LISIN STANDARD;
Q01836;
Q1-APR-1993 (Rel. 25, Created)
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SIGNAL
CHAIN
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REPEAT
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Pfam; PF01476; LysM; 3.
SMART; SM00257; LysM; 3.
SMART; SM00287; SH3b; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the European Bioinformatics Institute. There are no rest
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J. Bacteriol. 174:8166-8171 (1992).

- FUNCTION: THIS MAJOR EXTRACELLULAR PROTEIN MAY BE
- INVASION OF NONPROPESSIONAL PHAGOCYTIC CELLS BY LI
- I- DOMAIN: LYSM REPEATS ARE THOUGHT TO BE INVOLVED IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bubert A., Koehler S., Goebel W.;
"The homologous and heterologous regions within the iar
genus- and species-specific identification of Listeria
polymerase chain reaction.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR002482; LysM.
InterPro; IPR000064; NLPC P60.
InterPro; IPR003646; SH3 bac.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a obstween the Swiss Institute of Bioinformatics and the EMBL
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Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein p60 precursor (Invasion-associated protein). IAP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEROPS; C40.UPW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; M80352; AAA25285.1; -.
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-1- SIMILARITY: CONTAINS 2 LYSM REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=93094153; PubMed=1459966;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DISCUSSION OF SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                        YKVKSGDTIWALSVKYGVPVQKLIEWNNLSSS-SIYVGQ-----TIAVKEAAAKAAPT
                                                                                                                                                                                    T-----PAVDTNAATYKVQN----GDSLGKIASLFKVSVADLTNWNNLNATI
                                                                                                                                                                                                                                    TGSSGVMQFRYPVGATNPVVRRFGTATVAGSTVTSNGMWFSGRDGDLINASNAGTVI
                                                                                                                                                                                                                                                                                      TVKQAAPAKVAPKQEVKQTAPAKQEQAKPAAKETVKPAVSKPKAATPAPTAKPAVEQKAS
                                                                                                                                                                                                                                                                                                                                      TAHTPSPVAVQSSRPPVQQHPAVQKPTPPVV-VVKKPTPTPPVVQQPAPVAPPVTEAPFA 191
                                                                                                                                                                                                                                                                                                                                                                                                                                        YQVKQGDTVSKIAQRYGLNWREIGHINNLNSSYTIYTGQWLTLWSGDLKVRERSISSGVN
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511
219
342
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24;
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PROTEIN P60.
LYSM 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 140.5; DB
Pred. No. 0.011;
4; Mismatches
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of the p60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             83;
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Y LISTERIA.
D IN PEPTIDOG
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SETAIN-CLIP 11262 / Serovar 6a;

X MEDLINE-21537279; PubMed-11679669;

X MEDLINE-21537279; PubMed-11679669;

X Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,

Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,

A Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,

A Domann E., Dominguez-Bernal G., Buchaud E., Durant L., Dussurget O.,

A Domann K.-D., Fshih H., Garcia-del Portillo F., Garrido P.,

A Jones L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,

A Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,

A Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,

A Madueno E., Maitournam A., Mata Vicente J., Perez-Diaz J.-C., Purcell R.,

A Nardsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,

A Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,

Vacquez-Boland J.-A., Voss H., Wehland J., Cossart P.,

"Comparative genomics of Listeria species.";

EL Science 294:849-852(2001).
InterPro; IPR002482; Lysm.
InterPro; IPR00064; MLPC_P60.
InterPro; IPR00064; MLPC_P60.
InterPro; IPR003346; SH3_Dac.
Pfam; PF00877; MLPC_P60; 2.
Pfam; PF00476; Lysm; 2.
SMART; SM00257; Lysm; 2.
SMART; SM00257; Lysm; 2.
SMART; SM00287; SH3b; 1.
Repeat; Signal; Complete proteosional 27
CHAIN 28 467 PR
CHAIN 28 467 PR
DOMAIN 330 343 7
REPEAT 201 243 LY
REPEAT 201 243 LY
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15-JUN-2002 (Rel. 41, I
Protein p60 precursor i
IAP OR LIN0591.
                                                                                                                                                                                                                                                                                                                                                          BINDING.

I: SIMILARITY: BELONGS TO THE E.COLI NLPC / LISTERIA P60 FAMILY.

I: SIMILARITY: CONTAINS 2 LYSM REPEATS.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIINE=93094153; PubMed=1459966;
Bubert A., Kuhn M., Goebel W., Koehler S.;
Bubert A., Kuhn M., Goebel W., Koehler S.;
"Structural and functional properties of the p60 prodifferent Listeria species.";
J. Bacteriol. 174:8166-8171(1992).
J. Bacteriol. 174:8166-8171(1992).
INVASION OF NONPROPESSIONAL PHAGOCYTIC CELLS BY
-I- DOMAIN: LYSM REPEATS ARE THOUGHT TO BE INVOLVED
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[3]
DISCUSSION OF SEQUENCE.
MEDLINE=93094153; PubMe
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Bubert A., Koehler S., Goebel W.;
"The homologous and heterologous regions within the iap gene allow
genus- and species-specific identification of Listeria spp. by
polymerase chain reaction.";
                                                                                                                                                                                                                                                                    EMBL; M80349; AAA25283.1; -.
EMBL; AL596165; CAC95823.1;
ListiList; LIN00591; -.
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[2]
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Protein p60
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SEQUENCE
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MEDITINE=33094153; PubMed=1459966;

Bubert A., Kuhn M., Goebel W., Koehler S.;

"Structural and functional properties of the p60 proteins from different Listeria species.";

J. Bacteriol. 174:8166-8171(1992).

J. BACTERIOL. THIS MAJOR EXTRACELLULAR PROTEIN MAY BE INVOLVED IN INVASION OF NORPROFESSIONAL PHAGOCYTIC CELLS BY LISTERIA.

INVASION OF NORPROFESSIONAL PHAGOCYTIC CELLS BY LISTERIA.

OMAIN: LYSM REPEATS ARE THOUGHT TO BE INVOLVED IN PEPTIDOGLYCE.
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"The homologous and heterologous regions within the iap gene genus- and species-specific identification of Listeria spp. b polymerase chain reaction.";
Appl. Environ. Microbiol. 58:2625-2632(1992).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=92384582; PubMed=1514809;
MEDLINE=92384582; PubMed=1514809;
Koehler S., Goebel W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Listeria welshimeri.
Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria
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SIMILARITY: BELONGS TO THE E.COLI NLPC / LISTERIA
SIMILARITY: CONTAINS 3 LYSM REPEATS.
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InterPro; IPR00064; NLPC_P60.
InterPro; IPR000064; SH3 bac.
Pfam; PF00877; NLPC_P60; 1.
Pfam; PF00476; Lysm; 3.
SWART; SM00287; SH3b; 1.
SEQUENCE FACE A.A.

STRAIN-Rd / KW20 / ATCC 51907;

STRAIN-Rd / KW20 / ATCC 51907;

MEDLINE-95350630; PubMed=7542800;

Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,

Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,

McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,

Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,

Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,

Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,

Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
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01-NOV-1995
15-JUN-2002
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AAA25281.1;
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LYSM 3.
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Pred. No. 0.017;
7; Mismatches 103;
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01-NOV-1995
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        MEDLINE-95350630; PubMed-7542800;
MEDLINE-95350630; PubMed-7542800;
Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Smith H.O., Smith H.O., Smith H.O., Smith H.O., Smith H.O., Smith H.O., Smith H.O., Smith H.O., Smith H.O., Smith H.O., Smith H.O., Smith H.O., Smith H.O., Smith H.O., Smith H.O., Smith H.O., Smith H.O., Smith H.O., Smith H.O., Smith H.O., Smith H.O., Smith H.O., Smith H.O., Smith H.O., Smith H.O., Smith H.O., Smith H.O., Smith H.O., Smith H.O., Smith H.O., Smith H.O., Smith H.O., Smith H.O., Smith H.O., Smith H.O., Smith H.O., Smith H.O., Smith H.O., Smith H.O., Smith H.O., Smith H.O., Smith H.O., Smith H.O., Smith H.O., Smith H.O., Smith H.O., Smith H.O., Smith H.O., Smith H.O., Smith H.O., Smith H.O., Smith H.O., Smith H.O., Smith H.O., Smith H.O., Smith H.O., Smith H.O., Smith H.O., Smith H.O., Smith H.O., Smith H.O., Smith H.O., Smith H.O., Smith H.O., Smith H.O., Smith H.O., Smith H.O., Smith H.O., Smith H.O., Smith H.O., Smith H.O., Smith H.O., Smith H.O., Smith H.O., Smith H.O., Smith H.O., Smith H.O., Smith H.O., Smith H.O., Smith H.O., Smith H.O., Smith H.O., Smith H.O., Smith H.O., Smith H.O., Smith H.O., Smith H.O., Smith H.O., Smith H.O., Smith H.O., Smith H.O., Smith H.O., Smith H.O., Smith H.O., Smith H.O., Smith H.O., Smith H.O., Smith H.O., Smith H.O., Smith H.O., Smith H.O., Smith H.O., Smith H.O., Smith H.O., Smith H.O., Smith H.O., Smith H.O., Smith H.O., Smith H.O., Smith H.O., Smith H.O., Smith H.O., Smith H.O., Smith H.O., Smith H.O., Smith H.O., Smith H.O., 
                                                                                                                                                                               SEQUENCE F
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Pfam; PF01551; Peptidase_M37; 1.
Hypothetical protein; Complete prot
SEQUENCE 410 AA; 45983 MW; B28D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HAEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Science 269:496-512(1995).
                                                                                                                                                                                                                                    NCBI_TaxID=727;
                                                                                                                                                                                                                                                                                  Bacteria;
                                                                                                                                                                                                                                                                                                  Haemophilus influenzae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (S or send an email to license@isb-sib.ch).
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between the Swiss Institute of Bioinformatics and the EMBL
                                                                                                                                                                                                                                                                 Haemophilus
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  McDonald L.A.,
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                                                                                                                                                                                                                                                                                                                                                       32, Created)
32, Last sequence update)
41, Last annotation updat
                                                                                                                                                                               ATCC 51907;
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Pred. No. 0.02;
6; Mismatches 111
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B28D93E4E813BCA9 CRC64;
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  ×. v.,
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Matches 67
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Q48603; O52362;
Q48603; O52362;
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Probable N-acetylmuramidase precursor (BC 3.2.1.17)
Probable N-arrolysin) (Lysosyme).
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"Whole-genome 1
Rd.";
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or send a
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  MEDLINE=95189733; PubMed=7883712; Buist G., Kok J., Leenhouts K.J., Dabrowska M., Venema Haandrikman A.J.; embouride sequence of the gene "Molecular cloning and nucleotide sequence of the gene major peptidoglycan hydrolase of Lactococcus lactis, a needed for cell separation."; J. Bacteriol. 177:1554-1563(1995).
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-i- FUNCTION: COULD BE INVOLVED IN CELL WALL D.
-i- FORMATION (BY SIMILARITY).

-i- SIMILARITY: STRONG, TO E.COLI YEBA.

-i- SIMILARITY: TO STAPHYLOCOCCUS LYSOSTAPHIN.
                                                                                                                                                                SEQUENCE FROM N.A. STRAIN=MG1363;
                                                                                                                                                                                                                         NCBI_TaxID=1359;
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MEROPS; M37.UI
                                                                                                                                                                                                                                              Lactococcus lactis (subsp. cremoris) (;
acteria; Firmicutes; Lactobacillales;
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PP01551; Peptidase M37; 7
hetical protein; CeII wall
NCE 475 AA; 53255 MW;
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MW; 143C10F92233939D CRC64;
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37; Mismatches
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3; Streptococcaceae; Lactococcus
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     WNHLSSDTIYIGQNLIVSQSAAASNP
                                            EAPFATGSSGVMQ----FRYPVGATNPVVRRFGTATVAGSTVTSNGMWFSGRDGDLINASN
                                                                                                                                    SGVNTAHTPSSVAVQSSRPRVQQHPAVQXPTPTVVVVVXXPTPT--PVVVQQPAPVAPPVT
                                                                                                                                                                                SSTTYTVKSGDTLWGISQRYGISVAQIQSANNLKST-IIYIGQKLVLTGS----ASSTNS
                                                                                                                                                                                                                      ---RYQVKQGDTVSKIAQRYGLNWREIGHINNLNSSYTIYTGQWLTLWSGDLKVRERSIS
                                                                                                                                                                                                                                                                        TAALTGRYATDPSYGASLNRIISQYNLTRFDGASSAGNTNSGG---STTTITNNNSGTNS
                                                                                                                                                                                                                                                                                                              TTCILAGCASKPTYNST------SGSGSHRTSGSGGLAIGSQVITDSQGVPN-
                                                                                                                                                                                                                                                                                                                                                             Conservative
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В S 멼 Ş 밁 Ś 밁 Ś 밁 Ś

46564 7.8%;

MW.

39;

Score 130.5; Pred. No. 0.04 9; Mismatches

.043

Indels Length

Gaps

DB 1; 119;

437; 59;

CRC64;

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ASTTPTTSVTPA--KPTSQTTVKVKSGDTLWALSVKYKTSIAQLKS

186

295 128 240 71

-STGSGSTATINISNSTSSNSNASIHKVV

398

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EMBL; U17696; AAC33367.1; -.
EMBL; AF036720; AAB93629.1; -.
InterPro; IPR002901; Amidase_4.
InterPro; IPR002482; LysM.
Pfam; PF01476; LysM; 3.
Pfam; PF01832; Amidase_4; 1.
SMART; SM00047; LYZ2; 1.
SMART; SM00057; LysM; 3.
Hydrolase; Glycosidase; Bacteriolytic enzyme; Ce Cell division; Septation; Signal; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDINE-200; Sobal P.K., Sullivan P.A., Pillidge C.J.;
Govindasamy-Lucey S., Gopal P.K., Sullivan P.A., Pillidge C.J.;
Govindasamy-Lucey S., Gopal P.K., Sullivan P.A., Pillidge C.J.;
"Varying influence of the autolysin, N-acetyl muramidase, and the ce
envelope proteinase on the rate of autolysis of six commercial
Lactococcus lactis cheese starter bacteria grown in milk.";
J. Dairy Res. 67:885-596(2000).

1- FUNCTION: HYDROLYZES THE CELL WALL OF L.LACTIS AND
M.LYSODERKTICUS. REQUIRED FOR CELL SEPARATION DURING GROWTH.
M.LYSODERKTICUS. REQUIRED FOR CELL SEPARATION DURING GROWTH.

1- CATALYTIC ACTIVITY: Hydrolysis of the 1,4-beta-linkages between
acetyl-D-glucosamine and N-acetylmuramic acid in peptidoglycan
heteropolymers of the prokaryotes cell walls.

1- DOMAIN: THE LYSM REPEATS ARE THOUGHT TO BE INVOLVED IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collable between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/anor.send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               [2]
SEQUENCE FROM N.A.
STRAIN=2250;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PEPTIDOCLYCAN BINDING.

SIMILARITY: BELONGS TO FAMILY 73 OF GLYCOSYL HYDROLASES SIMILARITY: CONTAINS 3 LYSM REPEATS.
                               LYSM 1.

LYSM 3.

LYSM 3.

LYSM 3.

A -> T (IN REF 2).

A -> V (IN REF 2).

A -> V (IN REF 2).

A -> V (IN REF 2).

A -> V (IN REF 2).

A -> K (IN REF 2).

T -> A (IN REF 2).

T -> A (IN REF 2).

T -> A (IN REF 2).

T -> S (IN REF 2).

A -> T (IN REF 2).

A -> T (IN REF 2).
                                                                                                                                                                                                                                                                                                                                                                                          PROBABLE N-ACETYLMURAMIDASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cell wall;
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                                                                                                                                                                                                                                                                                                                                                                                                                           the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.,
STRAIN=M497-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; Achromobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-AUG-1992 (Rel.
15-JUL-1999 (Rel.
                                                                                                                                                                                                                                                                                     SIGNAL
                                                                                                                                                                                                                                                                                                Hydrolase;
                                                                                                                                                                                                                                                                                                                                 MEROPS; M23.001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=91035265;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Molecular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Achromobacter lyticus.
                                                                                                                                                                                                                                                                                                                       interPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S.L., Norioka S., Sakiyama F.;
lolecular cloning and nucleotide sequence of the beta-lytic
ne from Achromobacter lyticus,";
ne from Achromobacter lyticus,";
carteriol. 172:6506-6511(1990).
- CATALYTIC ACTIVITY: Cleavage of N-acetylmuramoy1-|-Ala,
insulin B chain at 23-Gly-|-Phe-24 > 18-Val-|-Cys(SO(3)F-
COPACTOR: BINDS ONE ZINC ION.
                                                                                                                                                                                                                                                                                                                                                                                                                           European
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: BELONGS TO PEPTIDASE FAMILY M23.
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A37151; LYYXLY.
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 289
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                                                                                                                                                                                                                                                                                                            PR00933;
                                                                                                                                                                       Similarity
 QRIASMKNQPSGA
                                         MWFSGRDGDLINASNAGTVIQADHNMDGASIVIQHTNGFVSSYIHIKDAQVKTGDTVRTG
                                                                                       QPAPVAPPVTEAPFATGSSGVMQFRYPVGATNPVVRRFGTATVAGS-----TVTSNG
                                                                                                                AGGRAARRRVPAGL-
                                                                                                                                   SGDLKVRERSISSGVNTAHTPSPVAVQSSRPPVQQHPAVQKPTPPVVVVKKPTPTPPVVQ 176
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                      GWGSNONGNWVSASAAGSFKR--HSSCFAEIV--HTGGWSTTYYHLMNIOYNTGANVSMN
                                                                                                                                                                                                                                                                                                                    IPR000841; Blytic_Mendpep.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 (Rel. 23, Last sequence update)
9 (Rel. 38, Last annotation update)
metalloendopeptidase precursor (EC
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196
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318
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Bioinformatics Institute.
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23,
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                                                                                                                                                          Score 126.5;
Pred. No. 0.06
29; Mismatches
                                                                                                                                                                                                                                      BETA-LYTIC METALLOENDOPEPTIDASE.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          subdivision; Alcaligenaceae;
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                                                                                                              RPPVQRTAPGQGGFGP-
                                                                                                                                                                      .068;
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                                                                                                                                                                                                                                                                                               Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of the beta-lytic
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                                                                   -GGAHTNTGSGNYPMSSLDMSRGG
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Db 293 TAIANPANTQAQA 305
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RESULT 20
GUNA_CALSA
   InterPro; IPR001956; CBD 3.
InterPro; IPR001701; GH 9.
InterPro; IPR001701; GH 9.
InterPro; IPR000556; Glyco_hydro_48.
Pfam; PF00759; Glyco_hydro_9; 1.
Pfam; PF00942; CBM 3; 3.
Pfam; PF000942; CBM 3; 3.
PRINTS; PR00844; GLHYDRLASE48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-91247819; PubMed-2039230;
Leuthi E., Jasmat N.B., Grayling R.A., Love D.R., Bergquist P.L.;
"Cloning, sequence analysis, and expression in Escherichia coli of
gene coding for a beta-mannanase from the extremely thermophilic
bacterium 'Caldocellum saccharolyticum'.";
Appl. Environ. Microbiol. 57:694-700(1991).
-1-FUNCTION: THE N-TERMINAL DOMAIN OF CEHA ENCODES FOR AN
ENDOGLUCANASE ACTIVITY ON CARBOXYMETHYLCELLULOSE. THE C-TERMIN
DOMAIN PROBABLY ACT SYNERGISTICALLY TO HYDROLYZE CRYSTALLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE 95336703; PubMed=7612247;
Te'O V.S., Saul D.J., Bergquist P.L.;
Te'A V.S., Saul D.J., Bergquist P.L.;
Te'Color another gene coding for a multidomain cellulase extreme thermophile Caldocellum saccharolyticum.";
Appl. Microbiol. Biotechnol. 43:291-296(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ul-AUG-1991 (Rel. 19, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Endoglucanase A precursor (EC 3.2.1.4) (Endo-1,4-beta-glucanase (CP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GUNA CALSA
P22534;
ProDom; PD001947; CBD 3; 2.

ProDom; PD011903; Glyco hydro 48; 1.

PROSITE; PS00592; GLYCOSYL_HYDROL_F9_1; 1.

PROSITE; PS00698; GLYCOSYL_HYDROL_F9_2; 1.

Cellulose degradation; Hydrolase; Glycosidase; SIGNAL 1 23 POTENTIAL.

CHAIN 24 1742 ENDOGLUCANASE A.
                                                                                                                                                                                                                                                       EMBL; L32742; AAA91086.1; --
EMBL; M36063, AAA72860.1; --
EMBL; L01257; -, NOT_ANNOTATI
PIR; A43745; A43745.
HSSP; P26221; ITF4.
                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement (Some send an email to license@isb-sib.ch).
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SIMILARITY: IN THE N-
E (FAMILY 9 OF GLYCOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CELLULOSE.

CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-glucosidic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linkages in cellulose.
PTM: THE LINKER REGION (ALSO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IMILARITY: IN THE N-TERMINAL SECTION; BELONGS (FAMILY 9 OF GLYCOSYL HYDROLASES).

MILARITY: IN THE C-TERMINAL SECTION; BELONGS (FAMILY 48 OF GLYCOSYL HYDROLASES).
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irmicutes; Clostridia; Clostridiales; Syntrophomonadace
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                                                                                                             SEQUENCE FROM N.A., AND SEQUENCE OF STRAIN-ARCC 9799; STRAIN-ARCC 9799; MEDILINE-92165737; PubMed=1347040; Chu C.-P., Kariyama R., Daneo-Mooru "Cloning and sequence analysis of Enterococcus hirae."; Bacteriol. 174:1619-1625(1992).
                                                                                                                                                                                                                                                 MUR2_ENTHR STANDARD; PRT; 666 AA P39046; 01-FEB-1995 (Rel. 31, Created) 01-FEB-1995 (Rel. 31, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation updat Muramidase-2 precursor (EC 3.2.1.17) (1,4-b acetylmuramoylhydrolase) (Peptidoglycan hydacetylmuramoylhydrolase)
                                                                                                                                                                                                                                                                                                                                 ENTHR
                  FUNCTION.

STRAIR-AFCC 9790;

MEDLINE-89327152; PubMed=2753858;

MEDLINE-89327152; PubMed=2753858;

Shock "The second peptidoglycan hydrolase covalently binds penicilin.";

J. Bacteriol. 171:4355-4361(1989).
                                                                                                                                                                                                     NCBI_TaxID=1354;
                                                                                                                                                                                                             Enterococcus hirae.
Bacteria: Firmicutes; Lactobacillales;
FUNCTION
                                                                                                                                                                                                                                         (Lysosyme) .
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Similarity 23.5%;
76; Conservative 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOTVTATETETETETETETETETEVSTEAT----SGQIKVLYANKETNSTTNTIREW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AIGSQVITDSQGV---PNRYQVKQGDTVSKIAQRYGLNWREIGHINNLN------
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643
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halysis of the m
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LINKER ("HINGE") (PRO-THR BOX).

CELLULOSE-BINDING (BY SIMILARITY).

LINKER ("HINGE") (PRO-THR BOX).

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CATALYTIC 2.

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(1,4-beta-N-
can hydrolase)
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                                            n G.D.;
Streptococcus
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 RESULT 22
LA17_YEAST
ID LA17_YEAST
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CC CAN COVALENTLY BIND PENICILLIN.

CC CANALYTIC ACTIVITY: Hydrolysis of the 1,4-beta-linkages between N-cc actevyl-p-glucosamine and N-acetylmuramic acid in peptidoglycan.

CC -I- SANALNE LOCATION: Secreted.

CC -I- SUNILARITY: BELONGS TO FAMILY 73 OF GLYCOSYL HYDROLASES.

CC -I- SIMILARITY: CONTAINS 6 LYSM REPEATS.
                                                                                                                                                                                                                                                                                                  Query Match
Best Local S
Matches 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR002901; Amidase_4.
InterPro; IPR002402; LysM.
Pfam; pP01476; LysM; 6.
Pfam; PP01832; Amidase_4; 1.
SMART; SM00047; LYZ2; 1.
SMART; SM00257; LysM; 6.
Hydrolase; Glycosidase; Bacteriolytic en
Cell division; Septation; Repeat; Signal
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Del Mar Lleo M.,
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353
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36; Conser
                                                                                                                                                 HGISMNQLIEWNNIKNNF-VYPGQQLVVSKGSSSA--SGSTSNTSTGNTSSNTA
                                             YGLNWREIGHINNLNSSYTIYTGQWLTLWSGDLKVRERSISSGVNTAHTPSPVA
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ilarity 31.6%;
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!1; Mismatches
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A FORMATION
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(Rel. 35, Created)
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protein LAS17.

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                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hughes B., Pohl T.M.;
Submitted (JUL-1996) to the EMBL
-!- SIMILARITY: TO S.POMBE WSP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Sacch
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (See or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001960; WH1. InterPro; IPR003124; WH2.
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SM00246;
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                                                                               GMWFSGRDGDLIN---ASNAGTVIQADHN-MDGASIVIQHTNG
                                                                                                               AFLTQQPQSGGAPAPPPPPQMP-ATSTSG
                                                                                                                                    P-VVQQP----APVAPPVTEAPFATGSSGVMQFRYPVGATNPVVRRFGTATVAGSTVTSN
                                                                                                                                                           DLKV-----RERSISSGVNTAHTPSPVAVQSSRPPVQQHPAVQKPTPPVVVVKKPTPTP
                                                                                                                                                                                                         PPPRASRPTPNVTMQQNPQQYNNSNRPFGYQTNSNMSSPPPPPVTTFNTLTPQ-MTAATG
                                                                                                                                                                                                                              -VPNRYQVKQGDTVSKIAQRYGLNWREIGHINNLNSS-----YTIYTGQWLTLWSG
                                                                                                                                                                                                                                                     PMRTTTEGSGVRLPAPPPPPRRGPAPPPPPHRHVTSNTLNSAGGNSLLPQATGRRGPAPP
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WH2; 1.
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STANDARD; PRT; 1192 AA. 
Q9H212; Q9H3I3; Q9BXG5; Q9Y2Y7;
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Pred. No. 0.47
%4; Mismatches
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  Q9UQ42; Q9Y293;
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                                                                   584
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                                                                                                                 GGSFAETT
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Q9Y5U6;
15-JUN-2002
15-JUN-2002
15-JUN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last sequence update)
Reticulon 4 (Neurite outgrowth inhibitor) (Nogo protein) (Foocen)
(Neuroendocrine-specific protein) (NSP) (Neuroendocrine specific
protein C homolog) (RTM-x) (Reticulon 5) (My043 protein).
RTM4 OR NOGO OR ASY OR KIAAO886.
 Nagase T., Ishikawa K.-I., Suyama M., Kiku
Miyajima N., Tanaka A., Kotani H., Nomura
"Prediction of the coding sequences of uni
                                                                                                                                        SEQUENCE FROM N.A. (ISOFORM 3).
Gu J.R., Wan D.F., Zhao X.T., Zhou X.M.,
Qin W.X., Huang Y., Qiu X.K., Qian L.F.,
Yu J., Han L.H.;
                                                                                                                                                                                                             "Human neuroendocrine-specific protein C (NSP) homolog gene. Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yang J., Yu L., Bi A.D., Zhao S.-Y.;
"Assignment of the human reticular agene
2p14--2p13 by radiation hybrid mapping.";
Cytogenet. Cell Genet. 88:101-102(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Prinjha R., Moore S.E., Vinson M., Blake S., Michalovich D., Simmons D.L., Walsh F.S.; "Inhibitor of neurite outgrowth in humans."; Nature 403:383-384(2000).
                                       MEDLINE=99156230; PubMed=10048485;
                                                                                                                                                                                                                                         Song H., Peng Y., Zhou J.,
Luo B., Hu R., Chen J.;
                                                                                                                                                                                                                                                                                                            "Isolation of a cell
Submitted (JUN-1998)
                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Placenta, and Ito T., Schwartz S.M. "Cloning of a member Submitted (FEB-1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Developmentally-regulated alternative splicing in a novel Nogo-A."; Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jin W.-L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
Jin W.-L., Ju G.,
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MEDLINE=20237542; PubMed=10773680;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                          TISSUE=Brain;
                                                                     SEQUENCE FROM N.A.
                                                                                                                            "Novel
                                                                                                                                                                                                                                                                   TISSUE=Pituitary;
                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                        Yutsudo M.,
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                                                                                                ubmitted
                                                                                                                           human cDNA clone with
                                                                                                  (AUG-1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PubMed=11126360;
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nd Skeletal muscle;
                                                                                                                                                                                                                                                                                  (ISOFORM 3).
                                                                                                                                                                                                                                                                                                                                                                      (ISOFORM
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to the EMBL/GenBank/DDBJ
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Nomura N., Ohara O.; of unidentified human
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He L.P., Li H.N.,
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                             Ξ.
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Yu Y.,
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SEQUENCE FROM N.A. (ISOFORM 3).

**BEDLINE=20499367; PubMed=11042152;
Zhang Q.-H., Ye M., Wu X.-Y., Ren S.-X., Zhao M., Zhao C.-J., Fu G.,
Zhang Q.-H., Ye M., Wu X.-Y., Ren S.-X., Lao M., Zhao C.-J., Fu G.,
Shen Y., Fan H.-Y., Lu G., Zhong M., Xu X.-R., Han Z.-G., Zhang J.-W.,
Tao J., Huang Q.-H., Zhou J., Hu G.-X., Gu J., Chen S.-J., Chen Z.,
"Cloning and functional analysis of cDNAs with open reading frames for 300 previously undefined genes expressed in CD34+ hematopoietic stem/progenitor cells.";
Genome Res. 10:1546-1560(2000).
                                                                                                                                                                                                                                                                                                                                                                          block the regeneration of the nervous central system in adults.

Isoform 2 reduces the anti-apoptotic activity of Bcl-xl and Bcl-2.

Instorm 2 reduces the anti-apoptotic activity of Bcl-xl and Bcl-2.

This is likely consecutive to their change in subcellular location, from the mitochondria to the endoplasmic reticulum, after binding and sequestration.

Isografic binding and sequestration.

Isografic Interacts with Bcl-xl and Bcl-2.

Isografic Interacts with Bcl-xl and Bcl-2.

Isografic Interacts with Bcl-xl and Bcl-2.

Isografic Interacts with Bcl-xl and Bcl-2.

Isografic Interacts interacts of the endoplasmic reticulum through 2 putative transmembrane of the endoplasmic reticulum through 2 putative transmembrane of the endoplasmic reticulum through 2 putative transmembrane of the endoplasmic reticulum through 2 putative in the membrane of the endoplasmic reticulum through 2 putative transmembrane of the endoplasmic reticulum through 2 putative transmembrane of the endoplasmic reticulum through 2 putative transmembrane of the endoplasmic reticulum through 2 putative transmembrane of the endoplasmic reticulum through 2 putative transmembrane of the endoplasmic reticulum through 2 putative transmembrane of the endoplasmic reticulum through 2 putative transmembrane of the endoplasmic reticulum through 2 putative transmembrane processed in brain and testis and weakly in heart and skeletal muscle. Isoform 2 is widely expressed in brain, skeletal muscle and adipocytes. Isoform 4 is testis-
    EMBL;
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                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/anor send an email to license@isb-sib.ch).
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-!- FUI
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Sha J.H., Zhou
Submitted (JAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 482-1192 FROM N.A. (ISOFORM 1/4) TISSUE-Brain, Mao Y.M., Xie Y., Zheng Z.H.; Submitted (MAY-1998) to the EMBL/GenBank/DDB
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Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complete sequences of 100 large proteins in vitro.", Res. 5:355-364(1998).
                                                                                                                                                                                                                                                                                                 SIMILARITY: CONTAINS 1 RETICULON DOMAIN. CAUTION: Ref.11 sequence differs from the frameshifts in positions 1149 and 1156.
                                                                                                                                                                                                                                                                                                                         specific.
SIMILARITY: CONTAINS 1
CAUTION: Ref.11 sequence
    AJ251383;
AJ251384;
AJ251385;
AB040462;
AB040463;
AF148537;
AF148538;
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403:439-444(2000).
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(JAN-2001)
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(MAY-1998) to the EMBL/GenBank/DDBJ databases.
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CAB99248.1;
CAB99249.1;
CAB99250.1;
BAB189227.1;
BAB18928.1;
AAG12176.1;
AAG12177.1;
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                                                           Mus musculus (Mouse).
Eukaryota; Metazoa; C
Mammalia; Eutheria; I
NCBI TaxID=10090;
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P35428;
01-JUN-1994
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                                                                                                                                   Transcription 
HES1 OR HES-1.
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01-JUN-1994 (Rel. 29, Last seq
15-DEC-1996 (Rel. 37, Last ann.
Transcription factor HES-1 (Ha
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AAH14366.1;
AAH12619.1;
AAH10737.1;
AAH10737.1;
AAD39920.1;
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annotation update)
(Hairy and enhancer
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ALT_INIT.
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MISSING (IN ISOFORM 2).

S -> C (IN REF. 6).

E -> Q (IN REF. 1).

N -> S (IN REF. 1).

N -> S (IN REF. 1).

N -> S (IN REF. 1).
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Pred. No. 0.90
3; Mismatches
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ANTENALISKTS -> MDGQR
3).
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W; CDE239BBF31589CA CRC64;
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=94148977; PubMed=7906273;
MCDLINE=94148977; Sakai Y., Sakai Y.,

Watanabe

Η.,

Nakanishi

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RESULT 25
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                                                                                                                                                                                                                                                                                        Query Match
Best Local S
Matches 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001092; HLH basic.
InterPro; IPR003650; Orange.
Pfam; PF00010; HLH; 1.
SMART; SM00351; HLH; 1.
SWART; SM00351; ORANGE; 1.
PROSITE; PS00038; HLH 1; 1.
PROSITE; PS00038; HLH 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collat between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is no modified and this statement is not removed. Usage by and for con entities requires a license agreement (See http://www.isb-sib.ch/ar or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kageyama R.;
"Structure, Chromosomal locus, and promoter analysis of the gene encoding the mouse helix-loop-helix factor HES-1. Negative autoregulation through the multiple N box elements.";
J. Biol. Chem. 269:5150-5156(1994).
                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRANSFAC; T01649; -. MGD; MGI:104853; Hes1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; D16464; BAA03931.1; PIR; A53336; A53336.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transcription
                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: NUCLEAR:

SUBCELLULAR LOCATION: NUCLEAR:

TISSUB SPECIFICITY: EXPRESSED AT HIGH LEVELS IN UNDIFFERENTIATED NEURAL PRECURSOR CELLS, BUT THE LEVEL OF EXPRESSION DECREASES AS NEURAL DIFFERENTIATION PROCEEDS.

DOMAIN: HAS A PARTICULAR TYPE OF BASIC DOMAIN (PRESENCE OF A HELLX-INTERRUPTING PROLINE) THAT BINDS TO THE N-BOX (CACNAG), RATHER THAN THE CAMONICAL E-BOX (CANNTG).

RATHER THAN THE CARONIL E-BOX (CANNTG).

DOMAIN: THE CARONYL-TERMINAL WAPW MOTIF IS A TRANSCRIPTIONAL REPRESSION DOMAIN NECESSARY FOR THE INTERACTION WITH GROUCHO, A TRANSCRIPTIONAL CO-REPRESSOR RECRUITED TO SPECIFIC TARGET DNA BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                        BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HAIRY-RELATED PROTEINS. SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY TRANSCRIPTION FACTORS. "HAIRY" SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: TRANSCRIPTIONAL REPRESSOR OF GENES THAT REQUIRE A BHIH PROTEIN FOR THEIR TRANSCRIPTION: MAY ACT AS A NEGATIVE REGULATOR OF MYOGENESIS BY IMHIBITING THE FUNCTIONS OF MYOD AND ASHI. SUBUNIT: TRANSCRIPTION REPRESSION REQUIRES FORMATION OF A COMPLEX SUBUNIT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WITH A CO-REPRESSOR PROTEIN (GROUCHO).
                                                                                                                                                                                            170
                                                                                               241
                                                                                                                                                              181
                                                                                                                                                                                                                          126
                                                                                                                                                                                                                                                                                     43;
                                                                                                                                                                                                                                                                                                       Similarity
                                                                                          AHSGPVIPVYTSNSGTSVGPNAVSPSSGSSLTSDSMW
                                                                                                                            --TNPVVRRF----GTAT-----VAGSTVTSNGMW 230
                                                                                                                                                          PFAPPPPPPLVPIPGGAAPPPGSAPCKLGSQAGEAAKVFGGFQVVPAPDGQFAFLIPNGAF
                                                                                                                                                                                          ----PTPPVVQQPAPVAPPVTEAPFATGS------SGVMQFRYPVGA-
                                                                                                                                                                                                                        STCEGVNTEVRTRLLGHLANCMTQINAMTYPGQAHPALQAPPPP----PPSGPAGPQHA
                                                                                                                                                                                                                                              SISSGVNT-----AHTPSPVA-VQSSRPPVQQHPAVQKPTPPVVVVKKPT------
                                                                                                                                                                                                                                                                                                                                                      282
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                                                                                                                                                                                                                                                                                                                                                                                   n regulation; 35 47 47 48 92 156 248 273 280
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                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                      29749
                                                                                                                                                                                                                                                                                                    7.0%;
                                                                                                                                                                                                                                                                                                                                                      MW;
                                                                                                                                                                                                                                                                                                                                                                                                DNA-binding; Nuclear protein; Repressor.
BASIC DOMAIN.
HELIX-LOOP-HELIX MOTIF (BY SIMILARITY PRO-RICH.
SER/THR-RICH.
                                                                                                                                                                                                                                                                                       15;
                                                                                                                                                                                                                                                                                                      Score 116.5;
Pred. No. 0.2
                                                                                                                                                                                                                                                                                                                                                                                   WRPW MOTIF (REQUIRED FOR ACTIVITY)
                                                                                                                                                                                                                                                                                                                                                                      (BY SIMILARITY
                PRT;
                                                                                                                                                                                                                                                                                                                                                      88C7700C5EF7DA26 CRC64;
                                                                                                                                                                                                                                                                                       Mismatches
               334 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                oved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                             ).24;
                                                                                                                                                                                                                                                                                                                      BB
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                                                                                                                                                                                                                                                                                                                   1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gh a collaboration
                                                                                                                                                                                                                                                                                                                      282;
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RESULT 26
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SEQUENCE
                                                          01-OCT-1996 (Rel. 34,
01-OCT-1996 (Rel. 34,
01-OCT-1996 (Rel. 34,
36.4 kDa proline-rich
Lycopersicon esculentum (Tomato).
Eukaryota; Viridiplantae; Streptophyta; Embryo
Spermatophyta; Magnoliophyta; eudicotyledons;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF01476; LysM; 1.
Pfam; PF01551; Peptidase_M37;
SMART; SM00257; LysM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                 TPRP-F1.
                                                                                                                       PRF1_LYCES
Q00451;
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Nature 407:81-86(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa "Genome sequence of the endocellular bacterial symbiont of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             symbiotic bacterium).
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-OCT-2001 (Rel.
16-OCT-2001 (Rel.
16-OCT-2001 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro;
InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=118099;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: BELONGS TO THE E.COLI NLPD / HAEMOPHILUS LPPB FAMILY.
                                                                                                                                                                                                                                                                      252
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                                                                                                                                                                                                                                                                                                                                                                                                                    TAHTESPVAVQSSRPPVQQHPAVQKPTPPVVVVKKPTPTPPVVQQPAPVAP----PVTEA 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    proteome.
                                                                                                                                                                                                            FEIRYLGESINPLSIL
                                                                                                                                                                                                                                                                      FVTNLFKKYGLLIIIKHDQNYLSIYAFNNSVLVKEKDRVYKNQQIATMGLSSDTNLARLY 311
                                                                                                                                                                                                                                                                                                 QADH--NMDGASIVIQHTNGFVSSYIHIKDAQVKTGDTVRTGQRIASM-KNQPSGAALFE
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                                                                                                                                                                                                                                                                                                                                                           PFATGSSGVMQFRYPVGATNPVVRRFGTATVAGSTVTSNGMWFSGRDGDLINASNAGTVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                   YIVKSKDTMYSIAKNSGYNYHELSKFNSIKKPYKIIIGO--KIWMGDFLIDKNNNDCSI-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YQVKQGDTVSKIAQRYGLNWREIGHINNLNSSYTIYTGQWLTLWSGDLKVRERSISSGVN 132
                                                                                                                                                                                                                                         FRISRNGVYVDPLTVL 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IPR002886; Peptidase_M37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      334 AA; 39788 MW; 4E4E4D2117FD6977 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                      STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6.9%;
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                                                                           Last sequence up
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             45; Mismatches 131;
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                                                                           on update)
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aphids
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Embryophyta; Tracheophyta; edons; core eudicots;

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SORRED DRAFT
  NLPD_YE
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Best Local S
Matches 33
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01-FEB-1996
01-FEB-1996
15-DEC-1998
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EMBL; X57076; CAA403661.1; -.
EMBL; X57076; CAA403661.1; -.
EMBL; X7076; CAA43666.1; -.
FINE PA4337; 11YP
ThterPro; IPR001768; Try/amyl inhbtr.
ThterPro; IPR001768; Try/amyl; 1.
C44E58
                            SEQUENCE FROM N.A.

STRAIN=#1024 / Serotype 0:9;

MEDLINE=95247270; pubMed=7729893;

Iriarte M., Stainier I., Cornells G.R.;

"The rpoS gene from Yersinia enterocolitica and its influence on expression of virulence factors";

Infect. Immun. 63:1840-1847(1995).

I- SUBCELLULAR LOCATION: Attached to the inner membrane by a lipid anchor (Potential).

-i- SIMILARITY: BELONGS TO THE E.COLI NLPD / HAEMOPHILUS LPPB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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STRAIN-CV. Arava;
MEDLINE=9139722; PubMed=1868217;
Salts Y., Wachs R., Gruissem W., Barg R.;
Salts Y., Wachs R., Gruissem W., Barg R.;
"Sequence coding for a novel proline-rich protein preferentially expressed in young tomato fruit.";
Plant Mol. Biol. 17:149-150(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPKUVL.VV, alpha amyl
Pfam; PF00234; tryp_alpha amyl
Pfam; Alpha AA; 36375 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRALN=cv. VFNT Cherry; TISSUE=Fruit;
STRALN=cv. VFNT Cherry; TISSUE=Fruit;
MEDLINE=92119262; PubMed=1731999;
MEDLINE=92119262; PubMed=1731999;
Salts Y., Wachs R., Kenigsbuch D., Gruissem W., Barg R.;
Salts Y., Wachs R., Kenigsbuch D., Gruissem W., Barg R.;
"DNA sequence of the tomato fruit texpressed proline-rich protein gene
TPNP-F1 reveals an intron within the 3 untranslated transcript.";
TPNP-F1 reveals an intron within the 3 untranslated transcript.";
TPNP-F1 reveals an intron within the 3 untranslated transcript.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Asteridae; euasterids
NCBI_TaxID=4081;
                                                                                                                                                                                                                                                               Yersinia enterocolitica.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                  Lipoprotein NLPD.
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  This SWISS-PROT entry is copyright.
                                                                                                                                                                                                                Yersinia.
NCBI_TaxID=630;
[1]
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33; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VIGGIVVGGSGVYGGGIVVGGNG
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(Rel. 33, Last seq
(Rel. 37, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                     (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Solanales; Solanaceae; Solanum.
                                                                                                                                                                                                                                                                 gamma
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; Pred. No. 0.33
6; Mismatches
                                                                                                                                                                                                                                                                                                                                 sequence update)
annotation update)
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                                                                                                                                                                                                                                                               subdivision; Enterobacteriaceae;
It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                              97
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MOZ_HUMA

ID MOZ_H

AC Q9279

DT 15-JU

DT 15-JU

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IN SECURICE FROM N.A.

IN MEDLINE-96376968; PubMed=8782817;

IN MEDLINE-96376968; PubMed=8782817;

IN MEDLINE-96376968; PubMed=8782817;

IN MEDLINE-96376968; PubMed=8782817;

IN MEDLINE-96376968; PubMed=8782817;

IN MEDLINE-96376968; PubMed=8782817;

IN MEDLINE-9637696; PubMed=8782817;

IN MET CARTON MAINTENERSE TO THE CREB-binding protein.";

IN MAIL GENERAL LOCATION: NUCLEAR:

CC -!- FUNCTION: MAY REPRESENT A CHROMATIN-ASSOCIATED ACETYLTRANSFERASE.

CC -!- SUBCELLULAR LOCATION: NUCLEAR:

CC -!- SUBCELLULAR LOCATION THAT PRODUCES A MOZ-CBP CHIMAERA OBSERVED IN THE TRANSLOCATION THAT PRODUCES A MOZ-CBP CHIMAERA OBSERVED IN THE CREB-BING SUBTYPE OF ACUTE MYELOID LEUGMIA.

CC -!- SIMILARITY: CONTAINS 2 PHD-TYPE ZINC FINGERS.

CC -!- SIMILARITY: BELONGS TO THE MYST (SAS/MOZ) FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           B
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Best Local S
Matches 28
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MOZ HUMAN

92794;
15-UIL-1998 (Rel. 36, Created)
15-UIL-1998 (Rel. 36, Last sequence update)
15-UIL-1998 (Rel. 41, Last annotation update)
15-UIM-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Inner mem
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR002886; Peptidase_M37.
InterPro; IPR000437; Prok lipoprot
Pfam; Pf01551; Peptidase_M37; 1
PROSITE; PS00013; PROKAR_LIPOPROTEIN; PARTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U16152; AAC43390.1; -. MEROPS; M37.UPW; -.
                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a copyred the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fentities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                  Genew; HGNC:1
                                                                               EMBL; U47742; AAC50662.1;
Genew; HGNC:13013; ZNF220.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CBI_TaxID=9606;
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ilarity 30.4%;
Conservative 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41;
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Tchauf A.M.,
D.E.;
                                                                                                                                                                                                                                                                           restrictions
                                                                                                                                                                                                                                                                                  collaboration - contstation - tions on its
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IPR001386; Histone_H1/H5 IPR002717; MOZ_SAS.

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Q04666;
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ZN_FING
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DOMAIN
       MEDLINE=93109293; PubMed=8417318; Feder J.N., Jan L.Y., Jan Y.-N.; "A rat gene with sequence homology
                                                     STRAIN=Sprague-Dawley; TISSUE=Embryo; MEDLINE=94040724; PubMed=1340473; MEDLINE=94040724; PubMed=1340473; Sasai Y., Kageyama R., Tagawa Y., Shigemoto "Two mammalian helix-loop-helix factors stru Drosophila hairy and Enhancer of split."; Genes Dev. 6:2620-2634(1992).
                                                                                                                                        Rattus norvegicus (Rat).
Eukaryota, Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                      HES1 OR HES-1 OR HL
                                                                                                                                                                                                 01-JUN-1994 (Rel.
01-JUN-1994 (Rel.
15-DEC-1998 (Rel.
                                                                                                                                                                                                                    01-JUN-1994
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Pfam; PF01853; MOZ SAS; 1.
SMART; SM00526; H15; 1.
SMART; SM00249; PHD; 2.
                                                                                                               SEQUENCE FROM N.A.
                                                                                                                               NCBI_TaxID=10116;
                                   SEQUENCE FROM N.A.
                                                                                                                                                                                      Transcription factor
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induced
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PS50016; ZF_PHD_2;
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                                                                                                                                                                                                                                                                                                                                            LNSSYTIYTGQWLTLWSGDLKVRERSISSGVNTA-------HTPSPVAV
                                                                                                                                                                                                                                                                                                                                                               SQQVVDSGFSDLGSIESTTENYENPSSYDSTMGGSICGNSSSQSSCSYG----GLSSSSS
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growth
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homology to the Drosophila factors known to influence
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(Hairy and enhancer of
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POLY-GLU.
POLY-LYS.
GLU-RICH.
GLU-RICH.
POLY-SER.
POLY-SER.
GLN/PRO-RICH.
MET-RICH.
BREAKPOINT FOR TRANSLOCATION TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          translocation;
                                                                                                                                                                                                                                                                                                                                                                                                    Score 114.5;
Pred. No. 3;
Pred. No. 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C2HC-TYPE
                                                                                                                                         Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                       PRT;
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                                                                                                                                                                                                                                       281
                                                                        structurally
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                                                                                                                                                                                                                                                                                                                                                                                                                      Length
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        hairy
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MANB CALSA P22533; 01-AUG-1991

(Rel. 19,

Created)

STANDARD;

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                                                                                                                                                                                                                                                                           CONFLICT
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001092;
InterPro; IPR003650;
Pfam; PF00010; HLH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      differentiation.";
Mol. Cell. Biol. 1
-!- FUNCTION: TRAN
                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00038; HLH_1; 1. PROSITE; PS50888; HLH_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                          SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART; SM00353; HLH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; D13417; BAA02682.1; EMBL; L04527; AAA41307.1;
                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FRANSFAC; T01648;
                                                                                                                                                                                                                                                                                                                                                                                   ranscription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    . Cell. Biol. 13:105-113(1993).

FUNCTION: TRANSCRIPTIONAL REPRESSOR OF GENES THAT REQUIRE PROTEIN FOR THEIR TRANSCRIPTION. MAY ACT AS A NEGATIVE RECOFMYOGENESIS BY INHIBITING THE FUNCTIONS OF MYOD AND ASHIOF MYOGENESIS BY THE TRANSCRIPTION DEPORTED FORMATION OF A
                                                                                                                                                                                                                                                                                                                                                                      BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN: HAS A PARTICULAR TYPE OF BASIC DOMAIN (F
HELIX-INTERRUPTING PROLINE) THAT BINDS TO THE N-
RATHER THAN THE CANONICAL E-BOX (CANNTG).
DOMAIN: THE CARBOXYL-TERMINAL WRPW MOTIF IS A TH
REPRESSION DOMAIN NECESSARY FOR THE INTERACTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HAIRY-RELATED
SIMILARITY: BE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: Nuclear:
TISSUE SPECIFICITY: PRESENT IN ALL TISSUES I
IN EFITHELIAL CELLS AND IN MESODERM-DERIVED
EMBRYONAL MUSCLE CELLS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBUNIT: TRANSCRIPTION REPRESSION REQUIRES WITH A CO-REPRESSOR PROTEIN (GROUCHO).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRANSCRIPTION FACTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRANSCRIPTIONAL CO-REPRESSOR RECRUITED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S36748;
                                                                                                        181
                                                                                                                                 170
                                                                                                                                                            126
                                                                                                                                                                                    126
                                                                                                                                                                                                                                                                                                                                                                                                                         SM00353; HLH; 1.
SM00511; ORANGE; 1.
                                                                                                                                                                                                              42;
                                                                                                                                                                                                                         Similarity
                                                      HSGPVIPVYTSNSGTSVGPNAVSPSSGSSLTADSMW
                                                                                                       PFAPPPPLVPIPGGAAPPPGSAPCKLGSQAGEAAKVFGGFQVVPAPDGQFAFLIPNGAFA
                                                                                                                                                          STCEGVNTEVRTRLLGHLANCMTQINAMTYPGQAHPALQAPPPP----PPSGPGGPQHA
                                                                                                                                                                                   SISSGVNT-----AHTPSPVA-VQSSRPPVQQHPAVQKPTPPVVVVKKPT-----
                                                                              -TNPVVRRF---
                                                                                                                                                                                                                                                                281
                                                                                                                                                                                                                                                                                                                    35
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                                                                                                                                 PTPPVVQQPAPVAPPVTEAPFATGS------SGVMQFRYPVGA--
                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                     DNA-binding; Nuclear BASIC DOMAIN.
                                                                                                                                                                                                          16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             THE BASIC HELIX-LOOP-HELIX (BHLH) "HAIRY" SUBFAMILY.
                                                                                                                                                                                                                                                                          HELIX-LOOP-HELIX MOTIF

PRO-RICH.

SEK/THR-FICH.

SEK/THR-FICH.

SEK/THR-FICH.

KEP SIMILARITY).

K -> N (IN REF. 2).

R -> W (IN REF. 2).
                                                                                                                                                                                                             Score 114; DB Pred. No. 0.36; Mismatches
                                                                                                                                                                                                                                                                8A98C8964F075B0D
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                                                      276
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                                                                                                                                                                                                                                                                                                                                                                                 protein; Repressor.
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                                                                                                                                                                                                                                                                CRC64;
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SUCH AS
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EMBL; M36063; AAA72861.1; -.
PIR; B43745, B43745.
PIR; A48954; A48954.
HSSP; Q06851; INBC.
Intex-Pro; IPR001956; CBD 3.
Intex-Pro; IPR001547; GH 5.
Pfam; PF00150; Cellulase; 1.
Pfam; PF00150; Cellulase; 1.
Pfam; PF00942; CBM 3; 2.
ProDom; PD001947; CBD 3; 2.
PROSITE; PS00659; GLYCOSYL HYD;
Hydrolase; Glycosidase; Cellul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 1-346 FROM N.A.

SEQUENCE OF 1-346 FROM N.A.

MEDLINE=91247819; PubMed=2039230;

Luethi E., Jasmat N.B., Grayling R.A., Love D.R., Bergquist P.L.;

Luethi E., Jasmat N.B., Grayling R.A., Love D.R., Bergquist P.L.;

"Cloning, sequence analysis, and expression in Escherichia coli of a

gene coding for a beta-mannanse from the extremely thermophilic

bacterium 'Caldocellum saccharolyticum'.";

Appl. Environ. Microbiol. 57:694-700(1991)

-i-FUNCTION: DEGRADATION OF HEMICELLICOSES, THE SECOND MOST ABUNDANT

POLYSACCHARIDES IN NATURE. CONTAINS TWO CATALYTIC DOMAINS WITH

MANNANASE AND ENDOGLUCANASE ACTIVITIES.

-i- CATALYTIC ACTIVITY: Random hydrolysis of 1,4-beta-D-mannosidic

linkages in mannans, galactomannans, glucomannans, and
CHAIN
DOMAIN
DOMAIN
DOMAIN
DOMAIN
DOMAIN
DOMAIN
DOMAIN
ACT_SITE
ACT_SITE
CONFLICT
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MEDLINE=93119139; PubMed=1476429;

Gibbs M.D., Saul D.J., Luthi E., Bergquist P.L.;

"The beta-mannanase from 'Caldocellum saccharolyticum'
multidomain enzyme.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Firmicutes;
Caldicellulosiruptor.
NCBI_TaxID=44001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUL-1993 (Rel. 26, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Beta-mannanase/endoglucanase A precursor [Includes: Mannan endo
beta-mannosidase A (EC 3.2.1.78) (Beta-mannanase) (Endo-1,4-
mannanase); Endo-1,4-beta-glucanase (EC 3.2.1.4) (Cellulase)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO CELLULASE FAMILY A (FAMILY 5 OF GLYCOSYL HYDROLASES).

SIMILARITY: IN THE C-TERMINAL SECTION, BELONGS TO CELLULASE FAMILY J (FAMILY 44 OF GLYCOSYL HYDROLASES).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    galactoglucomannans.
CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-glucosidic
linkages in cellulose.
MISCELLANEOUS: THIS ENZYME IS MOST ACTIVE AT PH 6 AND 80 DE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Microbiol. 58:3864-3867(1992).
                                                                                                                                                                                                                                                                                                                                                                 enzyme
   1331
325
361
518
564
720
780
1331
162
257
                                                                                                                                                                                                                                                                                                                                                                                         SYL_HYDROL_F5; 1.
Cellulose_degradation;
EETA-MANNANASE/ENDOGLUCANASE A.
CATALYTIC (MANNANASE ACTIVITY).
PRO/SER/THR-RICH (PT BOX).
SUBSTRATE-BINDING (POTENTIAL).
PRO/SER/THR-RICH (PT BOX).
SUBSTRATE-BINDING (POTENTIAL).
PRO/SER/THR-RICH (PT BOX).
CATALYTIC (ENDGLUCANASE ACTIVITY).
PRO/FON DONOR (BY SIMILARITY).
NUCLEOPHILE (BY SIMILARITY).
T -> P (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                             Signal;
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Best Local S
Matches 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      like) (HHL) (Hairy homolog).
HES1 OR HRY OR HL.
HOMO SAPIENS (Human).
Eukaryota; Metazoa; Chordata; C.
Mammalia; Eutheria; Primates; C.
NCBI TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HUMAN
HESL HUMAN
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2009 (Rel. 41, Last annotation update)
15-JUN-2009 (Rel. 41, Last annotation update)
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SEQUENCE
WALDIAGE K., KUNGGAI A., ILAKURA S., YAMAZAKI M., TASHIYO H.,
SUZUKI Y., Obayashi M., Nishi T., Shibahara T., Tanaka T.,
Nakamura Y., Isogai T., Sugano S.;
"NEDO human cDNA sequencing project.";
SUBMILTED (FEB-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: TRANSCRIPTIONAL REPRESSOR OF GENES THAT REQUIRE
PROTEIN FOR THEIR TRANSCRIPTION. MAY ACT AS A NEGATIVE REG
OF MYOGENESIS BY INHIBITING THE FUNCTIONS OF MYOD AND ASH1
SIMILARITY).
-!- SUBUNIT: TRANSCRIPTION REPRESSION REQUIRES FORMATION OF A
WITH A CO-REPRESSOR PROTEIN (GROUCHO) (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

MEDLINE=94292187; PubMed=8020957;

Feder J.N., Li L., Jan L.Y., Jan Y.-N.;

"Genomic cloning and chromosomal localization of HRY, homolog to the Drosophila segmentation gene, hairy.";

Genomics 20:56-61(1994).
                                                                                                                                                                                                                                                                                                                                                                                       Submitted
                                                                                                                                                                                                                                                                                                                                                                                       Yao J., Yeung S., Sur
"Functional analysis
Submitted (MAY-2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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76; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AEVKFKKDAPLSLNPDLNDNFVYMD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --NASNAGTVIQADHNM----DGASIVIQHTNGFVSSYIHIKD---AQVKTGDTVRTGQRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TQISPYIYGANQDIEGVVHSARRLGGNRLTGYNWENNFSNAGNDWYHSSDDYLCWSMGIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VMQFRYPVGATNPV-----VRRFGTATVAGSTVTSN-----GMWFSGRDGDLI-----
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ilarity 23.4%;
Conservative 3
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                                                                                                                                                                                                                                                                                                                                                                                 n H., Chen N.;
of human HRY in Drosophila.";
to the EMBL/GenBank/DDBJ databases.
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pred. No. 2.2;
4; Mismatches 156;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     937
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                                                                 COMPLEX
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RESULT 32
MYSC DICDI
ID MYSC D
AC P42522
DT 01-NOV
DT 16-OCT
DB MYOSIN
GN MYOC 0
OS Dictyc
OC Eukary
OX NCBI 1
RN [1]
RP SEQUEN
RX MEDLIN
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Best Local S
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DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00010; HLH; 1.
SMART; SM00353; HLH; 1.
SMART; SM00511; ORANGE; 1.
PROSITE; PS00038; HLH 1; 1.
PROSITE; PS50888; HLH 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
 MEDLINE=95348228; PubMed=7622596;
               STRAIN=AX2
                                                                    Dictyostelium discoideum Eukaryota; Mycetozoa; Dic
                                                                                                        01-NOV-1995 (Rel. 32,
01-NOV-1995 (Rel. 32,
16-OCT-2001 (Rel. 40,
Myosin IC heavy chain.
                                                                                                                                                  P42522;
01-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR003650; O
InterPro; IPR003650; O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; L19314; AAA65220.1; -.
EMBL; AF264785; AAF73060.1; -.
EMBL; AK000415; BBA91149.1; -.
TRANSFAC; T04892; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -
                             SEQUENCE FROM N.A
                                                     NCBI_TaxID=44689;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transcription
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF TRANSCRIPTION FACTORS. "HAIRY" SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN: HAS A PARTICULAR TYPE OF BASIC DOMAIN (PRESENCE OF A HELIX-INTERRUPTING PROLINE) THAT BINDS TO THE N-BOX (CACNAG), RATHER THAN THE CANONICAL E-BOX (CANNYG).

DOMAIN: THE CARBOXYL-TERMINAL MERPW MOTIF IS A TRANSCRIPTIONAL REPRESSION DOMAIN NECESSARY FOR THE INTERACTION WITH GROUCHO, TRANSCRIPTIONAL CO-REPRESSOR RECRUITED TO SPECIFIC TARGET DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HAIRY-RELATED PROTEINS
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                                                                                                                                                                                                                                                                                                                                                                                     126
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                                                                                                                                                                                                                                               PVYTSNSGTSVGPNAVSPSSGPSLTADSMW 275
                                                                                                                                                                                                                                                                          RRF----GTAT-----VAGSTVTSNGMW
                                                                                                                                                                                                                                                                                                    PLVPIPGGAAPPPGGAPCKLGSQAGEAAKVFGGFQVVPAPDGQFAFLIPNGAFAHSGPVI
                                                                                                                                                                                                                                                                                                                             PVVQQPAPVAPPVTEAPFATGS-------SGVMQFRYPVGA---TNPVV
                                                                                                                                                                                                                                                                                                                                                        STCEGVNTEVRTRLLGHLANCMTQINAMTYPGQPHPALQAPPPPPPGPGGPQHAPFAPPP
                                                                                                                                                                                                                                                                                                                                                                                  SISSGVNT-----AHTPSPVA-VQSSRPPVQQHPAVQKPTPPVVVVKKP-----TPTP
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48
156
249
275
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92
246
273
278
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Last
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                                                                                                                                                  Created)
                                                                  pum (Slime mold).
Dictyosteliida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA-binding; Nuclear protein; Repressor.
BASIC DOMAIN.
HELIX-LOOP-HELIX MOTIF (BY SIMILARITY PRO-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                              15;
                                                                                                                       sequence update) annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                           Score 109.5;
Pred. No. 0.7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WRPW MOTIF (REQUIRED
                                                                                                                                                                             PRT;
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F93'42A88FC749E3C
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                                                                    Dictyostelium
                                                                                                                       update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                             49;
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RESULT 33
VGP3_EBV
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Matches
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                                                                                                                                                                                                                                                       VGP3 EBV STANDARD P03200; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P03201; P032
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DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Molecular genetic analysis of myoC, a Dictyostelium myosin I.";
J. Cell Sci. 108:1093-1103(1995).

-i- function: myoSin Is a protein that binds to actin & has atpase activity that is activited by actin.

-i- Subunit: myoSin I heavy charles single-headed. Dimer of a heavy and a light chain. Imability to self-assemble into filaments.

-i- Similarity: Contains 1 myoSin-like globular head domain.

-i- Similarity: Contains 1 sh3 domain.
                   SEQUENCE FROM N.A.
MEDLINE=84270667; PubMed=6087149;
Baer R., Bankier A.T., Biggin M.D
Gibson T.J., Hatfull G., Hudson G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00242; MYSC; 1
SMART; SM00326; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ProDom; PD000066; SH3; 1.
ProDom; PD000355; myosin_head;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF0001B; SH3; 1.
Pfam; PF00063; myosin head; 2
PRINTS; PR00193; MYOSINHEAVY.
PRINTS; PR00452; SH3DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP;
                                                                                                                                      NCBI_TaxID=10377;
                                                                                                                                                               Viruses; dsDNA viruses, no RNA stage;
Gammaherpesvirinae; Lymphocryptovirus
                                                                                                                                                                                                               Epstein-barr virus (strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DictyDb; DD01090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
Tuffnell P.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
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InterPro; IPR001609; myosin_head.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro;
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Pred. No. 3.6;
17; Mismatches
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NON ALPHA-HELICAL,
ATP (POTENTIAL).
SH3.
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                   Deininger P.L., Farrell P.
., Satchwell S.C., Seguin O
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antigen)
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"DNA sequence and expression of the B95-8 Epstein-Barr virus genome."; Nature 310:207-211(1984). -!- FUNCTION: RESPONSIBLE FOR EBV BINDING TO THE CR2 RECEPTOR ON HUMAN

B-CELLIS.
SUBCELLULAR LOCATION: MOST ABUNDANT COMPONENT OF THE VIRAL ENVELOPE.

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PIR; A03762; QQBE21. 
PIR; A03763; QQBE22. 
PIR; S33008; S33008.
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RESULT 35 GP1_CHLRE

Db	γ	Db	Ş	Query Best 1 Match	-											2000 2000				RESULT EXTN S AC P	рь	Ş	DЬ	Q.	da Vo
174 PPVTKPPTHTPS 185	183 PPVTEAPFATGS 194	117 YTPSPKPPATKPPTYFTPKPPATKPPTPPVYTPSPKPPVTKPPTPKPTPPVYTPNPK 173	PVAVQSSRPPVQQHPAVQKPTPPVVVVKKI	6.5%; Score 108.5; DB 1; Length 283; st Local Similarity 37.5%; Pred. No. 0.86; ches 27; Conservative 7; Mismatches 23; Indels 15; Gaps 3;	1 24 POTEN 25 283 EXTEN 283 AA; 29593 MW; 8D7	IS; PRO1217; PRICHEXTENS at; Cell wall; Glycoprotoxylation.	MBL; X56010; CAA39485.1; TR; S14449; S14449. nterPro, IPR002965; P rich extensn.	n equires a license agreement (See non meail to license@isb-sib.ch).	in the titrions as long as its content is in no we statement is not removed. Usage by and for commerci	s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation in	D. THE FRUITING PROTECTS AS ALLEGATION OF THE PROTECTS AND ALL	STRUCT	requence of a hydroxyproline-rich glycoprotein gene re."; wol miol 16.365,367(1991)	0882; PubMed=1893107; in C., Puigdomenech P., Martinez-Izquierdo J.A.;	SEQUENCE FROM N.A.	.a; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC Andropogoneae; Sorghum. 1558;	ulgare). ta; Embryophyta; Tracheophyta	precursor (Proline-rich s	nce update)	T 34 SORBI STANDARD; PRT; 283 AA. P24152:	SOPKNATSAVTTGOHNITSSST	N	581 SAVTTPTPNATSPTLGK-TSPTSAVTTPTPNATGPTVGETSPQANATNHTLG 631	198 MQFRYPV-GATNPVVRRFGTATVAGSTVTSNGMWFS-GRDGDLINASNAGTVIQADHNMD 255	149 VQQHBAVQKETPPVVVVKKPTPTPPVVQQPAPVAPPVTEAPFATGSSGV 197

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RESULT 36
FHAB_BORPE
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Best Local S
Matches 25
 P12255;
01-OCT-1989
01-FEB-1996
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15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Vegetative cell wall protein gpl precursor (Hydroxyproline-rich glycoprotein 1).
GP1.
GP1.
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                                                  FHAB
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SIGNAL
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GlycoSuiteDB; O9FPQ6; -.
InterPro; IPR002965; Prich extensn.
InterPro; IPR003882; Pistil_extensin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         entities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 encoding cell wall hydroxyproline-rich glycoproteins.", Proc. Natl. Acad. Sci. U.S.A. 87:7355-7359(1990).
-!- FUNCTION: Major component of the outer cell wall W6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-91017504; PubMed=1699225;
Adair W.S., Apt K.E.;
"Cell wall regeneration in Chlamydomonas: accumulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Glycosylated polyproline II rods-with-kinks plant hydroxyproline-rich glycoproteins."; Biochemistry 40:2978-2987(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ferris P.J., Woe Goodenough U.W.,
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                                                                                                                                                                                                                                                               DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=21159092; PubMed=11258910;
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                                                                                                                                                                                                                                                                                                                                                                                                           ruitles requires a license agreement (See http://www.isb-sib.ch/announce/send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PTM: N-glycosylated and O-glycosylated.
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                                                  BORPE
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Pred. No. 1.8;
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N-LINKED (GLCNAC. . .)
N-LINKED (GLCNAC. . .)
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VEGETATIVE CELL WALL PROTEIN GP1.

49 X 5 AA APPROXIMATE PPSPX REPEATS.

POLY-PRO.
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AT12 HUMAN
P58397;
15-JUN-2002
15-JUN-2002
15-JUN-2002
ADAMTS-12 Pro-
                                                 15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
ADAMTS-12 precursor (EC 3.4.24.-) (A disintegrin metalloproteinase with thrombospondin motifs 12)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antigen;
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M60351; AAA22974.1; --
EMBL; M60351; AAA22975.1; ALT_INIT.
EMBL; M60351; AAA22976.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Relman D.A., Doménighini M., Tuomanen E., Rappuoli R., Filamentous hemagglutinin of Bordetella pertussis: nus sequence and crucial role in adherence." Proc. Natl. Acad. Sci. U.S.A. 86:2637-2641(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            ADAMTS12.
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for con
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MEDLINE=90355839; P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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                                                                                                                                                                                                                                                                                                      TLWSG---DLKVRERSI--SSGVNTAHTPSPVAVQS--SRP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hemagglutinin.
3591 AA; 36
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             (Human)
                                                                                                                                            STANDARD;
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Pred. No. 15
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Interpro; IPR001762; Disintegrin.
Interpro; IPR001870; Pep_M12B_propep.
Interpro; IPR001890; RepTolysin.
Interpro; IPR001894; TSP1.
Interpro; IPR000184; TSP1.
Interpro; IPR000184; TSP1.
Interpro; IPR000180; Zn_MTpeptdse.
IPR000190; Tsp1; 6.
Pfam; PF01421; RepTolysin; 1.
Pfam; PF01421; RepTolysin; 1.
Pfam; PF01562; Pep_M12B_propep; 1.
SMART; SM00209; TSP1; 8.
PROSITE; PS01215; ADAM MEPRO; 1.
PROSITE; PS01215; ADAM MEPRO; 1.
PROSITE; PS01215; TSP1; 2.
PROSITE; PS01215; TSP1; 2.
PROSITE; PS01215; TSP1; 2.
PROSITE; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215; PS01215;
Répeat; Extracellular
SIGNAL 1 24
PROPEP 26 24
CHAIN 465 54
DOMAIN 545 59
DOMAIN 597 70
DOMAIN 886 94,
DOMAIN 947 99
DOMAIN 947 99
DOMAIN 947 99
DOMAIN 1316 136
DOMAIN 1316 136
DOMAIN 1316 142
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MEDLINE=21264577; PubMed=11279086;
Cal S., Argueelles J.M., Fernandez P.L., Lopez-Otin C.;
Cal S., Argueelles J.M., Fernandez P.L., Lopez-Otin C.;
Cal S., Argueelles J.M., Fernandez P.L., Lopez-Otin C.;
Identification, characterization, and intracellular processing of ADAM-TS12, a novel human disintegrin with a complex structural organization involving multiple thrombospondin-1 repeats.";
J. Biol. Chem. 276:17932-17940(2001).
J. Biol. Chem. 276:17932-17940(2001).
-i- COPACTOR: BINNS 1 ZINC ION (BY SIMILARITY).
-i- SUBCELLULAR LOCATION: Secreted. Associated with the extracellular matrix (By similarity).
-i- TISSUE SPECIFICITY: Expressed exclusively in fetal lung. Is widely expressed in gastric carcinomas and in cancer cells of diverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no was modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Genew; HGNC:14605; ADAMTS12.
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FOR A TIGHT INTERACTION WITH THE EXTRACELLULAR MATRIX (BY FOR: THE PRECURSOR IS CLEAVED BY A FURIN ENDOPEPTIDASE.

PTM: IS SUBJECTED TO AN INTERACELLULAR MATURATION PROCESS LEADIND TO A FRACMENT CONTAINING THE N-TERMINAL REGION INCLUDING THE METALLOPROTEINASE DISINTEGRIN-LIKE, CYS-RICH AND TS-1 DOMAINS AND THE C-TERMINAL FRAGMENT CONTAINING THE SPACER 2 AND THE FOUR TS-1 DOMAINS.

SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12B.

SIMILARITY: CONTAINS 8 TSP TYPE-1 DOMAINS.
     matrix.
                                                                                                                                                                                                                                                                                                                                                                                             Zinc; Signal; Glycoprotein; Zymogen;
  SPACER 2.
TSP TYPE-1
TSP TYPE-1
TSP TYPE-1
TSP TYPE-1
TSP TYPE-1
POLY-GLU.
CYSTEINE SW
                                           SPACER 1.
SPACER 1.
TSP TYPE-1 2.
TSP TYPE-1 4.
SPACER 2.
TSP TYPE-1 6.
TSP TYPE-1 6.
TSP TYPE-1 8.
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BY SIMILAR
ADAMTS-12.
                                                                                                                                                                                                                                                                TSP TYPE-1 1.
                                                                                                                                                                                                                                                                                                                                  SIMILARITY.
     SWITCH (POTENTIAL).
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ID ALYS_ENTFA STAN
AC P37710;
AC P37710;
DT 01-OCT-1994 (Rel. 3
DT 01-OCT-2001 (Rel. 4
DT 16-OCT-2001 (Rel. 4
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Best Local S
Matches 57
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O1-OCT-1994 (Rel. 30, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Autolysin precursor (EC 3.2.1.-) (Peptidoglycan hydrolase)
(Beta-glycosidase).
Enterococcus faccalis (Streptococcus faccalis).
Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Ent
                                                                                                                              SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLLINE=91358349; PubMed=1679432;

Beliveau C., Potvin C., Trudel J., Asselin A., Bellemare G.;

"Cloning, sequencing, and expression in Escherichia coli of a Streptococcus faecalis aurolysin.";

J. Bacteriol. 173:5619-5623(1991).

J. Bacteriol. 173:5619-5623(1991).

M.LYSODEIKTICUS. MAY PLAY AN IMPORTANT ROLE IN CELL WALL
AND CELL SEPARATION.

-I- SUBCELLULAR LOCATION: Secreted (Prob-
-I- DOMAIN: LYSM REPEATS ARE THOUGHT TO
BINDING.
-I- SIMILARITY: BELONGS TO FAMILY 73 OF
-I- SIMILARITY: CONTAINS 5 LYSM REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1264 NRNHLKLPNNMNQTKSSEPVLTEEDATSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1114 SEGGLVATTTSGSGLSSSRNPITWPVTPFYNTLTKGPEMEIHSGSGEEREQPEDKDESNP
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57; Conserv
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                                                                    Secreted (Probable)
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  McCleary W.R.,
                   SEQUENCE FROM N.A. MEDLINE=90332690;
                                                                                                 Bacteria; Proteobacteria; delta
Myxococcales; Cystobacterineae;
                                                                                                                                               Myxococcus xanthus.
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PF01832; Amidase 4; 1.
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1 53 POTENTIAL.

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    Zusman D.R.;
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                                                                                                                         subdivision; Myxobacteria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Purification and characterization of the Myxococcus xanthus FrzE protein shows that it has autophosphorylation activity.";

J. Bacteriol. 172:6661-6668(1990).
-i- FUNCTION: FRZE IS INVOLVED IN A SENSORY TRANSDUCTION PATHWAY THAT CONTROLS. THE FREQUENCY AT WHICH CELLS REVERSE THEIR GLIDING
                                                                                                                                                                                                                                                                            PROSITE; PS50109; HIS KIN; 1.

PROSITE; PS50110; RESPONSE REGULATORY; 1.

Sensory transduction; Transferzase; Kinase; Phosph DOMAIN

270

509

HISTIDINE KINASE.

DOMAIN

60

76

RESPONSE REGULATORY.

170

HISTIDINE KINASE.

REGULATORY.

POSPHORYATION (AUT)

DOMAIN

130

197

ALA/PRO-RICH (POSSIB
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-1- SIMILARITY: SIMILAR TO BOTH CHEA AND CHEY.
-1- SIMILARITY: CONTAINS 1 RESPONSE REGULATORY DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                McCleary W.R., Zusman D.R.;
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; PD003142; Hpt; 1.
SM00260; CheW; 1.
SM00387; HATPase_C; 1.
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SM00448; REC; 1.
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SSYIHIKDAQVKTGDTVRTGQRIASMKNQPSGAALFEFRISRNG
                                                                                                              VQKPTPPVVVVKKPTPTPPVVQQP----APVAPPVTEAPFA-TGSSGVMQFRYPVGATN
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                                                                                                                                                                        GQWLTLWSGDLKVRERSISSGVNT----AHTPSPVA-----VQSSRPP--VQQHPA
                                                       PVVRRFGTATVAGSTVTSNGMWFSGRDGDLINASNAGTVIQADHNMDGASIVIQHTNGFV 268
                                                                                    APPPAPPAPVAAPVVTPAAVAAPPAPVQAPVAPPPTQAPVAEPGAHAAAAAPHPAAA---
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IPR001789;
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Bact_sens_pr_C.
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Pred. No. 3.1;
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                EMBL; AF102855; AAD04569.2; -
EMBL; AF31951; AAD29417.1; A
EMBL; AF159046; AADA2975.1; -
EMBL; AF159046; AADA2975.1; A
EMBL; AF141904; AAF02498.1; A
HSSP; P00519; IABL.
InterPro; IPR001210; ANK.
InterPro; IPR001478; PDZ.
InterPro; IPR001478; PDZ.
InterPro; IPR001452; SAM.
InterPro; IPR001452; SAM.
InterPro; IPR001452; SAM.
INTERPRO; IPR001452; SAM.
Pfam; PF000595; PDZ; 1.
Pfam; PF00536; SAM; 1.
Pfam; PF00018; SH3; 1.
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RX PhDMed=10806096;
RA Sheng M., Kim E.;
RA Sheng M., Kim E.;
RY "The Shank family of scaffold proteins.";
RI "The Shank family of scaffold proteins.";
RI "The Shank family of scaffold protein in the postsynaptic
CC clel Sci. 113:1851-1856(2000).
RL J. Cell Sci. 113:1851-1856(2000).
RL J. Cell Sci. 113:1851-1856(2000).
RL J. Cell Sci. 113:1851-1856(2000).
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RC Cell Sci. 13:1851-1856(2000).
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Sala C., Piech V., Wilson N
"Regulation of dendritic sp
Shank and Homer.";
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Bockers T.M., Mameza M.G., Kreutz M.R., Bockmann J., Weise C.,
Bockers T.M., Mameza M.G., Kreutz M.R., Bockmann J., Weise C.,
Buck F., Richter D., Gundelfinger E.D., Kreienkamp H.-J.,
Buck F., Richter D., Gundelfinger E.D., Kreienkamp H.-J.,
"Synaptic scaffolding proteins in rat brain. Ankyrin repeats of
"Synaptic scaffolding protein family interact with the cytoskeletal
protein alpha-fodrin.",
J. Biol. Chem. 276:40104-40112 (2001).
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SIMILARITY: BELONGS TO THE SHANK FAMILY.
SIMILARITY: CONTAINS 7 ANK REPEATS.
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PROSITE; PS501097; ANK REP REGION,
PROSITE; PS50106; PDZ; 1.
PROSITE; PS50105; SAM_DOMAIN; 1.
PROSITE; PS50105; SAM_DOMAIN; 1.
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                                                                                               PVTEAPFATGSSGVMQFRYPVGATNPVVRRFGTATVAGSTVTSNGMWFSGRDGDLINASN 243
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                    FE 305
                                        ----STDSHHGGASYIPERTSSLQRQRLS-EDSQ-----
                                                          AGTVIQADHNMDGASIVIQHTNGFVSSYIHIKDAQVKTGDTVRTGQRIASMKNQPSGAAL 303
                                                                             PQASA-LATVKASI-----ISELSSKLQQFGGSSTAGGALP----WARGGSGG-----
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MISSING (IN ISOFORM 5).

S -> T (IN REF. 1).

S -> N (IN REF. 2).

R -> K (IN REF. 1).

A -> T (IN REF. 1).

S -> D (IN REF. 1).

S -> N (IN REF. 2).

S -> N (IN REF. 2).
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MISSING (IN ISOPORM 2).
SQEGRQESRSDKAKRLFRHYTYGSYDSFDAPSLIDGIDSG
SQEGRQESRSDKAKRLFRHYTYGSYDSFDAPSLIDGIDSG
-> MALSAVGGGPGGALPQPPPALSSSWPALGPRRRSVWY
                                                                                                                                                                                                                                                                                                                                                                                   MISSING (IN ISOFORM 3).
MISSING (IN ISOFORM 4).
LSEDSCTSLLSKPS -> QYRIVVKSSDFGDF (IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alternative splicing
                                                                                                                                                                                                                                                                                                                                                                                                                    (IN ISOFORM 2)
                                                                                                                                                                                                                                                                                          3F478B5A7B18BA86 CRC64;
                                                                                                                                                                                                                                                                   Length 2167;
                                                                                                                                                                                                                                                 Indels
                                        ----TSLLSKPS-SSI 1946
                                                                                                                                                                                                                                                 81;
                                                                                                                                                                                                                                                Gaps
                                                                               1906
                                                                                                                                                                                                                           78
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Search completed: July 8, 2003, 11:06:05

Job time : 25 secs

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Result
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Gapop 10.0 , Gapext 0.5
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sp_phage:*
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               116
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Q9jp90 rhodocyclus
Q9pf23 xylella fas
Q9ckkl pasteurella
Q8x2t2 escherichia
Q8x2t2 escherichia
Q8x2t2 escherichia
Q8x2t3 eschoronas
Q8z3y0 salmonella
Q8zm83 salmonella
Q91528 pseudomonas
Q9k120 coxiella bu
Q9wwv6 pseudomonas
Q9x44 azotobacter
Q8w038 ralstonia s
Q9r836 deinococcus
Q8zbq1 yersinia pe
Q9ku17 vibrio chol
Q8y989 brucella me
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45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17
136.5	138.5	139.5	141	141	145	147.5	152	152.5	153	153.5	155	158	158	158.5	165.5	167	169	171	171.5	172.5	174	174.5	188.5	196	196.5	198	202.5	203
8.2	8.3	8.4	8.4	8.4	8.7	8.8	9.1	9.1	9.2	9.2	9.3	9.5	9.5	9.5	9.9	10.0	10.1	10.2	10.3	10.3	10.4	10.4	11.3	11.7	11.8	11.9	12.1	12.2
285	715	512	164	162	247	176	760	203	228	176	437	375	321	436	401	371	223	449	312	392	512	512	562	609	515	415	379	415
16	16	N	N	N	N	N	16	N				16	16	16	N	16	16	16	16	N	16	N	16	16	16	16	16	16
Q9PEP1	P74517	Q03491	Q9APL3	Q9R3D9	Q9S4T2	Q9F7X9	Q8YRU0	Q9X6S4	Q9X8M5	052606	Q927Y9	Q9RW21	Q8RG41	Q8Y4E2	Q9KJW8	083190	Q8X3L6	Q8R6U3	Q9X7W8	Q8RNB5	Q926D2	008251	Q8UEQ5	Q9A6T7	Q98LD1	Q9JYP9	Q8X7Z3	Q9JTP1 .
Q9pep1 xylella fas	7	Q03491 listeria gr		Q9r3d9 escherichia	Q9s4t2 legionella	Q9f7x9 escherichia	Q8yru0 anabaena sp	<	Q9x8m5 streptomyce	7	Q927y9 listeria in	_	_		oartonella	O83190 treponema p	Q8x316 escherichia			Q8rnb5 bartonella	Q926d2 rhizobium m	008251 rhizobium m	Q8ueq5 agrobacteri	Q9a6t7 caulobacter	Q98ld1 rhizobium l		Q8x7z3 escherichia	Q9jtpl neisseria m

ALIGNMENTS

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mechanisms and effects (Proceedings of the 11th international congress	(in) Garab G. (eds.);	*	c gene cluster in purple bacteriu	Igarashi N., Shimada K., Matsuura K., Nagashima K.V.;	STRAIN=IL144;	SEQUENCE FROM N.A.	[3]	J. Biol. Chem. 269:2477-2484(1994).	gelatinosus.";	photosynthetic reaction center apoproteins from Rubrivivax	"Primary structure and transcription of genes encoding B870 and	Nagashima K.V., Matsuura K., Ohyama S., Shimada K.;	007; PubMed=8300574;	STRAIN=IL144;	SEQUENCE FROM N.A.		Photosyn. Res. 36:185-191(1993).		of horizontal g	"Phylogenetic analysis of photosynthetic genes of Rhodocyclus	Nagashima K.V., Shimada K., Matsuura K.;	STRAIN=IL144;	SEQUENCE FROM N.A.	[1]	NCBI_TaxID=28068;		D)	Rhodocyclus gelatinosus (Rhodopseudomonas gelatinosa).	NLPD.	NlpD protein.	N-2001 (TrEMBLrel. 17, Last annotation	(TrEMBLrel. 15,	-2000 (TrEMBLrel.		O9JP90 PRELIMINARY; PRT; 314 AA.	IT 1

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Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,

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Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer J

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Q9PF23;
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Bacteria; Proteobacteria; gamma subdivision; Xanthomonas
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Dordrecht (1999).
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PF01551; Peptidase M37; 1.
%; SM00257; LysM; 1.
%NCE 314 AA; 32355 MW; 8
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RA Garrier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
RA HO P.L., Hoheisel J.D., Junqueira M.H.S., Gomes S.L., Gruber A.,
RA Lemos B.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,
RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
RA Menck C.F.M., Miracca E.C., Miyaki C.Y., Monetiro-Vitorello C.B.,
RA Mond D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Mond D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Month A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
RA Metalon M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
RA Ge Oliveira M.C., de Oliveira R.C., Palmieri D.A., Pesquero J.B.,
RA Quaggio R.B., Roberto P.G., Santelli R.V., Sawasaki H.E.,
RA Ge Solva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,
RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A., Jr.,
RA da Silva A.C.R., Meidanis J., Setubal J.C.;
RA Zago M.A., Zatz M., Meidanis J., Setubal J.C.;
RA Zago M.A., Zatz M., Meidanis J., Setubal J.C.;
RHEL; AE003925; AAP83665.1; -
DR HSSP; P23931; 1E0G.
DR InterPro, IPR002482; LysM.
ROMANT; SN00257, LysM; 1.

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                                                                                                                                                                                                                                                                   PRELIMINARY;
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Last sequence that annotation
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Pred. No. 8.6e-11;
2; Mismatches 108;
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                                                           subdivision;
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annotation update
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EMBL; AE006198; AAX03698.1; -.
InterPro; IPR002482; LysM.
InterPro; IPR002886; Peptidase_M37.
Pfam; PF01476; LysM; 2.
Pfam; PF01551; Peptidase_M37; 1.
R SMART; SM00257; LysM; 2.
W Hypothetical protein; Complete protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protec
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Q8X2T2;
Q1-MAR-2002 (TrembLrel. 2
01-MAR-2002 (TrembLrel. 2
01-JUN-2002 (TrembLrel. 2
                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-21156231; PubMed-11258796;
Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoy;
Hayashi T., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe '
Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasuna;
Kuhara S., Shiba T., Hattori M., Shinagawa H.;
Kuhara S., Shiba T., Hattori enterohemorrhagic Escherichia coli
O157:H7 and genomic comparison with a laboratory strain K-12.";
DNA Res. 8:11-22(2001)
                                                                                      EMBL; AP002563; BAB37161.1; -.
InterPro; IPR002482; LysM.
InterPro; IPR002488; Peptidase_M37.
Pfam; PF01476; LysM; 1.
Pfam; PF01551; Peptidase_M37; 1.
SMART; SM00257; LysM; 1.
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STRAIN=0157:H7 / RIMD 0509952;
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Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
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May B.J., Zhang Q., Li L.L., Paust
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SEQUENCE FROM N.A.
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Tanaka M., Tobe T.,
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InterPro; IPR002886; Peptidase_M3
Pfam; PF01476; Lysm, 1.
Pfam; PF01551; Peptidase_M37; 1.
SMART; SM00257; Lysm; 1.
                                                                                                                                                          EMBL; AE004905; AAG08309.1; HSSP; P23931; 1E0G.
                                                                                                                                                                                 opportunistic pathogen."
Nature 406:959-964(2000)
                                                                                                                                                                                                                                                                                                                                                Pseudomonas aeruginosa.
Bacteria; Proteobacteria;
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                                                                                  Hypothetical protein; Complete SEQUENCE 231 AA; 25174 MW;
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VRGEYRVKRGDTLYSIATRHGWNYKDLARANGIRPPYAVKVGQ-VVRFDGRKSTYVASSR
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                                                                                    Complete
                                                                                                                                      Peptidase_M37
                                                                                                                                                                                                                                                                                                                                                gamma subdivision; Pseudomonadaceae;
                                        37;
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Pred. No. 1.9e
37; Mismatches
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Q8Z3Y0;
Q1-MAR-2002
01-MAR-2002
01-JUN-2002.
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Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis B., Davies R.M., Dowd L., White N., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.; Moule S., Davis S., Barrell B.G.; Minterica serovar Typhi CT18.", Nature 413:848-852(2001).
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InterPro; IPR002482; LysM.
InterPro; IPR002886; Peptidase_M37.
Pfam; PF01476; LysM; 1.
Pfam; PF01551; Peptidase_M37; 1.
SMART; SM00257; LysM; 1.
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Salmonella.
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                                                                                                                                     AHT-PSPVAVQSSRPPVQQHPAVQKPTPPVVVVKKPTPTPPVVQQPAPVAPPVTEAPFAT 192
                                                                                                                                                                                                                                                 GDTVSKIAQRYGLNWREIGHINNLNSSYTIYTGQWLTLWSGDLK----VRERSISSGVNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FÄVNNMRGYGNLVIIQHGTSYTSTYAHNSRLLVKEGQMVGKGQKIAEAGSSDADRVQLYF
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                                                                                    GDTLYRISRATGTSVKELARLNGISPPYTIEVGQRIKV-RGSAKSSSSTRKTSNKTATKT
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(TrEMBLrel.
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250 AA; 26426 MW; 9A57CF6117BE76C4 CRC64;
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EMBL; AE008839; AALZ1913.1; -.
EMBL; FR002482; LysM.
InterPro; IPR002486; Peptidase_M37.
InterPro; IPR002486; Peptidase_M37.
Pfam; PF01476; LysM; 1.
Pfam; PF01551; Peptidase_M37; 1.
SMART; SM00257; LysM; 1.
Hypothetical protein; Complete proteome.
Hypothetical protein; Complete proteome.
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76; Conser
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                                                                                    NGVYVDPLTVL 321
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                                RATAIDPLRYL 243
                                                                                                                                         QLRGYGNLIMIKHNEDYITAYAHNDTMLVNNGQSVKAGQKIATMGSTDAASVRLHFQIRY 232
                                                                                                                                                                         NMDGAS--IVIQHTNGFVSSYIHIKDAQVKTGDTVRTGQRIASMKNQPSGAALFEFRISR 310
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9; Mismatches 99;
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Indels

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Gaps

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SEQUENCE FROM N.A.

STRAIN=IT2 / SGSC1412 / ATCC 700720;

STRAIN=IT7 / SGSC1412 / ATCC 700720;

MEDLINE=21534948; PubMed=11677609;

MEDLINE=21534948; PubMed=11677609;

MCClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,

Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.

Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,

Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,

Waterston R., Wilson R.K.;

Waterston R., Wilson R. W.;

"Complete genome sequence of Salmonella enterica serovar Typhimurium

"Complete genome sequence of Salmonella enterica
                                                                                                                                                                                                                                                                                                                                                                                                                                  Salmonella typhimurium.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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01-MAR-2002 (TrEMBLrel. 20, Last sequence up
01-JUN-2002 (TrEMBLrel. 21, Last annotation
Putative metalloendopeptidase.
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u S., Layman D.,
Mulvaney E.,
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RESULT 9
Q9XI20
ID Q9XI
AC Q9XI
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DE Lip
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                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

MEDITINE=21340372; PubMed=11447163;

Seshadri R., Samuel J.E.;

Seshadri R., Samuel J.E.;

"Characterization of a Stress-Induced Alternate Sigma Factor, RpoS,

"Characterization and Its Expression during the Development Cycle.";

Infect. Immun. 69:4874-4883 (2001).
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InterPro; IPR002886; Peptidase_M37.
Pfam; PF01476; LysM; 1.
Pfam; PF01551; Peptidase_M37; 1.
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Ojangu E., Tover A., Kivisaar M.;
"Sequence of Pseudomonas putida nlpD gene (complete sequence)
similar to E. coli pcm gene (partial sequence).";
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF266132; AAF70311.1; -...
                                                                                                                                                                                                                                                                 Coxiella group;
NCBI_TaxID=777;
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Bacteria; Proteobacteria;
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36; Mismatches 95;
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01-NOV-1999
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EMBL; Y19122; CAB46190.1; -.
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InterPro; IPR002886; Peptidase_M
Pfam; PF01476; Lysm; 1.
Pfam; PF01551; Peptidase_M37; 1.
SMART; SM00257; Lysm; 1.
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Bacteria; Proteobacteria;
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                                                                                                                                                                                                                                                                                            Pfam;
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Kojic M., Degrassi G., Venturi V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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PF01551; Peptidase_M37;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GSSGVMQFRYPVGATNPVVRRFGTATV--AGSTVTSNGMWFSGRDGDLINASNAGTVIQA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YOVKOGDTVSKIAORYGLNWREIGHINNLNSSYTIYTGOWLTLWSGDLKVRERSISSGVN 132
                                           LVLALAMGTLLAGCSST---SSTS------ARVVDRNNAAPKRPTVTSGQ
                                                                                     LIFGVITTCILAGCASKPTYNSTSGSGSHRTSGSGGLAIGSQVITDSQGVPNR------
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                                                                                                                                                                                                                         244 AA; 25191 MW; 6F9B5BA39CD739AE CRC64;
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Last
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Pred. No. 7.2e-09;
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Q93AG4;
Q93AG4;
O1-DEC-2001 (TrEMBLrel. 1:
O1-DEC-2001 (TrEMBLrel. 1:
O1-UNI-2002 (TREMBLRel. 2:
Murein endopeptidase.
Q8Y038;
Q8Y038;
01-MAR-2002
01-MAR-2002
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"The stationary phase sigma factor (rpoS) of Azotobacter vinelandii.";
Submitted (SEP-201) to the EMBL/GenBank/DDBJ databases.
EMBL; AP421551; AAL16090.1; -.
InterPro; IPR002482; LysM.
InterPro; IPR002886; Peptidase_M37.
Pfam; PF01476; LysM; 1.
Pfam; PF01551; Peptidase_M37; 1.
SEQUENCE 217 AA; 22675 MW; ASAAEB0F64886945 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=UW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=354;
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                                                                                                                                                                                                                                                           DHWMDGAS--IVIQHTNGFVSSYIHIKDAQVKTGDTVRTGQRIASMKNQPSGAALFEFRI 308
                                                                                                                                                                                                                                                                                                                                                         SGVMQFRYPVG----ATNPVVRRFGTATVAGSTVTSNGMWFSGRDGDLINASNAGTVIQA
                                                                                                                                                                                                                                                                                                                                                                                                                                  PPVQQHPAVQKPTPPVVVVKKPTPTPPVVQQPAPVA------PPVTEAPFATGS 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RYGWEWRELAAHNGIAAPYVIHPGQXIQL-------
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                                                                                                                                                                                                                                       GGGLRGYGELIIKHSDVYVSAYGHNRRLLVREGQQVKAGQVIAEMGSTGTDRVKLHFEI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VVYDGSGLRGYAELIIIKHSDTYVSAYGHNRRLLVREGQQVKAGQSIA 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
(TrEMBLrel. 20, (TrEMBLrel. 20,
                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13.2%; Score 221; DE 28.9%; Pred. No. 1.56 tive 30; Mismatches
                                                                                                                                                                                                321
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19,
21,
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Created)
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Last seq
Last ann
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                                                           PRT;
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sequence update)
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                                                             268
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 217;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58;
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RESULT 13
Q9RS36
ID Q9RS3
AC Q9RS3
DT 01-MA
DT 01-MA
DT 01-MA
DT 01-MB
DT C011
DE C011
DE C010
GN DE100
OC Bacte
OC Deinc
OX NCBI-
RN [1]
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Best Local S
Matches 78
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X MEDLINE=2168879; PubMed=11823852;

X Salamoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,

A Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L.,

A Arlat M., Billault A., Brottier P., Camus J.C., Cantolico L.,

A Chandler M., Choisne N., Claudel-Renard C., Cunnac S., Demange N.,

A Siguier P., Thebault P., Woisan A., Robert C., Saurin W., Schiex T.,

A Siguier P., Thebault P., Whalen M., Wincker P., Levy M.,

Weissenbach J., Boucher C.A.;

"Genome sequence of the plant pathogen Ralstonia solanacearum.";

IN Auture 415;497-502(2002).

R BEMBL, Al546063; CAD14908 l; -.

R InterPro; IPR002482; LysM.

InterPro; IPR002482; LysM.

InterPro; IPR002486; Peptidase M37.

InterPro; IPR002886; Peptidase M37.

InterPro; IPR002886; Peptidase M37;

R Pfam; PF01456; LysM; 1.

PFAm; PF01551; Peptidase M37; 1.

R Pfam; PF01551; Peptidase M37; 1.

R PFAN; PF01551; Peptidase M37; 1.

R PFAN; PF01551; Peptidase M37; 1.

SMART; SM00257; LysM; 1.

Complete Proteome.

268 AA; 27918 MW; ECE0386D88E367CE CRC64;
OPRS36

PRELIMINARY; PRT; 454 AA.

C Q9RS36;

C Q9RS36;

T Q1-MAY-2000 (TrEMBLrel. 13, Created)

T Q1-MAY-2000 (TrEMBLrel. 13, Last sequence update)

T Q1-MAY-2002 (TrEMBLrel. 21, Last annotation update)

Cell wall glycyl-glycine endopeptidase, putative.

B Cell wall glycyl-glycine endopeptidase, putative.

DR2291.

DR2291.

DR2291.

DR2291.

DR2291.

DR2291.

DR2291.

DR200cccus radiodurans.

Deinococcus radiodurans.

Deinococcus radiodurans.

C Bacteria; Thermus/Deinococcus group; Deinococci; Deinococcaceae; Deinococcus.

NCBI TaxID=1299;

N [1]
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Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
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Probable lipoprotein NLPD/LPPB homolog.
RSC1206 OR RS02686.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RRNGKPVDPMRFL 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GVNTAHTPSPVAVQSSRPPVQQHPAVQKPTPPVVVVKKPTPTPPVVQQPAPVAPPVTEAP 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SRNGVYVDPLTVL 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VGPLRGYGNLVIIKHNDTFLTAYGNNDKVLVTEQSTVKKGQKIAEMGSTDADRVKLHFEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SAGATDGAIALAWP--AHGQVIGRF-----DDKANKGIDIGGKRGDAVTAADDGKVIH 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FATGSSGVMQFRYPVGATNPVVRRFGTATVAGSTVTSNGMWFSGRDGDLINASNAGTVIQ 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATGAVATP------VRPP-------NTTTQPIDAAPAATPPVVSSGA 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PNRYQVKQGDTVSKIAQRYGLNWREIGHINNLNSSYTIYTGQWLTLWSGDLKVRERSISS 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PARAGRLAVAMVSAALLAACASSGNQAPVLDRTSRAGS------APAAPLEPPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADHNMD-GASIVIQHTNGFVSSYIHIKDAQVKTGDTVRTGQRIASMKNQPSGAALFEFRI 308
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24.9%; Pred. No. 2
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                                                                                                Deinococci; Deinococcales;
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2.4e-08;
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Best Local Similarity
Matches 73; Conserv
  SEQUENCE FROM N.A.

STRAIN=CO-92 / BIOVAR ORIENTALIS;

STRAIN=CO-92 / BIOVAR ORIENTALIS;

MEDLINE=21470413; PubMed=11586360;

Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,

Prentice M.B., Sebaihia M., James K.D., Churcher C., Mungall K.L.,

Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M.,

Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,

Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,

Chillingworth T., Cronin A., Davies R.M., Narlyshev A.V.,

Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,

Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.,

Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q8ZBQ1
Q8ZBQ1;
01-MAR-2002
01-MAR-2002
01-JUN-2002
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STRAIN-R1;

MEDLINE-20036896; PubMed-10567266;

Mitte O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,

Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,

Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,

Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C.,

Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.

Ketchum K.A., Nelson K.B., Salzberg S., Smith H.O., Venter J.C.,

Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lipoprotein.
NLPD OR YPO3356.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART; SM00257; LysM; 3.
Complete proteome.
SEQUENCE 454 AA; 4855
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                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Science 286:1571-1577(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                        Yersinia pestis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro;
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PF01551; Peptidase_M37; 1.
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454 AA; 48550 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HQGIDVAAPPGTPVIAARSGRVIQA--HLDETYGWGWTVVIQHPDGWQTRVAHLSRISVE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ARPSPAQPAPPRVAQATPEHHARVVVRQTSSHSLWQWPLPGYGRITSDFGWRVLDGEREK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QQPAPVAPPVTEAPFAT------GSSGVMQFRYPVGATNPVVRRFGTATVAGSTVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LKVRERSISSGVNTAHTPSPVAVQSSRP-PVQ---QHPAVQKPTPPVVVVKKPTPTPPVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AQLAAAKKPKPTTHRVEIGDTFYSVARRYGINPIALQEYNPRLAGQTLNVGAVLSLVAPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SQVITDSQGVPNRYQVKQGDTVSKIAQRYGLNWREIGHINNLNSSYTIYTGQWLTLWSGD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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Yersinia pestis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13.1%;
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Pred. No. 5.2e
50; Mismatches
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Pfam; PF01551; Peptidase M37; 1.
PRINTS; PR01561; EDGERECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE 333 AA
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SMART; SM00257; LysM; 1.
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EMBL; AJ414156; CAC92586.1; -.
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            OHTNGFVSSYIHIKDAOVKTGDTVRTGQRIASMKNQPSGAALFEFRISRNGVYVDPLTVL
                                                                                                                                                                                                             RIVYNRSYDNIPKGSYSGNTYTVKRGDTLFYIAWITGNDFRDLAAKNNIAEPYSLNVGQS
                                                                        RRFGTATVAGSTVTS------NGMWFSGRDGDLINASNAGTVIQADHNMDGAS--IVI
                                                                                                      SAYSGNSGKONVGKMLPSSGAVVATTAPVTAPSSSVSEPASNGGPVSGWRWPTD-----
                                                                                                                                                                                    LTLWSGD----LKVRERSISSGVNTAHTPSPVAVQSSRPP--VQQHPAVQKPTPPV----
                                                                                                                                                                                                                                                                                             PIKRLGLIFG-VITTCILAGCASKPTYNSTSGSGSHRTSGSGGLAIG---SQVITDSQG-
KHNDDYLSAYAHNDTMLVREQQEVKAGQKIATMGSTGTSSVRLHFEIRYKGKSVNPLRYL
                                                                                                                               ------VVVKKPTPTPPVVQQPAPVAPPVTEAPFATGSSG-VMQFRYPVGATNPVV
                                                                                                                                                          IQLGNGSGGGMLAATDATSSGI
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                                                                                                                                                                                                                                                                   PMIRLRVAACTVVSLWLVGCTND----NSTSAP----ISSVGGDRSGTMLSKANTDSSGG
                                                                                                                                                                                                                                                                                                                                                                          333 AA;
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                                                   ·GKTIDSFSASEGGNKGIDIAGSRGQPILATASGRVVYAGNALRGYGNLIII
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                                                                                                                                                                                                                                                                                                                       52; Mismatches 130;
                                                                                                                                                                                                                                                                                                                                  Score 218.5;
Pred. No. 4.1
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330
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MEDLINE=20406833; PubMed=10952301;
Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwir Dodson R.U., Haft D.H., Hickey E.K., Peterson J.D., Umayam I Dodson R.E., Nelson K.E., Read T.D., Tettelin H., Richardson i Gill S.R., Nelson K.E., Read T.D., Tettelin H., Dragoi I., Bass S., Qin H., Dragoi I., Bass S., Qin H., Dragoi I., McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., McDonald C., Smith H.O., Colwell R.R., Mekalanos J.J., Ve 01-OCT-2000 01-OCT-2000 Pfam; Pfam; InterPro; IPR002482; InterPro; IPR002886; TIGR; VC0533; -. Nature 406:477-483(2000). EMBL; AE004139; AAF93701.1; -. Vibrio cholerae. Bacteria, Proteobacteria; Lipoprotein NlpD. VC0533. 01-DEC-2001 Q9KUI7; Q9KUI7 NCBI_TaxID=666; 15 PF01476; LysM; 1. PF01551; Peptidase_M37; SM00257; Lysm; (TrEMBLrel. (TrEMBLrel. PRELIMINARY; (TrEMBLrel. of both chromosomes of Peptidase_M37. 15, 19, gamma Last Last Created) PRT; subdivision; sequence up the cholera pathogen Vibrio 311 A update) update) Vibrionaceae; R.A., Gwinn M.L.,

White

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L.A.,

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RESULT 16
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RC STRAIN=16M / ATCC 23456 / BIOTYPE 1;

RX MEDLINE=20020109; PubMedell1756688;

RD DelVecchio V.G., Kapatral V., Redkar R.J., Patra G., Mujer C., Los T.,

RA DelVecchio V.G., Kapatral V., Redkar R.J., Lykidis A., Reznik G.,

RA Jahlonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltsman E.,

RA Jahlonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltsman E.,

RA Jahlonski L., Kyrpides N., O'Callaghan D., Letesson J.-J.,

RA Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,

RA Haselkovn R., Kyrpides N., O'verbeek R.;

"The genome sequence of the facultative intracellular pathogen

RT Brucella melitensis.";

RT Brucella melitensis.";

Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).

RKL Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).

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BMEI1079.

Brucella melitensis.

Bactteria, Proteobacteria, alpha subdivision; Rhizobiaceae

Brucellaceae; Brucella.

MCBI TaxID=29459;
           162
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                                                                 30 LĄGCASKPTYNSTSGSGSHRTSGSGGLĄIGSQVITDSQGVPNRYQVKQGDTVSKIĄQRYG
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IAGVPQAPAVNGKKSSPTNMASAGGAIA-----TPPSVGGAYVVKSGDSLFSIAKKHN
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427 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RLGLIFGVITTCILAGCASKPTYNSTSGSGSHRTSGSGGLAIGSQVITDSQGVPNRYQVK 76
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311 AA;
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(TrEMBLrel. 20,
(TrEMBLrel. 21,
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larity 25.8%; Pred. No. 2e-07.
Conservative 48; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                         43604 MW; 48912D48846E6BD7
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                                                                                                                                      12.3%; Score 205; DB 16; 26.2%; Pred. No. 5.4e-07; tive 45; Mismatches 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          48; Mismatches 138; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
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Matches 71
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Q9JTP1,
Q9JTP1,
Q9JTP1,
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=22491 / SEROGROUP A / SEROTYPE 4A;

MEDLINE=20222555; PubMed=10761919;

Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,

Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,

Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd

Jagels K., Leather S., Moule S., Mungall K., Quail M.A.,

Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,

Whitehead S., Spratt B.G., Barrell B.G.;

"Complete DNA sequence of a serogroup A strain of Neisseria meningitidis 22491.";

Nature 40.550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Neisseria meningitidis (serogroup A).
Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
NCBI_TaxID=65699;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Complete proteome. SEQUENCE 415 AA;
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EMBL; AL162756; CAB84920.1; -.
InterPro; IPR002483; LysM.
InterPro; IPR00286; Peptidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF01476; LysM; 2.
Pfam; PF01551; Peptidase_M37;
SMART; SM00257; LysM; 2.
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       240 NASNAGTVIQADHNMDGAS--IVIQHTNGFVSSYIHIKDAQVKTGDTVRTGQRIASMKNQ
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                                                                                                                                                                                                                                                                      TAHTPSPVAVQSSRPPVQQHPAVQKPTPPVVVVKKPTPTPPVVQQPAPVAP------
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                                                                                                                   PVTEAPFA----TGSSGVMQFRYPVGATNPVVRRFGTATVAGSTVTSNGMWFSGRDGDLI
                                                                                                                                                                                                        ----PKAAAVK-SRPAVP--AAVOTPV-----KPAAQPPVQSAPQPAAPAAENKAVPA
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                                                                         PAPQSPAASPSGTRSVGGIVWQRP--TQGKVVADFGG-----NNKGVDIAGNAGQPV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 203; DB 16;
Pred. No. 7.2e-07;
2; Mismatches 97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 415;
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Best Local S
Matches 72
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EMBL; AB005502; AAG57849.1; -.

EMBL; AP002562; BAB37019.1; -.

InterPro; IPR002482; LysM.

InterPro; IPR002886; Peptidase_M37.

Pfam; PF01476; LysM; 1.

Pfam; PF01551; Peptidase_M37; 1.

SMART; SM00257; LysM; 1.
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Q8X7Z3;
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D., Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirpatrick H.A., Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L., Grotbeck B.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K., Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R.;
"Genome sequence of enterohaemorrhagic Escherichia coli O157:H7."
"Ganaly S. S. Schwartz D.C., Wature 409:529-533 (2001).
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NLPD OR Z4050 OR ECS3596.
NLPD OR Z6050 OR ECS3596.
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Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
Hayashi T., Makino K., Ohnishi M., Murata T., Tanaka M., Tobe T.,
Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
Kuhara S., Shiba T., Hattori M., Shinagawa H.;
"Complete genome sequence of enterohemorrhagic Escherichia coli
"Complete genome sequence of enterohemorrhagic Escherichia coli
0157:H7 and genomic comparison with a laboratory strain K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. STRAIN=0157:H7 / F
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SEQUENCE 379 AA;
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            281
                                                                                                                                                                                                                                                                                                133 TAHTPSPVAVQSSRPPVQQHPAVQKP--TPPVVVVKKPT-----------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity 26.:
72; Conservative
                                                      GMWFSGRDGDLINASNAGTVIQADHNMDGAS--IVIQHTNGFVSSYIHIKDAQVKTGDTV
                                                                                                                   TATTVTAPVTVPTASTTEPTVSSTSTSTPISTWRWP--TEGKVIETFG-ASEGG----NK
                                                                                                                                                                                                                                      ASGTPITGGNAITQADAAEQGVVIKPAQNSTVAVASQPTITYSESSGEQSANKMLPNNKP
                                                                                                                                                                                                                                                                                                                                                      YTVKKGDTLFYIAWITGNDFRDLAQRNNIQAPYALNVGQ-
      GIDIAGSKGQAIIATADGRVVYAGNALRGYGNLIIIKHNDDYLSAYAHNDTMLVREQQEV
                                                                                                                                                                            TPPVVQQPAPVAPPVTEAPFATG---SSGVMQFRYPVGATNPVVRRFGTATVAGSTVTSN
                                                                                                                                                                                                                                                                                                                                                                                                                   YQVKQGDTVSKIAQRYGLNWREIGHINNLNSSYTIYTGQWLTLWSGDLKVRERSISSGVN 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             379 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40172 MW; F664459AA1D90720 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12.1%; Score 202.5; DB 16; Length 26.1%; Pred. No. 7e-07; tive 42; Mismatches 113; Indels
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01-OCT-2000
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tettelln H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E., Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J., Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K., Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A., Haft D.H., Ciecko A., Parksey D.S., Blair E., Cittone H., Clark E.B., Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J., Gill J., Scarlato V., Masignani V., Pizza M., Grandi G., Sun L., Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.; "Complete genome sequence of Neisseria meningitidis serogroup B strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=MC58 / SEROGROUP B;
MEDLINE=20175755; PubMed=10710307;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Complete proteome. SEQUENCE 415 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Science 287:1809-1815(2000).
SMBL: AE002497; AAF41839.1; -.
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Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lipoprotein NlpD, putative. NMB1483.
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PF01551; Peptidase_M37; 1.
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                                                                                                                                                                                                                                                                 SMKNOPSGAALFEFRISRNGVYVDP
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; Pred. No. 1.7e-06;
38; Mismatches 95
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Best Local Similarity 25.7
Matches 69; Conservative
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Q9A6T7;
01-JUN-2001
01-JUN-2001
01-MAR-2002
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SEQUENCE FROM N.A.
STRAIN-ATCC 19089 / CB15;
MEDLINE-21173698; PubMed=11259647;
Nierman W.C., Feldblyum T.V., Laub
Eisen J., Heidelberg J.F., Alley M.
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SEQUENCE
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EMBL; AP002996; BAB48532.1; -.

INTERPO; IPR002482; LysM.

InterPro; IPR002486; Peptidase_M37.

Pfam; PF01476; LysM.;

Pfam; PF01551; Peptidase_M37; 1.

SMART; SM00257; LysM; 2.
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Batteria, Proteobacteria, alpha subdivision;
Phyllobacteriaceae; Mesorhizobium.
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001 (TrEMBLrel. 17, 1
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0, M23/M37 family.
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  Paulsen I.T.,
Ohta N., Madd
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  Maddock J.R.,
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                     X.E.,
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Q8UEQ5;
01-JUN-2002
01-JUN-2002
01-JUN-2002
                                                              Nester E.W.;
"The genome C58.";
                                                                                                                                               SBÖURNCE FROM N.A.

MEDLINE=21608550; PubMed=11743193;

MEDLINE=21608550; PubMed=11743193;

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Okura V.K., Zhou Y., Chen L., Mood G.E., Almeida N.F. Jr., Woo L.

Chen Y., Paulsen I.T., Eiseen J.A., Karp P.D., Bovee D. Sr.,

Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,

Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,

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Kutyavin T., Levy R., Li M.-J., McClelland R., Mc
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BMBL, AE005873; AAK23971.1; -.

TIGR, CC1996; -.
   Science
[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lipoprotein.
ATU1700 OR AGR C 3124.
Agrobacterium tumefaciens
Bacteria; Proteobacteria;
Rhizobiaceae; Rhizobium.
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InterPro; IPR002886; Peptidase
Pfam; PF01476; LysM; 4.
Pfam; PF01551; Peptidase M37;
SMART; SM00257; LysM; 4.
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l Similarity 23.6%;
66; Conservative 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        proteome.
609 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APQGTPVLSSADGEIAYAGNQVPTFGNLVLVKHADGWVTAYAHLSSTNVKMRQQVKQGEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GRDGDLINASNAGTVIQADHNMD--GASIVIQHTNGFVSSYIHIKDAQVKTGDTVRTGQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P-SSGRTIIETAAAPTEAEIIASGKGKFAWPL--RGDIISSFG---VKGTGQRNDGLNIR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PFATG------SSGVMQFRYPVGATNPVVRRFGTATVAGSTVTSNGMWFS
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(TrEMBLrel.)
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                                                                                        natural genetic
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Peptidase_M37.
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; Pred. No. 3.8e-06;
54; Mismatches 110
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Last sequence update)
Last annotation update)
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Rhizobiaceae
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                                                                                               tumefaciens
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M., White
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Matches 81
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01-JUL-1997
01-JUN-2002
                                                                                                                                                                                                                                                                                                                      008251;
        Mol. Plant Microbe Interact. 10:933-937(1997).
EMBL; U81296; AAB88077.1; -.
InterPro; IPR002482; LysM.
InterPro; IPR002488; Peptidase_M37.
Pfam; PF01476; LysM; 2.
Pfam; PF01551; Peptidase_M37; 1.
SMART; SM00257; LysM; 1.
                                                                                                                                                                                                              Rhizobium meliloti (Sinorhizobium meliloti). Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae; Sinorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cielo C., Slater S.;
"Genome sequence of the plant pathogen and biotechnology agent Agrobacterium tumefaciens C58.";
Science 294:2323-2328(2001).
EMBL; AE009126; AAL42700.1; ALT_INIT.
EMBL; AE008091; AAK87473.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M., Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L. Houmiel K., Gordon J., Vaudin M., Iartchouk O., Bpp A., Liu F., Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B., Filangan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G.,
                                                                                                      "A biotin-regulated | Rhizobium meliloti."
                                                                                                                                 Streit W.R.,
                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                   Lipoprotein.
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MEDLINE=21608551;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             ERSISSGVNTAHTPSPVAVQSSRPPVQQHPAVQKPTP---PVVVVKKPTPTPPVVQQPAP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PPSGG----YKVQPGDSLAKIARANGVSVAALKAANGI-SNESIRVGQTLAM---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TDSQGVPNRYQVKQGDTVSKIAQRYGLNWREIGHINNLNSSYTIYTGQWLTLWSGDLKVR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NASNAGTVIQADHNMD--GASIVIQHTNGFVSSYIHIKDAQVKTGDTVRTGQRIASMKNQ 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VAPPVTEAPFATGSSGVMQFRYPV-GATNPVVRRFGTATVAGSTVTSNGMWFSGRDGDLI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                              llips D.A.;
                                                                                                                                            PubMed=9304864;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57218 MW; B6479E31F9579A84 CRC64;
                                                                                                                 locus, bioS,
52431 MW;
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                                                                                                                                                                                                                                                                                Created)
Last sequence up
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Pred. No. 1.2
0A870A76EBCE7D8B CRC64;
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Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).

EMBL, AL59187; CAC46115.;

TILENGAG. 115.4.
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01-DEC-2001 (TrEMBLrel. 19,
01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                                                    Pfam;
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Rhizobiaceae; Sinorhizobium.
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Rhizobium meliloti (Sinorhizobium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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InterPro; IPR002886;
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PF01551; Peptidase_M37; 1.
                                                                                  l Similarity
79; Conserv
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512 AA; 52003 MW; 6BBADDD3290125D0 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PVVQQPAPVA-PPVTEAPFATG-----SSGVMQFRYPV-GATNPVVRRFGTATVAGST
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Pred. No. 0
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Pred. No. 0.00011;
8; Mismatches 128
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subdivision;
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Fiskus W., Padmalayam I., Baumstark B.;
"Molecular cloning, sequencing, and characterization of the homolog in Bartonella henselae.";
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.

EMBL, AF48425, AA,1897611;
-
SEQUENCE 392 AA; 42635 MW; CF71E6B91FDA206C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bartonella henselae (Rochalimaea henselae).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Bartonellaceae; Bartonella.
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GVSGDVKTPRVYFEVRENSLPVDPIKYLE
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                                               QPSG---AALFEFRISRNGVYVDPLTVLK 322
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                                                                                                                                                                                                               ----ATGISKMRWPV--RGRLLSQFGQKR---GTTMSRGIDIAVPEGSS
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-UN-2002 (TrEMBLrel. 21, Last annotation update)
Putative secreted peptidase.
SC06773 OR SCGA5.22.
Streptomyces coelicolor.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
NCBI TaxID=1902;
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STRAIN=A3(2) / M145;

Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,

Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,

Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,

Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,

Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,

Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Weil S.,

Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,

Reeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,

Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,

Hopwood D.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                     "Complete genome sequence of the model actinomycete Streptomyces coelicolor A3(2).",
Nature 417:141-147(2002).
EMBL; A104945; CAB39706.1; .
InterPro; IPR002482; LysM.
InterPro; IPR002482; LysM.
Pfam; PF01476; LysM; 1.
Pfam; PF01551; Peptidase_M37; 1.
PRINTS; PR01574; TUBBYPRÖTEIN.
SMART; SM00257; LysM; 1.
SMART; SM00257; LysM; 1.
SMART; SM00257; LysM; 1.
SMART; SM00257; LysM; 1.
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Redembach M., Kieser H.M., Denapaite D., Eichner A.,
Rinashi H., Hopwood D.A.;
"A set of ordered cosmids and a detailed genetic and
the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
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Oliver K., Harris D.;
Submitted (MAR-1999)
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Bentley S.D.,
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STRAIN=A3(2);
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Submitted (MAR-1999) to the
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                                                  RSISSGVNTAHTPSPVAV--OSSRPPVOOHPAVOKPTPPVVVVKKPTPTPPVVOOPAPVA
                                                                                                                                                                                                                                                                    GSHR-----TSGSGGLAIGSQVITDS------
EAVGSDPSLIHPGLKLSIDGQAAKPSAPSSAQSQKPA-----QKSAEKPAEKTAAKPA 155
                                                                                                          EKNSDSRTYTVKSGDYLSKIADEQDVD--
                                                                                                                                                                                                               GKHRRTRAMRLTRTIAVAGTGGAALALPLMGAAAANAAPAHSVSEQAVQSVPASAKKAAA
                                                                                                                                                         -----NRYQVKQGDTVSKIAQRYGLNWREIGHINNLNSSYTIYTGQWLTLWSGDLKVRE
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e EMBL/GenBank/DDBJ databases.
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                                                           182
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SEQUENCE FROM N.A. STRAIN=HOUSTON-1; NCBI_TaxID=38323; Q8RNB5; Q8RNB5; Q1-JUN-2002 01-JUN-2002 01-JUN-2002 N1pD. NLPD.

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                     Q8X3L6;
Q8X3L6;
Q1-MAR-2002
01-MAR-2002
01-JUN-2002
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01-JUN-2002
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Membrane proteins related to metalloendopeptidases.
NLPD6 OR TTE2691.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong Chen Y., Xue Y., Lai X., Huang L., Dong X., P Tan H., Chen R., Wang J., Yu J., Yang H.;
"A complete sequence of T. tengcongensis genome.",
Genome Res. 12:689-700(2002).
EMBL; AE013208; AAM25810.1; -.
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STRAIN-MB4T / JCM11007;
MEDLINE=21992816; PubMed=11997336;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thermoanaerobacter tengcongensis.
Bacteria; Firmicutes; Bacillus/Clostridium
Thermoanaerobacteriales; Thermoanaerobactes
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     Putative
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lipoprotein
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                                                                                                                                                                                                                                                                                                                                                              PIYASDGGTVIFAGWESGYGYLVKIDHHNGYVTYYGHASKLLVKVGDKVEKGQKIALV--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GÓQVGLSGATGNVTGPHLHFEIRTTPDYGSDIDPLAFLR 306
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                        (TrEMBLrel. (TrEMBLrel. (TrEMBLrel.
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ilarity 27.6%;
Conservative 4
                                                                                                                              PRELIMINARY;
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Thermoanaerobacteriaceae; Thermoanaerobacter.
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                        Created)
Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 171; DB 16;
Pred. No. 0.00017;
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f., Ling
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EMBL; AEGOSSIG; AAGS7994.1; -.
InterPro; IPRO02482; LysM.
InterPro; IPRO02886; Peptidase_M37
Pfam; PF01476; LysM; 1.
SMART; SM00257; LysM; 1.
Lipoprotein; Complete proteome.
SEQUENCE 223 AA; 23472 MW; 774
MEDIAIN=MILHOUS;
MEDIAINE=9332770; PubMed=9665876;
MEDIAINE=9332770; PubMed=9665876;
Praser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G.,
Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A.,
Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J.,
Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T
McDonald L., Artiach P., Bowman C., Cotton M.D., Fujii C., Garland
McDonald L., Artiach P., Bowman C., Cotton M.D., Fujii C., Garland
                                                                                                                                                                                                           083190;
01-NOV-1998
01-NOV-1998
01-JUN-2002
                                                                                                                                                     Treponema pallidum.
Bacteria; Spirochaetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Perna N.T., Plunkett G. III, Burland V., Mau B., Gl
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirl
Posfai G., Hackett J., Klink S., Boutin A., Shao Y.
Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schw
Welch R.A., Blattner F.R.;
                                                                                                      SEQUENCE FROM N.A. STRAIN=NICHOLS;
                                                                                                                                                                                  Hypothetical TP0155.
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                                                                                                                                          NCBI_TaxID=160;
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Escherichia
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Escherichia coli
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                                                                                                                                                                                                                                                                                                                                                                                                    VGATNPVVRRFGTATVAGSTVTSNGMWFSGRDGDLINASNAGTVIQADHNMDGAS--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GLNWREIGHINNLNSSYTIYTGQWLTLWSGDLK----VRERSISSGVNTAH-TPSPVAVQ 143
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                                                                                                                                                                                                                                                                                                                                 KHSEDYITAYAHNDTMLVNNGQS
                                                                                                                                                                                                                                                                                                                                                           QHTNGFVSSYIHIKDAQVKTGDT 284
                                                                                                                                                                                                                                                                                                                                                                                                                                          SSWPPVGQRCWLWPTTGKVIM-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SSRPPVQQHPAVQKPTPPVVVVKKPTPTPPVVQQPAPVAPPVTEAPFATGSSGVMQFRYP
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                                                                                                                                                                                               (TrEMBLrel. 08, 0
(TrEMBLrel. 08, 1
(TrEMBLrel. 21, 1
al protein TP0155.
                                                                                                                                                                                                                                                                 PRELIMINARY;
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                                                                                                                                                        Spirochaetaceae; Treponema
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Pred. No. 9.3e-05;
5; Mismatches 79;
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                                                                                                                                                                                                           sequence update) annotation updat
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Kirkpatrick
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., Potamousis K.,
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                                                             Query Match
Best Local S
Matches 83
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Best Local
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Q9KJW8;
01-OCT-2000 (TYEMBLrel. 15, Created)
01-OCT-2000 (TYEMBLrel. 15, Last sequence update)
01-DEC-2001 (TYEMBLrel. 19, Last annotation update)
43 kDa antigen.
Bartonella bacilliformis.
Bacceria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Bartonellaceae; Bartonella.
                                                                                                                                                                   MEDLINE-20407302; PubMed=10948113;
Padmalayam I., Kelly T., Baumstark B., Massung R.;
Padmalayam I., Kelly T., Baumstark B., Massung R.;
Padmalayam I., Kelly T., Baumstark B., Massung R.;
"Molecular cloning, sequencing, expression, and characterization of an immunogenic 43-kilodalton lipoprotein of Bartonella bacilliformis that has homology to NlpD/LppB.";
Infect. Immun. 68:4972-4979(2000).

EMBL; AF157831; AAF80360.1; -.
InterPro; IFR002482; LysM.
InterPro; IFR0024886; Peptidase_M37.
Pfam; PF01476; LysM.
1.
Pfam; PF01476; LysM.; 1.
Pfam; PF01551; Peptidase_M37; 1.
SMART; SM00257; LysM.; 1.
SMART; SM00257; LysM.; 43418 MW; C5ABFB0E8575FBDE CRC64;
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Pfam; PF01551; Peptidase M37; 1.
SMART; SM00257; LysM; 2.
Hypothetical protein; Complete proteome.
SEQUENCE 371 AA; 40664 MW; 8BB00C5E5E3A82A8 CRC64;
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TIGR; TP0155; -.
Interpro; IPR002482; LysM.
Interpro; IPR002886; Peptidase
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Science 281:375-388(1998)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Complete genome sequence of Treponema pallidum, the syphilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         130 GVNTAHTESEVAVQSSREEVQQHEAVQKETEEVV-VVKKE-----TETE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87
   31 AGCASKPTYN-STSGSGS----HRTSGSG-----GLAIGSQVITDSQGVPNRYQV
                                                                83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                             Similarity 25.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YEVREGDVVGRIAQRYDISQDAIISLNKLRSTRALQVGQLLKIPSVDGILYTVKNGDTFS
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                                                                                        9.9%; Score 165.5; DB 2; 25.0%; Pred. No. 0.00036;
                                                                51;
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                                                             Mismatches
                                                             141; Indels
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                                                                                                                    Length
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Q8Y4E2;
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NCBI_TaxID=1639;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Listeria monocytogenes.
Bacteria; Firmicutes; Bacillus/Clostridium
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          255 AKQEAAIKAAEEKRMQEAAAASSAKSAAVVK----
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OPSSSSNEATE---TVSS

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RP SEQUENCE FROM N.A.

RP STRAIN-EGD-E / SEROVAR 1/2A;

RX MEDILINE-2153729; PubMed=11679669;

RX MEDILINE-2153729; PubMed=11679669;

RA Glaser P., Frangeul L., Buchrieser C., Rusnick C., Amend A.,

RA Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,

RA Baquero F., Chetouani F., Couve E., de Daruvar A., Dehoux P.,

RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,

RA Domann K.-D., Fishi H., Garcia-del Portillo F., Garrido P.,

RA Domes L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,

RA Madueno E., Maitournam A., Mata Vicente J., Ng E., Nadjari H.,

RA Madueno E., Novella S., de Pablos B., Perze-Diaz J.-C., Purcell R.,

RA Nordsiek G., Novella S., de Pablos B., Perze-Diaz J.-C., Purcell R.,

RA Vazquez-Boland J.-A., Voss H., Webland J., Cossart P.;

RC Varguez-Boland J.-A., Voss H., Webland J., Cossart P.;

RC Comparative genomics of Listeria species.";

RI Science 294:849-852 (2001).

RI EMBL; AL591983; CAD00582.1; -.

DR Listilist; LN002504; -.

RI Listilist; LN002504; -.

RI InterPro; IPR00286; Peptidase M37; 1.

RFAm; PF01551; Peptidase M37; 1.

RFA ROMEN RAS AA; 47049 MM; 2D36887C1098E167 CRC64;
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical protein lmo2504.
LMO2504.
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TPSPVAVQSSRPPVQQHPAVQKPTPPVVVVKKPTPTPPVVQQPAPVAPPVTEAPFATGSS 195
                                                                     EKNDLVMALANKKDLT-----KSEQTILLASE-----QGALTDEEKRLASNIAGEK 254
                                                                                                                                    KQGDTVSKIAQRYGLNWREIGHINNLNSSYTIYTGQWLTLWSGDLKVRERSISSGVNTAH 135
                                                                                                                                                                                                  ; Score 158.5; DB 16; Length 436; ; Pred. No. 0.0013; 33; Mismatches 100; Indels 67;
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Q8RG41;
01-JUN-2002
01-JUN-2002
01-JUN-2002
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01-UUN-2002 (TrEMBLrel. 21, Last sequence update)
01-UUN-2002 (TrEMBLrel. 21, Last annotation update)
Cell wall endopeptidase family M23/M37.
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Kapatral V., Anderson I., Ivanova N.,
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                                                                                                                                                                                                                                                                                                                                                  VAPPVT-----EAPFATGSSGVMQFRYPV---GATNPVVRRFGTATVAGSTVTSNGMWF 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                      -VRERSISSGVNTAHTPSPVAVQSSRPPVQQHPAVQKPTPPVVVVKKPTPTPPVVQQPAP
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                                                                                                                                                TVRTGQRIASMKN--QPSGAALFEFRISRNGVYVDPLTVLK 322
                                                                                                                                                                                                                                                 SGRDGDLI-----NASNAGTVIQADHNMDGAS--IVIQHTNGFVSSYIHIKDAQVKTGD
                                                                                                                                                                                                                                                                                                     --PPDTGGGDDGGAPASYSGEG---FAFPVRYAGITSPFGNRY--HPVLKRYILHTGV--
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Pred. No. 0.00093;
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Q927Y9;
01-DEC-2001
01-DEC-2001
01-MAR-2002
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01-JUN-2002
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Lipoprotein; Complete proteome.
SEQUENCE 375 AA; 39107 MW;
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PF01551; Peptidase_M37; 1.
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                       (TIENBLIEE). 19, Created)
(TIENBLIEE). 19, Last sequence update)
(TIENBLIE). 20, Last annotation updat
protein lin2647.
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6; Mismatches
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Pred. No. 0.
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Hypothetical LIN2647.

update)

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RESULT 35
052606
ID 05260
AC 05260
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DT 01-JU
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DT Novell
GN NLPD.
OS Ralist
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A Claser P., Frangeul L., Buchrieser C., Rusnick C., Amend A.,

A Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,

A Charbit A., Chetouani F., Couve B., de Daruvar A., Dehoux P.,

Charbit A., Chetouani F., Couve B., de Daruvar A., Dehoux P.,

Charbit A., Chetouani F., Couve B., de Daruvar A., Dehoux P.,

Charbit A., Chetouani F., Couve B., de Daruvar A., Dehoux P.,

Charbit A., Chetouani F., Couve B., de Daruvar A.,

Charbit A., Dominguez-Bernal G., Durant L., Dussurget O.,

Charbit A., Dominguez-Bernal G., Durant L., Dussurget O.,

Charbit A., Chetouani G., Darutillo F., Garrido P.,

Charbit A., Kaerst U., Kreft J., Kuhn M., Kuns F., Kurapkat G.,

Charbit A., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,

Charbit G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,

Charbit G., Novella S., Chiueter T., Simoes N., Tierrez A.,

Comparative genomics of Listeria species.";

Comparative genomics of Listeria species.";

Comparative genomics of Listeria species.";

Comparative G., 24:949-852 (2001).
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Best I
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052606;
01-JUN-1998
01-JUN-1998
01-JUN-2002
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Interpro; IPR002017; Spectrin.
Pfam; PF01551; Peptidase_M37; 1.
Hypothetical protein; Complete prot
SEQUENCE 437 AA; 47301 MW; F3FD
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STRAIN=CLIP 11262 / SEROVAR 6A;
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Bacteria; Firmicutes;
STRAIN=AW1;
MEDLINE=98294041; PubMed=9632252;
Flavier A.B., Schell M.A., Denny T.P.;
"An RpoS (sigmaS) homologue regulates
                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                               NCBI_TaxID=305;
                                                                                                                                                                                                                                                Ralstonia solanacearum (Pseudomonas solanacearum)
Bacteria; Proteobacteria; beta subdivision; Ralst
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                                                                                                                                                                                                                                                                                                                                         . 06, Created)
. 06, Last sequence update)
. 21, Last annotation update)
(Fragment).
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F3FD028682428C57 CRC64;
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   acylhomoserine
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                                                                                                                                                                                                                                                Ralstonia group;
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   lactone-dependent
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Best Local
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01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 21, Last annotation update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Putative peptidase.
SC03368 OR SCE94.19C.
Streptomyces coelicolor.
Streptomyces coelicolor.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Bacteria; Streptomycineae; Streptomycetaceae; Streptomyces.
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Q9X8M5;
01-NOV-1999
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EMBL; AF042351; AAC38576.1; -.
InterPro; IPR002886; Peptidase M37.
Pffam; PF01551; Peptidase_M37; 1.
                                                     Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L., Thomson N.R., James K.D., Harris D.E., Quail M.A., Kleser H., Harris D.E., Quail M.A., Kleser H., Collins M., Erown S., Chandra G., Chen C.W., Collins M., Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S., Huang C.-H., Kleser T., Larke L., Murphy L., Oliver K., O'Neil S., Rabbinowitsch E., Rajandream M.A., Rutherford K., Kutter S., Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K., Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lipoprotein.
                                                                                                                                                                                                                       MEDLINE=97000351, PubMed=8843436;
Redembach M., Kieser H.M., Denapaite D., Eichner A.,
Kinashi H., Hopwood D.A.;
"A set of ordered cosmids and a detailed genetic and
the 8 Mb Streptomyces coelicolor A3(2) chromosome.",
Mol. Microbiol. 21:77-96(1996).
                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. STRAIN=A3(2);
                                                                                                                                                                                                                                                                                                                                                        STRAIN=A3(2);
Bentley S.D., Parkhill J., I
Submitted (APR-1999) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                 Oliver K., Harris D., Submitted (APR-1999)
               "Complete genome sequence coelicolor A3(2).";
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STRAIN=A3(2) / M14
                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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Oliver K., Ha
                                            poomdog
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   417:141-147 (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      176 AA,
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s EMBL/GenBank/DDBJ databases.
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Pred. No. 0.0
                                the model
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hes 79;
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RESULT 38
Q8YRU0
ID Q8YRU
AC Q8YRU
DT 01-MA
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   Q8YRU0;
Q8YRU0;
01-MAR-2002
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1999
01-NOV-1999
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "RNA polymerase sigma factor RpoS of Vibrio parahaemolyticus.";
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AP144608; AAD3392.1; -.
InterPro; IPR002886; Peptidase M37.
Pfam; PF01551; Peptidase M37; I.
NON TER 1 1 1
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Q9X6S4;
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InterPro; IPR002886; Peptidase
Pfam; PF01551; Peptidase M37; I
SEQUENCE 228 AA; 22817 MW;
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|:
LR 222
                                                                                                                                                                                    RTGORIASMKNOPSGAALFEFRISRNGVYVDP
                                                                                                                                                                                                                     GIDIAGQRGQPIVSTAAGTVVYSGNALRGYGNLIIVKHNDNYLSAYAHNDKLLVTEGQSV
                                                                                                                                                                                                                                                                                              KEYVGSKDNQHTKPKPPTT----TVQNDKVSKWLWP--TKGRVIKNFS----AGEQ-GNK
                                                                                                                                                                                                                                                                                                                                  -----VAPPVTEAPFATGSSGVMQFRYPVGATNPVVRRFGTATVAGSTVTSN
                                                                                                                                                                                                                                                                                                                                                                                               PSPVAVQSSRPPVQQHPAVQKP----TPPVVVVK----KPTPTPPVVQQPAP-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NGFVSSYTHIKDAQVKTGDTVRTGQRIASMKN--QPSGAAL-FEFRISRN-GVYVDPLTV 320
                                                                                                                                                                                                                                                             GMWFSGRDGDLINASNAGTVIQADHNMDGAS--IVIQHTNGFVSSYIHIKDAQVKTGDTV
                                                                                                                                                                                                                                                                                                                                                                      PVVVPVVTTTP-----PPVVKPTTTTKPVTSSKNSSQKPTTTPTKVAQKEPPKKVEQTKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NGTYSQYAHLSRINVKIGQIVKTGQSIAKSGNTGNSSGPHLHFEIRTTPNYGSAVDPVAF 220
                                                                                                                                                 KSGQKIATMGSSGAKSVKLHFEIRYQGKSVNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proteobacteria;
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(TrEMBLrel. 12, I
(TrEMBLrel. 19, I
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                                                         PRELIMINARY;
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, Last sequence up
, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                 34; Mismatches
 Created)
Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 152.5; DB 2;
Pred. No. 0.0013;
""smatches 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 153; DB 16;
Pred. No. 0.0014;
6; Mismatches 42;
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                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33EE174EADFA2360 CRC64;
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                                                         760
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AC Q9
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DT 01
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Best Local S
Matches 95
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A Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,

A Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,

A Kishida Y., Kohara M., Matsumoto M., Matsumo A., Muraki A.,

A Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,

Yasuda M., Tabata S.;

T "Complete genomic sequence of the filamentous nitrogen-fixing

T "Complete genomic sequence of the filamentous nitrogen-fixing

T cyanobacterium Anabaena sp. strain PCC 7120.";

DNA Res. 8:205-213 (2001).

DNA Res. 8:205-213 (2001).

R EMBL, AP003592, BABF0052.1; -.

R InterPro; IPR002482; LysM.

R InterPro; IPR002486; Peptidase_M37.
                                                   Q9F7X9;
01-MAR-2001
01-MAR-2001
01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF01476; LysM; 1. — Pfam; PF01551; Peptidase M37; 1. SMART; SM00257; LysM; 1. — Hypothetical protein; Complete proteome. SEQUENCE 760 AA; 80569 MW; FB62A0DDFC6A573B
 Escherichia coli
                   Lipoprotein NLPD.
                                                                                                                              Q9F7X9
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95; Conserv
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                                                                                                                                                                                                                                                                                              GWRWGRMHRGIDIAAPVGTPVFÄAADGVVEKSGWNRGGYGNLVDIRHPDGSLTRYAHNSR
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                                                                                                 MEDINE-9936966; PubMed-10438758;
Hales L.M., Shuman H.A.;
"The Legionella pneumophila rpoS gene is required for growth within Acanthamoeba castellanii.";
J. Bacteriol. 181:4879-4889 (1999).
EMBL; API17715; AAD51395 1; -.
InterPro; IPR002482; LysM.
InterPro; IPR002482; LysM.
InterPro; IPR002486; Peptidase_M37.
Pfam; PP01551; Peptidase_M37; 1.
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Lipoprotein.
SEQUENCE 247 AA; 27535 MW; 6C36631BD5BC9675 CRC64;
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Culham D.E., Wood J.M.;
"An Escherichia coli reference collection group B2- and uropathogen-
associated polymorphism in the rpoS-mutS region of the E. coli
chromosome.";
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Escherichia.
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Bacteria; Proteobacteria; gamma subdivision; Legionellaceae group;
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NCBI_TaxID=446;
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EMBL; AF270497; AAG27176.1; -.
InterPro; TER002886; Peptidase M37.
Pfam; PF01551; Peptidase M37; I.
NON TEP
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-VMY-2001 (TrEMBLrel. 17, Last annotation update)
Novel lipoprotein homolog.
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1 Similarity
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8.7%; Score 145; DB 2; Length 247;
1larity 24.3%; Pred. No. 0.0058;
Conservative 43; Mismatches 104; Indels
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Search completed: July 8, 2003, 11:07:35 Job time: 85 secs

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(c) 1993 - 2003 Compugen Ltd
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Drosophila melanog
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      Moraxella catarrhalis BASB110 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                               VAPPVTEAPFATGSSGVMQFRYPVGATNPVVRRFGTATVAGSTVTSNGMWFSGRDGDLIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ASNAGTVIQADHNMDGASIVIQHTNGFVSSYIHIKDAQVKTGDTVRTGQRIASMKNQPSG
                                                                                                                                                                                                                                      AALFEFRISRNGVYVDPLTVLK 322
                                                                                                                                                                                                                                                                                                                                                                 VAPPVTEAPFATGSSGVMQFRYPVGATNPVVRRFGTATVAGSTVTSNGMWFSGRDGDLIN
                                                                                                                                                                                                                                                                                                                                                                                                                                         KVRERSISSGVNTAHTPSPVAVQSSRPPVQQHPAVQKPTPPVVVVKKPTPTPPVVQQPAP
                                                                                                                                                                                                                                                                                          ASNAGTVIQADHNMDGASIVIQHTNGFVSSYIHIKDAQVKTGDTVRTGQRIASMKNQPSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               322 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 322; DB 22; llarity 100.0%; Pred. No. 1.2e-310; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BEECHAM BIOLOGICALS
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Length Indels

322; 0;

Gaps

120

120

60 60

180

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                                                                                                                                                                                                                                                                                                                                                                               CC catarrhalis strain MC2931 (ATCC 43617), a causative agent of otitis comedia in children and pneumonia in adults. The sequence is a crain MC2931 (ATCC 43617), a causative agent of otitis cranslation of a BASB110 PCR product (see AAR30047). It differs by classified from the predicted polypeptide sequence (see AAB20166) of the BASB110 gene product, having Gly rather than Ser at position composition provides BASB110 polypeptides, and composition provides BASB110 polypeptides using recombinant methods for producing BASB110 polypeptides using recombinant methods. Also claimed is a vaccine composition comprising a BASB110 polypeptide, an immunogenic fragment of a BASB110 polypeptide, or a polypeptide having at least 85% amino caid sequence identity to BASB110, or comprising a polynucleotide encoding such a polypeptide. A claimed method of diagnosing a comprased infection involves identifying a BASB110 polypeptide or antibody. A claimed therapeutic composition useful in treating humans with M. catarrhalis infection comprises at least 1 antibody cdirected against a BASB110 polypeptide. BASB110 polypeptides also chave utility in raising specific antibodies, and in screening for antibacterial drugs.
                                                                                                                                                                                                                                                                                                    Query Match
Best Local :
                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence is that of BASB110 protein from Moras catarrhalis strain Mc2931 (ATCC 43617), a causative agent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 83-84; 88pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel BASB110 polypeptides of Moraxella catarrhalis, useful vaccine for treating Moraxella catarrhalis infections -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers Misc-difference 104
                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Moraxella catarrhalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BASB110; infection; otitis media; pneumonia; therapy; diagnosis; antibacterial; antimicrobial; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS
                                                                                                                                                                                                                                                                                                Local
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)B; AAF30047.
   181
                                  181
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                                                                                                                                           61
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                                                                                                                                                                                                                                                                                 321;
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                                                                                                                                                                                                                                                                                                    Similarity
                      VAPPVTEAPFATGSSGVMQFRYPVGATNPVVRRFGTATVAGSTVTSNGMWFSGRDGDLIN
                                                                                          KVRERSISSGVNTAHTPSPVAVQSSRPPVQQHPAVQKPTPPVVVVKKPTPTPPVVQQPAP 180
                                                                                                                                                                                                                                MTVTIAINSQNQKPIKRLGLIFGVITTCILAGCASKPTYNSTSGSGSHRTSGSGGLAIGS
                                                                    KVRERSISSGVNTAHTPSPVAVQSSRPPVQQHPAVQKPTPPVVVVKKPTPTPPVVQQPAP
                                                                                                                                        QVITDSQGVPNRYQVKQGDTVSKIAQRYGLNWREIGHINNLNSGYTIYTGQWLTLWSGDL
                                                                                                                                                                         QVITDSQGVPNRYQVKQGDTVSKIAQRYGLNWREIGHINNLNSSYTIYTGQWLTLWSGDL
                                                                                                                                                                                                            MTVTIAINSQNQKPIKRLGLIFGVITTCILAGCASKPTYNSTSGSGSHRTSGSGGLAIGS
 VAPPVTEAPFATGSSGVMQFRYPVGATNPVVRRFGTATVAGSTVTSNGMWFSGRDGDLIN
                                                                                                                                                                                                                                                                                                                                                       322
                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                  68.6%;
                                                                                                                                                                                                                                                                                Score 221; DB 22;
Pred. No. 1.7e-210;
0; Mismatches 1;
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tive agent of otitis
                                                                                                                                                                                                                                                                                                                   Length 322;
                                                                                                                                                                                                                                                                                 Indels
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                                 240
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240
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RESULT 4
AAG90076
ID AAG9
XX

AAG90076 standard; Protein; 223

밁 S

Matches

Conservative

0

Mismatches

٥,

Indels

0

Gaps

0

217 ATVAGSTVT 225

ATVAGSTVT

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RESULT 3
ABB61691
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           Query Match
Best Local
                                                                                                                   capable of detecting 1000 or more genes from Drosophila. The invent useful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins (ABB57737-ABB72072)
                                                                                                                                                                                                 The invention relates to an isolated nucleic acid detection reagent canable of detecting 1000 or more genes from Drosophila. The invent
                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                    23-MAR-2000;
11-JUL-2000;
                                                                                         The sequence data for this patent did not form specification, but was obtained in electronic f
                                                                                                                                                                                                                                          Disclosure; SEQ ID NO 11865; 21pp + Sequence Listing;
                                                                                                                                                                                                                                                                                 New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                   Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-MAR-2001; 2001WO-US09231.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-SEP-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABB61691;
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                                                                                                                                                                                                                                                                                                                                                                                              (PEKE ) PE CORP NY.
                                                                          ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                            2001-656860/75.
DB; ABL05794.
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Similarity 9; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ASNAGTVIQADHNMDGASIVIQHTNGFVSSYIHIKDAQVKTGDTVRTGQRIASMKNQPSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ASNAGTVIQADHNMDGASIVIQHTNGFVSSYIHIKDAQVKTGDTVRTGQRIASMKNQPSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             melanogaster polypeptide SEQ ID NO 11865
                                                   968 AA;
                                                                                                                                                                                                                                                                                                                                                                   Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                     2000US-191637P.
2000US-0614150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein;
         2.8%;
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           Score 9;
Pred. No.
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           .22;
                                                                                         n part of the printed format directly from
                      Length 968;
                                                                                                                                                                                                                                          English.
                                                                                                                                                                                                    The invention
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RESULT 5
AAW94997
ID AAW9
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AC AAW9
DT 12-M
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Best Local S
Matches 8
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07-APR-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                 The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a protein described in the exemplification of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nakagawa
Tateishi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Coryneform bacterium; organic acid synthesi
 YAK-1; serine-threonine inflammatory disorder;
                                      YAK-1 related
                                                                  12-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 17; SEQ ID NO: 3830; 246pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-DEC-2000; 2000EP-0127688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-JUN-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Corynebacterium glutamicum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-SEP-2001
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                                                                                                                     AAW94997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (KYOW ) KYOWA HAKKO KOGYO KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         glutamicum
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DB; AAH65295.
                                                                                                                                                                                     130
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                                                                                                                                                                                                                                      Similarity
8; Conser
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                                                                                                                     standard;
                                                                                                                                                                                     HTPSPVAV 137
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                                                                                                                                                                                                                                                                                           223
                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99JP-0377484.
2000JP-0159162.
2000JP-0280988.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    synthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mizoguchi H, Ando S, Hayashi M,
Senoh A, Ikeda M, Ozaki A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein fragment SEQ ID NO: 3830.
                                                                  (first
                                      serine/threonine protein kinase-HTLAR33.
                                                                                                                                                                                                                                                                                             ₽,
                                                                                                                     Protein;
                                                                                                                                                                                                                                                    2.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid synthesis; vitamin;
 e protein kinase;
osteoporosis; Ad
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                                                                                                                                                                                                                                        Score 8; DB:
Pred. No. 18
0; Mismatches
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                                                                                                                                                                                                                                                      DB 22;
o. 18;
               HTLAR33; bone loss; ARDS;
                                                                                                                                                                                                                                        0,
                                                                                                                                                                                                                                                                 Length 223
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Adult Respiratory Disease

Syndrome;

23-MAR-1998

(first entry)

Peptide;

13 B

AAW31599; AAW31599 덩 Ś

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RESULT 6
AAW31599
ID AAW3
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AC AAW3
XX
AC AAW3
XX
AC AAW3
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                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      arthritis; psoriasis; dermatitis; asthma; allergy; infection; HIV-1; HIV-2; cachexia; immunodeficient disorder, septic shock; pain; injury; cancer; anorexia; bulimia; Parkinson's disease; cardiovascular disease; neurological disorder; Huntington's disease; gene therapy; gene mapping Gilles de la Tourette's syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New serine-threonine kinase (HTLAR33) polypeptides and polynucleotides - useful as diagnostic reagents and for prevention and treatment of bone loss, neurological and inflammatory disorders and cancer, HIV infections and angina pectoris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 15; 30pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1999-108353/10.
N-PSDB; AAX17774.
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28-JUL-1997;
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D
                                                                                                                                                                                                                                                             APVAPPVT 457
                                                                                                                                                                                                                                                                                                                  APVAPPVT 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      557 AA;
                                                                                                                                                                                                                                                                                                                                                                           2.5%; Soliarity 100.0%; I Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98US-0027064.
97US-0053924.
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; Pred. No. 42
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                    20;
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RESULT 7
AAU11448
ID AAU1
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AC AAU1
AC AAU1
AC AAU1
AC AAU1
AX
DT 12-W
XX
DB Synt
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      in trans, all virion proteins required for packaging such a retroviral vector. The helper DNA sequence encodes a ecotropic Moloney murine leukaemia virus (MMLV) or gibbon ape leukaemia virus (GALV) gag and pol; and a xenotropic, amphotropic, ecotropic or polytropic envelope protein. The packaging plasmids, designated KAT plasmids, are used with a second retroviral vector encoding a foreign gene of interest to produce mammalian cells with retroviral supernatants that express, e.g. a hormone, lymphokine, growth factor or coagulation factor. The plasmids are useful in construction of stable cell lines that constitutively
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   produce the retroviral proteins required in trans for the production of retrovirus particles: gag, pol and env. The stable producer cells continue to produce high titre retrovirus indefinitely in the absence of drug selection due to the stable integration of both packaging function and virus vector. The retroviral vector plasmids are constructed with sequences enabling the episomal persistence without the need for stable integration of the vector plasmid. The Env gene determines the host
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This linker peptide is used to construct a plasmid pIK98.6-K/L/H which is used in the construction of a retroviral packaging plasmid used for the production of high titres of recombinant retrovirus in human cells. The retroviral packaging plasmid comprises a retroviral halper DNA sequence derived from a replication incompetent retroviral genome that encodes, the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the c
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                             Synthetic peptide linker for chimaeric antibodies #1
                                                                                     12-MAR-2002
                                                                                                                                             AAU11448;
                                                                                                                                                                                                AAU11448 standard; Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 27; 157pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  foreign
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             High efficiency retroviral packaging system - used to transduce human cells, esp. haematopoietic stem cells, T or B cells with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1997-165307/15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cooke K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CELL-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-AUG-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-AUG-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-FEB-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9707225-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 retroviral packaging system; human; virion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Linker peptide used in the construction of pIK98.6-K/L/H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         primer;
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                                                                                                                                                                                                                                                                                                                                                                                          41 STSGSGS 47
                                                                                                                                                                                                                                                                                                                                           N
                                                                                                                                                                                                                                                                                                                                                                                                                                                  h 2.2%; So Similarity 100.0%; F 7; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CELL GENESYS INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13
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                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,
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k; Pred. No. 12;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zsebo KM;
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RESULT 8
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14-DEC-1990;
12-DEC-1991;
09-DEC-1992;
                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to treating viral or malignant diseases using modified T cells that express proteins comprising (in an N-terminal to C-terminal direction) single chain antibody binding domains (that bind to viral or tumour antigens), transmembrane domains and cytoplasmic signal transducing domains. When the single chain antibody domain binds to the viral or tumour antigen on the cell, the modified T cells kill cells expressing the antigens. The modified T cells are used for treating immunodeficiency virus (HIV), cytomegalovirus, hepatitis C, hepatitis B, and mycobacterium avium. The present sequence is peptide linker used to link together the functional peptides of the chimaeric antibody molecule
                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Virucidal; cytostatic; peptide linker; anti-HIV; human immunodeficiency virus infection; viral disease; malignant disease; T cell; single chain antibody; cytomegalovirus; hepatitis C; hepatitis B;
                                                                                         Mouse; monogenic audiogenic seizure-susceptible-1 gene; mass1;
                                                                                                                   Mouse massi protein conserved
                                                                                                                                               18-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 3; Column 23; 38pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Treating viral infections, e.g. HIV, and malignancies using T cells that express proteins which bind virus/tumour antigens and kill cells presenting the antigens, via the activity of a cytoplasmic signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-074399/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Capon DJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-JUN-1995;
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                         WO200165927-A1.
                                                                             transgenic
                                                                                                                                                                                                  AAE10936 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           transducing domain
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                                                                                                                                                                                                                                                                                            41 STSGSGS 47
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                                                                                                                                                                                                                                                                                                                       Similarity 7; Conserv
                                                                           animal; genetic abnormality; seizure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Weiss A,
                                                                                                                                                                                                                                                                                                                                                                            13 AA;
                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENESYS INC.
                                                                                                                                             (first entry)
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90US-0627643.
91WO-US09431.
92US-0988194.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95US-0479737
                                                                                                                                                                                                  peptide;
                                                                                                                                                                                                                                                                                                                                     2.2%; Score 7;
100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Irving
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Roberts MR,
                                                                                                                    acid repeat motif #11.
                                                                                                                                                                                                                                                                                                                                     DB 23;
5. 12;
                                                                                                                                                                                                                                                                                                                        0
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                                                                                                                                                                                                                                                                                                                                                  Length 13;
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13-SEP-2001.

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RESULT 9
ABPO408F
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to nucleic acid molecules designated monogenic audiogenic seizure-susceptible-1 (mass1) genes. The nucleic acid molecule may be used via recombinant DNA methodologies in the production of transgenic animal (especially mouse) models for studying genetic abnormalities related to mass1 which result in seizure susceptible phenotypes (mass1 is audiogenic seizures). The present sequence is mouse monogenic audiogenic seizure-susceptible (mass1) protein conserved amino acid repeat motif.

Note: The present sequence (SEQ ID NO.16) is incorrectly referred to as SEQ ID NO.15 in the sequence listing of the specification.
                                                                                                                                                                                                                                                                                                Human; open reading frame; OREX; gene thorapy; cancer; cirrhosis; hyperproliferative disorder; psoriasis; benign tumour; haemorrhage; degenerative disorder; osteoarthritis; neurodegenerative disorder; cardiovascular disease; diabetes mellitus; systemic lupus erythematosus; hypertension; hypothyroidism; cholesterol ester storage disease; immune deficiency; immune disorder; infectious disease;
                                                                               30-MAY-2000; 2000US-206132P.
29-AUG-2000; 2000US-228716P.
                                                                                                                                29-MAY-2001; 2001WO-US10836
                                                                                                                                                                                                  WO200192523-A2
                                                                                                                                                                                                                                                                 myasthenia gravis.
                                                                                                                                                                                                                                                                                                                                                                                                                   Human ORFX protein sequence SEQ ID NO:8156.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      24-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABP04087;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABP04087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-589903/66
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03-AUG-2000;
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                                                (CURA-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       287
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                                                CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     n 2.2%;
Similarity 100.0%;
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      standard; Protein; 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGQRIAS 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGORIAS 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Audiogenic Seizure-Susceptible-1 (mass1) genes, useful for animal models of audiogenic seizures -
                                                                                                                                                                                                                                                                                    disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        White S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000US-187209P
2000US-222898P
                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fu Y,
                                                                                                                                                                                                                                                                                    rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 7; DB 2; Pred. No. 31; 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 22;
o. 31;
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DR WPI; 2002-106308/14.

DR NPSDB; ABN19839.

XX Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, preventing and treating cardiovascular disease, neurodegenerative, preventing and treating cardiovascular disease, neurodegenerative, preventing and treating trame, Doglish.

CC Disclosure, SEQ ID 8156; 1037pp; English.

CC The present invention describes substantially purified human proteins of the specification). ABN15762 to ABN7782 encode the human DRFX corrections of the specification of the specification. ABN15762 to ABN77852 encode the human DRFX corrections of the specification of the specification of the specification of the specification of the specification of the specification of the specification of the specification of the specification of the specification of the specification of cardiovascular discorders of the section of the specification, cardiovascular discorders, discorders has no the used in the transplantation, cardiovascular discorders, discorders has not settled to organ transplantation, cardiovascular discorders, discorders infectious of the specification of the specification, hypothyroidism cholesterol ester storage disease, autoimmune discorders such as multiple sclerosis, rheumatoid disease, autoimmune thyroiditis, myasthenia gravis, graft-versus-host of disease and autoimmune inflammatory eye disease. ORFX proteins are also cardiovascular diseases, discorders, proteins are also cardiovascular discorders for treating osteoporosis, competition or regeneration and treatment of lung or liver fibrosis, reperituion injury in various tissues and conditions resulting from the specification, but was obtained in electronic format directly from WIPO cardiovascular discorders of the printed specification, but was obtained in electronic format directly from WIPO cardiovascular discorders.

So Sequence 54 AA;
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RESULT 10
AAM83197
ID AAM83
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AC AAM83
AC AAM83
XX
O7-NC
XX
DE Humar
XX
Humar
XX
Homo
XX
HOmo
XX
O9-At
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AC 17-JF
PR 01-JF
PR 02-NL
PR 16-NJ
PR 16-NJ
PR 16-NJ
PR 117-NJ
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Best Local S
Matches 7
 31-JAN-2000;
04-FEB-2000;
24-FEB-2000;
02-MAR-2000;
16-MAR-2000;
17-MAR-2000;
                                                                                                                                                                                                                                   AAM83197;
                                                                                                                                                                                                                                                         AAM83197 standard; Protein;
                                                                        17-JAN-2001; 2001WO-US01354.
                                                                                               09-AUG-2001.
                                                                                                                                                          Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis.
                                                                                                                                                                                                               07-NOV-2001 (first entry)
                                                                                                                  WO200157182-A2
                                                                                                                                                                                                                                                                                                                              178 PAPVAPP 184
                                                                                                                                                                                         immune/haematopoietic antigen
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                                                                                                                                                                                                                                                                                                                                                    Similarity 7; Conserv
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; 2000US-0179065.
; 2000US-0180628.
; 2000US-0184664.
; 2000US-0186350
; 2000US-0189874.
; 2000US-0190076.
                                                                                                                                                                                                                                                                                                                                                   2.2%;
|larity 100.0%
|Conservative
                                                                                                                                                                                                                                                                                                                                                0;
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; Pred. No. 46,
0; Mismatches
                                                                                                                                                                                           SEQ ID NO:10790
                                                                                                                                                                                                                                                                                                                                                              DB 23;
o. 46;
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18-APR-2000; 19-MAY-2000; 07-JUN-2000; 28-JUN-2000;

30-JUN-2000; 07-JUL-2000; 07-JUL-2000;

14-JUL-2000; 26-JUL-2000; 26-JUL-2000; 14-AUG-2000; 14-AUG-2000;

14-AUG-14-AUG-14-AUG-14-AUG-14-AUG-14-AUG-

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14-AUG-2000; 14-AUG-2000; 14-AUG-2000; 11-AUG-2000; 22-AUG-2000; 22-AUG-2000; 23-AUG-2000; 30-AUG-2000; 01-SEP-2000;

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RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foetal deficiency; blood; allergy; renal; immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma; inflammation; ischaemic shock; Alzheimer's disease; restencesis; AIDS; cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus; osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion; endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
                                                                                                                                                                                                                                                               01-APR-1998;
                                                                                                                                                                                                                                                                                                                                                       19-MAR-1998;
19-MAR-1998;
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19-MAR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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                                                         SM, Ni J, R
, Endress GA,
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Similarity 100.0%; Pred. No. 56
7; Conservative 0; Mismatches
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                                                                                                                                                                                              98US-0078574.
98US-0078574.
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98US-0078577.
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98US-0078579.
98US-0078591.
98US-0080313.
98US-0080314.
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                                                   Rosen CA, r
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Куаw
                                                      Young PE, F
H, Ebner R,
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                                                             Feng P, Soppet DR;
R, Lafleur DW;
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Matches 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 199
N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                             SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
                                                                                                           Skeiky YAW, Persing DH,
L'maisonneuve J, Zhang Y,
                                                                                                                                                                                       21-APR-2000; 2000US-199047P.
02-JUN-2000; 2000US-208841P.
07-JUL-2000; 2000US-216747P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 11; Page 387; 484pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated human genes, useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood
Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful treating acne vulgaris -
                                                               WPI; 2001-616774/71.
N-PSDB; AAS59618.
                                                                                                                                                                                                                                                      20-APR-2001; 2001WO-US12865
                                                                                                                                                                                                                                                                                                                                                   Propionibacterium acnes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Propionibacterium acnes immunogenic protein #22483.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAU61587;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAU61587 standard; Protein; 72
                                                                                                                                                                                                                                                                                                                     WO200181581-A2
                                                                                                                                                           (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1999-562050/47
DB; AAZ24858.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2.2%; Score 7; DB:
ilarity 100.0%; Pred. No. 57
Conservative 0; Mismatches
                                                                                                             Mitcham JL, Wang SS, Jen S, Carter D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   English.
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polypeptides. The proteins and

Example

1; SEQ ID No 22782; 1069pp; English.

AAU39105-AAU68017 represent Propionibacterium acnes

their associated DNA sequences

immunogenic are used in

CC the treatment, prevention and diagnosts of medical conditions caused by CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne, cC pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis. CC P. acnes is also involved in infections of bone, joints and the central CC nervous system, however it is particularly involved in the inflammatory CC lesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a cCC sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The cCC polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to covaregulate expression and activity of P. acnes polypeptides and ct therefore treat P. acnes infections. The antibodies may also be used as CC diagnostic agents for determining P. acnes presence, for example, by cnryme linked immunosorbent assay (ELISA).

CC Note: The sequence data for this patent did not form part of the printed as pecification, but was obtained in electronic format directly from WIPO care fern wino introduced and consense.

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178 PAPVAPP 184

Query Match

ftp.wipo.int/pub/published_pct_sequences.

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Local

Similarity
7; Conserv

2.2%; but 100.0%; Pr

Score 7; DB 2; Pred. No. 61; 0; Mismatches

DB 22;

Length 72;

0,

Indels

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Gaps

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Conservative

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                                                                                                                                                                                                                                                                                                    SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for treating acne vulgaris -
                                                                                                                                            21-APR-2000; 2000US-199047P.
02-JUN-2000; 2000US-208841P.
07-JUL-2000; 2000US-216747P.
                                                 WPI; 2001-616774/71.
N-PSDB; AAS59549.
                                                                                               Skeiky YAW,
                                                                                                                                                                                            20-APR-2001; 2001WO-US12865.
                                                                                                                                                                                                                       01-NOV-2001.
                                                                                                                                                                                                                                                                     Propionibacterium acnes.
                                                                                                                                                                                                                                                                                                                                                                                                         AAU50707;
                                                                                   L'maisonneuve
                                                                                                                                                                                                                                                                                         dermatological; osteopathic; neuroprotectant.
                                                                                                                                                                                                                                                                                                                                                      Propionibacterium acnes immunogenic protein #11603
                                                                                                                                                                                                                                                                                                                                                                                27-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                              AAU50707 standard; Protein; 80 AA
                                                                                                                     (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PAPVAPP 34
                                                                                 Persing DH,
e J, Zhang Y,
                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                  Mitcham JL, Wang
, Jen S, Carter
                                                                                            Wang SS,
                                                                                               Bhatia
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Example 6; Fig 1; 94pp; English

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AAY96225
ID AAY96
XX AAY96
XX T11-SE
XX Leafy
KW Belec
XX Leafy
KW Belec
XX Arabi
XX Leafy
KW Belec
XX Arabi
XX O9-NC
PF 09-NC
PF 10-NC
XX O9-NC
PR 10-NC
XX O9-NC
PR 10-NC
XX WPI;
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Matches
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by P. acnes. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis. P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention
                                            New HAP3-type CCAAT-box binding transcriptional activators, particularly Leafy cotyledon 1 transcriptional activator, u inducing somatic embryogenesis or apomixis in a plant cell
                                                                                                                                           Lowe KS, Gordon-Kamm
Sun X, Hoerster GJ,
                                                                                                                                                                                             (PION-)
                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-SEP-2000 (first entry)
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                                                                                                              WPI; 2000-376568/32
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10-NOV-1998;
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                                                                                                                                                                                                                                                                                                                                                             WO200028058-A2
                                                                                                                                                                                                                                                                                                                                                                                                                            Leafy cotyledon 1 transcriptional activator; LEC1;
selectable marker; transgenic plant; transgenic see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis LEC1 consensus region
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7; Conserv
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DU PONT DE NEMOURS & CO E
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98US-0107810.
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                                                                                                                                                                                                                                                                                                                                                                                                                          transgenic plant;
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                                                                                                                                                            WJ, Klein TM,
                                                                                                                                           Gregory CA,
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Pred. No.
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dimpalli R;
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The present invention is related to a Lactococcus lactis nucleotide sequence (ABA90521) and related proteins (ABB5300-ABB55621). The nucleic acid sequence is useful in the detection and/or amplification of nucleic acid sequence, particularly to identify Lactococcus lactis or related species. The proteins of the invention are useful for the biosynthesis or biodegradation of a composition of interest. The invention helps research in lactic bacteria, particularly useful in the production of yogurt and cheese.

Note: The sequence data for this patent is based on equivalent patent w0200177334 (published 18-OCT-2001) which is available in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is the leafy cotyledon 1 transcriptional activator, LEC1 consensus sequence from Arabidopsis. This sequence is a HAP3-type CCANT-box binding protein, LEC1 expression initiates the formation of rembryo-like structures and improves growth and recovery of transformants When appmixis occurs, i.e. the replacement of sexual reproduction by asexual reproduction, LEC1 expression in the muclellus integument, or cell specific expression in the megaspore mother cell would trigger embryo formation from maternal tissues only. This results in the production of seeds identical to the parent. Using LEC1, transgenic high yielding seeds could be developed. In addition, LEC1 could be used for positive selection of a transformed cell (transgenic plant), for increasing transformation efficiency and for increasing recovery of regenerated plants. The present sequence was used in the identification of the plant LEC1 consensus sequence (AAY96223).
                                                                                                                                                                                                                                                                             Claim 6; SEQ ID No 2144; 2504pp; French.
                                                                                                                                                                                                                                                                                                                 New nucleotide sequence useful in the identification or Lactococcus lactis and related species -
                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-043418/06.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lactococcus lactis IL1403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biosynthesis; biodegradation; lactic bacterium; yogurt; cheese.
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18-OCT-2000
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Arabidopsis thaliana protein fragment SEQ ID NO: 74962.
                                               (first entry)
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;

Arabidopsis thaliana.

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28-MAY-1999;
01-JUN-1999;
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Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis;
                                                                                     Human ORFX protein sequence SEQ ID NO:1822.
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                                                                                                                                                                                                                                                                                                                     ABP00920 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID NO 25194; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated nucleic acid genes from Drosophila and interactions -
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N-PSDB; ABL10237.
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11-JUL-2000; 2000US-0614150.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster polypeptide SEQ ID NO 25194
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ilarity 100.0%;
Conservative (
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2
5.92;
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RESULT 19 ABG04226 ID ABG04 XX

ABG04226 standard; Protein; 126

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64 99 Query Match Best Local S Matches 7

Similarity NNLNSSY 105

> .2%; Score 7; 0.0%; Pred. No. 0;

> > Length 114;

0;

Gaps

0

Mismatches DB 93, 23; ٥,

Conservative

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The present invention describes substantially purified human proteins CC (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1 CC in the specification). ABN15762 to ABN27252 encode the human ORFX CC proteins given in ABP00010 to ABN1500. ORFX proteins are useful for treating or preventing a pathology associated with an ORFX-associated CC disorder in humans, and in the manufacture of a medicament for treating a CC syndrome associated with ORFX-associated disorder. ORFX polynucleotide CC sequences can be used in gene therapy. ORFX sequences can be used in the CC treatment of cancer, hyperproliferative disorders, cirrhosis of liver, CC psoriasis, benign tumours, keloid, degenerative disorders related to organ CC transplantation, cardiovascular diseases, diabetes mellitus, systemic CC troage disease, various immune deficiencies and disorders, infectious CC diseases, autoimmune disorders such as multiple sclerosis, rheumatoid CC arthritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host CC disease and autoimmune thyroiditis, myasthenia gravis, graft-versus-host CC disease and autoimmune thyroiditis, myasthenia gravis, graft-versus-host CC disease and autoimmune thyroiditis, myasthenia gravis, graft-versus-host CC disease and autoimmune thyroiditis, myasthenia gravis, graft-versus-host CC disease and autoimmune thyroiditis, myasthenia gravis, graft-versus-host CC protection or regeneration and treatment of lung or liver fibrosis, CC protection or regeneration and treatment of lung or liver fibrosis, CC protection or regeneration and treatment of lung or liver fibrosis, CC protections of the printed constraint did not form part of the printed CC Albanese and conditions resulting from CC systemic Cytokine damage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and autoimmune disorders
                                      N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID 1822; 1037pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shimkets RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-MAY-2000;
29-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hyperproliferative disorder; psoriasis; benign tumour; haemorrhage; degenerative disorder; osteoarthritis; neurodegenerative disorder; cardiovascular disease, diabetes mellitus; systemic lupus erythematosus; hypertension; hypothyroidism; cholesterol ester storage disease; immune deficiency; immune disorder; infectious disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200192523-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         autoimmune disorder; rheumatoid arthritis; autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CURA:-) CURAGEN CORP.
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DB; ABN16672.
114 AA;
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2000US-228716P.
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RESULT 20
AAO05078
ID AAO05
XX
AC AAO05
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Best Local S
Matches 7
                                                                                                                                                                                                                                                                                                                                                                                                           and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WI at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                       AAC05078;
                                                                AAO05078 standard; Protein; 136
                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 20; SEQ ID No 34585; 103pp; English.
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23-AUG-2000; 2000US-0649167.
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                                                                                                                                                                                                                                                                            Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                       126
                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                       AA;
                                                                                                                                                                                                                                                                       2.2%; Score 7; DB:
100.0%; Pred. No. 1e-
tive 0; Mismatches
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o. 1e+02;
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                                      Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
                                                                                                           Arabidopsis
                     termination
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RESULT 21
AAG58103
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Best Local Similarity
Thes 7; Conserve
                                                                                                                                                                                                                                                                                         The invention relates to human polymucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polymucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity inhibin activity and may be useful in the diagnosis and/or activity in the diagnosis and/or activity and may be useful in the diagnosis and/or activity.
 18-OCT-2000
                                                                 AAG58103 standard; Protein; 138 AA
                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation.
                                 AAG58103;
                                                                                                                                                                                                                                                                                                                                         Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tang YT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 20; SEQ ID NO 18970; 1399pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-FEB-2000; 2000US-0515126.
18-MAY-2000; 2000US-0577409.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human polypeptide SEQ ID NO 18970
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                                                                                                                                                                                                                                                                                                                                                                                              treatment
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                                                                                                                                                                                                                                                                                                                                                                          nflammation.
                                                                                                                                                                                                                                                                                                                     ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                      28
                                                                                                                                                                                      KPTPTPP 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Liu C,
                                                                                                                                                                                                                                                                                                                                                                                          of cancer, leukaemia, nervous system
                                                                                                                                                                                                                                                                                       136 AA;
                                                                                                                                                                                                                       Conservative
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drmanac
                                                                                                                                                                                                                                      2.2%;
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0; Mismatches
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o. 1.1e+02;
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                                                                                                                                                                                                                                                                                                                                                                                          disorders, arthritis and
                                                                                                                                                                                                                       Indels
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thaliana protein fragment SEQ ID NO:

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25-FEB-2000;
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                                                           Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia;
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16-SEP-1999;
20-SEP-1999;
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23-SEP-1999;
                      WO200164835-A2
                                                                                            Human polypeptide SEQ ID NO 19767.
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                                     Homo sapiens.
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                                                     system disorders;
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ARESULT 23
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                                                                                                                                                                                                                                                                   03-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                 Staphylococcus aureus 'WCUH 29'.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                diagnosing and treating disorders -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to human
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No. 1.2e+02;
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(SMIK) SMITHKLINE

BEECHAM CORP.

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RESULT 24
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XX Prop:
XX SAPH
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KW infi:
KW infi:
KW WO20
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                     Skeiky YAW, Persing DH, Mitcham JL, Wang SS, L'maisonneuve J, Zhang Y, Jen S, Carter D;
                                                                                                                                                                                                             20-APR-2001; 2001WO-US12865
                                                                                                                                                                                                                                                      01-NOV-2001.
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                                                                                                                                                                                                                                                                                                                                      Propionibacterium acnes.
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DB; AAD05669.
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                                                                                                                        2000US-199047P.
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2000US-216747P.
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DR N-PSDB; AAS59749.

EX Propionibacterium acnes polypeptides and nucleic acids useful for PT Propionibacterium acnes polypeptides and nucleic acids useful for PT vaccinating against and diagnosing infections, especially useful for PT vaccinating against and diagnosing infections, especially useful for PT vaccinating against and diagnosing infections, especially useful for PT vaccinating acne vulgaris -

EXX Example 1; SEQ ID No 27900; 1069pp; English.

EXX Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic CC polypeptides. The proteins and their associated DNA sequences are used in CC the treatment, prevention and diagnosis of medical conditions caused by PS cacnes is also involved in infections of bone, joints and the central CC pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis. CC pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis. CC pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis. CC pustulosis system, however it is particularly involved in the inflammatory CC sample with a binding agent that binds co the proteins of the invention CC and determining the amount of bound protein in the sample. The cC polypeptides may be used as antigens in a patient comprises contacting the CC specific for P. acnes proteins. These antibodies can be used to compregulate expression and activity of P. acnes polypeptides and CC diagnostic agents for determining P. acnes presence, for example, by CC enzyme linked immunosorbent assay (ELEA).

CC Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO cat fire the protein and accordinate and concerns and accordinate directly from WIPO at the protein of the printed specific for the protein and accordinate accordinates. Score 7; DB 22; Length 159;

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                                   Skeiky YAW, Persing DH, I
L'maisonneuve J, Zhang Y,
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2000US-208841P.
2000US-216747P.
                                   Mitcham JL, Wang
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CC Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO cr at ftp.wipo.int/pub/published_pct_sequences.
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Best Local S
Matches 7
                          Telford J,
Tettelin H;
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24-NOV-2000; 2000GB-0028727.
07-MAR-2001; 2001GB-0005640.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae; group A streptococcus; Streptococcus pyogenes; antibacterial; antiinflammatory; infection; vaccine; meningitis; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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                                                                                                                                                                                                                                                                                                                                           29-OCT-2001; 2001WO-GB04789.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200234771-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptococcus pyogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptococcus polypeptide SEQ ID NO 132.
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                                                                                                                      (CHIR-) CHIRON SPA.
(GENO-) INST GENOMIC RES
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les 7; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2001-616774/71.
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                                                           Masignani V, Margarit Ros YI,
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100.0%; Pre
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Pred. No. 1.3e+02;
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are used in
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Best Local Similarity
                                                                                                                                            09-OCT-1998;
09-OCT-1998;
25-FEB-1999;
                                                                                                                                                                                                                          02-SEP-1998;
09-OCT-1998;
                                                                                                                                                                                                                                                                                         31-JUL-1998;
02-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                  01-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                           30-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antigenic; diagnosis;
antibacterial; gene tl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Neisseria meningitidis; Neisseria gonorrheae; antigenic; diagnosis; immunogenic; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Neisseria gonorrheae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the treatment or prevention of infection or disease caused by Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes. Nucleic acids encoding (I) are used to detect Streptococcus in a biological sample. (I) is used to determine whether a compound binds to (I). A composition comprising (I) or a nucleic acid encoding (I), may be used as a vaccine or diagnostic composition. The disease caused by Streptococcus that is prevented or performed may be meningitis. Nucleic acid encoding (I) may be used to recombinantly produce (I) and may be used in gene therapy. Antibodies to (I) are used for affinity chromatography, immunoassays, and distinguishing/identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a protein (ABP25413-ABP30895) from group B streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS (Streptococcus pyogenes), comprisione of 5483 sentences (S1), given in the specification. The proteins have antibacterial and antiinflammatory activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and antibodies that bind (I) are used in the manufacture of medicaments for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9957280-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Neisseria gonorrheae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New Streptococcus protein for the treatment or prevention of infection or disease caused by Streptococcus bacteria, such as meningitis, and for detecting a compound that binds to the protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptococcus proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 3167; 4525pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; ABN66109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7;
                                                        CHIRON CORP.
INST GENOMIC
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                                                                                                                                         98US-0103794.
98US-0103796.
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98US-0094869.
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98US-0099062.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene therapy.
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                                                           RES.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                immunogenic; infection;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO:2858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antigen; vaccine;
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Fraser C,

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Hickey E,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Petersen
Tettelin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel Neisserial polypeptides predicted vaccines and diagnostics -
                                 New isolated nucleic a
genes from Drosophila
interactions -
                                                                                                                       Venter JC,
                                                                                                                                                                       23-MAR-2000;
11-JUL-2000;
                                                                                                                                                                                                           23-MAR-2001; 2001WO-US09231.
                                                                                                                                                                                                                                   27-SEP-2001.
                                                                                                                                                                                                                                                            WO200171042-A2
                                                                                                                                                                                                                                                                                    Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                             pharmaceutical.
                                                                                                                                                                                                                                                                                                                       Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster polypeptide SEQ ID NO 11364.
                                                                                                                                                                                                                                                                                                                                                                        26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                       ABB61524 standard; Protein; 195 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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                                                                                                                                                (PEKE ) PE
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                                                                                   2001-656860/75.
DB; ABL05627.
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Similarity .100.0%; Pred. No. 1.:
7; Conservative 0; Mismatches
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2000US-0614150
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Venter JC;
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for elucidating co
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                                              nt for detecting cell signalling
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Best Local S
Matches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLIG176-ABLIG11), expressed DNA sequences (ABLIG176-ABLIG1); sepressed DNA sequences (ABLIG176-ABLIG1).
LEC1 polypeptide is encoded by the leafy cotyledon-1 (LEC1) gene (see ANG1022-24) of Arabidopsis thaliana. Full-length LEC1 polypeptide can act as a subunit of a protein capable of acting as a transcription factor in plant cells. The LEC1 gene is embryo-specific and can be used to modulate development (claimed) of embryos or other organs in plants. Inhibiting expression can be useful e.g. in weed control (by transferring an inhibitory sequence
                                                                                                                                       New isolated plant leafy cotyledon-1 gene - used for, e.g. increasing storage protein content in producing fruit with small and non-viable seed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                               19-FEB-1998;
21-FEB-1997;
                                                                                                                                                                                                                                                                                                                                        20-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                    27-AUG-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis leafy-cotyledon 1 (LEC1) polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-JAN-1999
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                                                                                                             Claim 15; Page 31; 55pp; English.
                                                                                                                                                                                                                                         Fischer RL,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Binding-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       transgenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LEC1; leafy-cotyledon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (ABB57737-ABB72072)
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DB; AAV61022-24.
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Larity 100.0%;
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                                                                                                                                                                                                                                         Goldberg
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97US-0804534.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "putative DNA binding site"
61..72
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                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "putative subunit interaction domain"
                                                                                                                                                                                                                                           RB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; embryo; transcription factor;
                                                                                                                                                                                                                                           Harada
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0; Mismatches
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RESULT 30
AAY54563
                       C LECI genes are thought to play a central role in late embryogenesis, in Specifying cotyledon identity during embryo development. LECI polypeptides may act as transcription factors. LECI polypucleotides are useful for modulating seed development and for inducing ecotopic development of embryonic tissue in a plant. In both cases, the LECI polynucleotide is introduced into the plant through a sexual cross and constructed is co-expressed in an antisense orientation with a second heterologous constructed from AP2 and RAP2 genes of Arabidopsis. The LECI polynucleotide selected from AP2 and RAP2 genes of Arabidopsis. The construction of the proparing expression cassettes for suppression in a seed, condition of the proparing expression, which is useful in weed control or for improving nutritional value of plant tissue respectively. LECI polypeptides and polynucleotides are especially used for increasing or analysis of the plant tissue respectively. LECI also accepted the plant tissue respectively. LECI also accepted the plant tissue respectively. LECI also accepted the plant tissue respectively. LECI also accepted the plant tissue respectively. LECI also accepted the plant tissue respectively. LECI also accepted the plant tissue respectively. LECI also accepted the plant tissue respectively. LECI also accepted the plant tissue respectively. LECI also accepted the plant tissue respectively. LECI also accepted the plant tissue respectively. LECI also accepted the plant tissue respectively. LECI also accepted the plant tissue respectively. LECI also accepted the plant tissue respectively. LECI also accepted the plant tissue respectively. LECI also accepted the plant tissue respectively. LECI also accepted the plant tissue respectively. LECI also accepted the plant tissue respectively. LECI also accepted the plant tissue respectively. LECI also accepted the plant tissue respectively. LECI also accepted the plant tissue respectively. LECI also accepted the plant tissue respectively. LECI accepted the plant tissue respecti
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 6; Page 53-54; 69pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New embryo-specific gene useful for producing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-160588/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence represents a Leafy Cotyledon 1 (LEC1) polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-JUN-1998;
17-NOV-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Leafy cotyledon 1 gene; LEC1 gene; embryogenesis; cotyledon identity,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Amino acid
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decreasing storage protein content in cotyledons or increases reproductive tissue mass, e.g., increases
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98US-0193931.
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100.0%; Pred. No. 1.6e+02;
tive 0; Mismatches 0;
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    increases fruit size, seed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         transgenic
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CC sequence that encodes LEC-1 protein comprising a subsequence that to LEC-1 B domain. LEC-1 sequences are used for modulating transcription resulting in the induction of embryonic characteristics core seed development in a plant. Polynuclectide sequences from LEC1 CC genes are used to direct expression of desired heterologous genes in cembryos, to modulate the development of embryos or the characteristics of an embryo on other organs (e.g., by embancing expression of the gene is cused to manipulate a number of useful traits, such as increasing or certain content in cotyledons or leaves. Inhibition of LEC1 gene expression is useful in weed control or teaves. Inhibition cof LEC1 gene expression is useful in weed control or to produce fruit with small and non-viable seed. Enhanced expression of LEC1 genes is cuseful to increase storage protein content in plant tissues. The LEC-1 gene promoters are useful for directing gene expression so that the casting desired gene product is located in embryos or seeds. Expression of LEC-1 genes in plant reproductive or vegetative tissue induce eccopic expression of cells and tissues, together with another plant nucleic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Harada J,
Kwong R;
                                                                                                                                                                                                                                                                                                                                                                                                                            Novel leafy cotyledon 1 polynucleotide encoding leafy cotyledon polypeptide for modulating transcription resulting in seed development in plant comprises providing in an expression cassette linked to LEC1
                                                                                                                                                                                                                                                                                                     polynucleotides encoding them. The invention also provides expres cassettes comprising a promoter operably linked to a heterologous
                                                                                                                                                                                                                                                                                                                                                                       Claim 2; Page 53-54; 73pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAD16914, AAD16915, AAD16916.
                                                                                                                                                                                                                                                                                                                                          The patent discloses novel leafy cotyledon 1 (LEC1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-565462/63.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            weed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Leafy cotyledon 1; LEC1; transcription modulator; seed development;
embryonic characteristic; transgenic plant; storage protein content;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Leafy cotyledon 1 (LEC1) protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-NOV-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (REGC ) UNIV CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           control;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              314 YVDPLTV 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               . Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lotan T, Ohto M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ectopic expression
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2.2%; Score 7; DB:
100.0%; Pred. No. 1.1
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                          English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Goldberg RB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 21; Lo
1.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fischer RL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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                                                                                                                                                                                                                                                                                                                                        polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bui A;
                                                                                                                                                                                                                                                                                                                       expression
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                                                                                                  The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The inventiuseful in developmental biology and in elucidating cell signalling cell-cell interactions in higher enkaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL101840-ABL16175) and the encoded proteins (ABB57037-ABB72072).

The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from vat ftp.wipo.int/pub/published_pct_sequences.
                                                                                Sequence
                                                                                                                                                                                                                                              Disclosure; SEQ ID NO
                                                                                                                                                                                                                                                                     New isolated nucleic acid genes from Drosophila and interactions -
                                                                                                                                                                                                                                                                                                                   N-PSDB;
                                                                                                                                                                                                                                                                                                                                                  Venter JC, Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                 23-MAR-2000; 2000US-191637P
11-JUL-2000; 2000US-0614150
                                                                                                                                                                                                                                                                                                                                                                                                                                   23-MAR-2001; 2001WO-US09231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster polypeptide SEQ ID NO 34800.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABB69336;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           acid and/or protein, such as the seed-mass enhancing antisense AP2 nucleic acid, generates a cell, tissue, or plant with increased fruit and seed mass, greater yields of embryonic storage proteins, etc. The present sequence is LEC-1 protein.
                                                                                                                                                                                                                                                                                                                                                                           (PEKE ) PE CORP NY.
                                                                                                                                                                                                                                                                                                                   2001-656860/75.
DB; ABL13439.
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            50
                                  n 2.2%; Similarity 100.0%; 7; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       h 2.2%; Sc Similarity 100.0%; P 7; Conservative 0;
            TSGSGGL 56
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                                                                                 213 AA;
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                                                                                                                                                                                                                                                                             detection reagent for detecting for elucidating cell signalling
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                                Score 7; DB 22; L
Pred. No. 1.7e+02;
0; Mismatches 0;
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Pred. No. 1.0
0; Mismatches
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                                                     Length 213;
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alling and
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AAU19650
ID AAU19
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RESULT 32
ABB69336
ID ABB69
XX ABB69
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31-JAN-2000;
04-FEB-2000;
24-FEB-2000;
02-MAR-2000;
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2000US-0226681

2000US-0227868

2000US-0227182

2000US-0227709

2000US-0229287

2000US-0229387

2000US-0229344
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2000US-0225214.
2000US-0225266.
2000US-0225267.
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; 2000US-0220964.
; 2000US-0224518.
; 2000US-0224519.
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2000US-0218290.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   300.
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05-SEP-2000; 06-SEP-2000; 06-SEP-2000; 08-SEP-2000; 08-SEP-2000; 08-SEP-2000; 08-SEP-2000; 08-SEP-2000;

2000US-0229513. 2000US-0230437.

08-SEP-2000; 08-SEP-2000; 12-SEP-2000; 14-SEP-2000;

2000US-0234997

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                                                                                                                                                                                RESULT 34
                                                                                                                                                                    The invention relates to isolated nucleic acid molecules encoding cover human secreted extracellular matrix proteins (SPB). The condition in e.g. humans, mice, rabbits, youts, horses, catts, dogs, condition in e.g. humans, mice, rabbits, youts, horses, catts, dogs, condition in e.g. humans, mice, rabbits, youts, horses, catts, dogs, condition in e.g. humans, mice, rabbits, youts, horses, catts, dogs, condition of SPB. The SP polynucleotide or a vector expressing them may compression of SPB. The SP polynucleotide or a vector expressing them may be administered to treat diseases by gene therapy. Antisense molecules can be administed to down regulate expression. The polynucleotides can be used as DNA probes in diagnostic assays. The SPB may also be used as antigens to produce antibodies and to identify modulators (agonists and antagonists) of the SPB. The anti-(SP) antibodies and antagonists may also be used to down regulate expression and activity of SPB and as diagnostic agents for detecting the presence of SPB in samples. The disorders include for example: immune/autoimmune diseases (e.g. HIV (human immunodeficiency virus) infections, anaemia, rheumatoid arthritis and multiple sclerosis), cancers and hyperproliferative disorders (e.g. cardiac, careat, tachycardia and angina), infections caused by bacteria, viruses can fungi and ocular disorders (e.g. corneal infections). Other uses circlude wound healing, maintenance of organs before transplantation,
                                                                                                                             Query Match
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                                                                                                                 Matches
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01-DEC-2000

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N-PSDB;
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17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
                                                                                                                                                                 arrest, tachycardia and angina), infecting and fungi and ocular disorders (e.g. c include wound healing, maintenance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acid molecules encoding human secreted extracellular matrix proteins, used in preventing, treating or ameliorating a disorder, e.g. Alzheimer's and Parkinson's diseases and cancers -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 11; SEQ ID No 300; 577pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2001-465572/50.
DB; AAS31221.
                                                                                167
                                                                                                            h 2.2%; Somilarity 100.0%; I 7; Conservative 0;
                                                 KPTPTPP
                                                                               KPTPTPP 173
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2000US-0251856.
2000US-0251868.
2000US-0251869.
2000US-0251989.
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2000US-0254097.
2001US-0259678.
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                                                                                                               Score 7; DB; Pred. No. 2e
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                                                                                                   , DB 22.
75. 2e+02;
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2000US-0240960.

14-SEP-2000 14-SEP-2000 14-SEP-2000 14-SEP-2000 14-SEP-2000 21-SEP-2000 21-SEP-2000 25-SEP-2000 26-SEP-2000 29-SEP-2000 29-SEP-2000 29-SEP-2000 02-OCT-2000 02-OCT-2000 02-OCT-2000 02-OCT-2000 02-OCT-2000 02-OCT-2000 02-OCT-2000 02-OCT-2000 02-OCT-2000 03-OCT-2000 04-NOV-2000 08-NOV-2000 09-NO

2000US-0246474. 2000US-0246475. 2000US-0246476. 2000US-0246477. 2000US-0246477.

2000US-0241826. 2000US-0244617.

2000US-0241809

2000US-0246523. 2000US-0246524.

2000US-0246527.

2000US-0249208. 2000US-0249209. 2000US-0249210. 2000US-0249211. 2000US-0249212. 2000US-0249213. 2000US-0249214. 2000US-0249214. 2000US-0249214. 2000US-0249214.

ABP47870 ID ABP4 XX

ABP47870

standard; Protein;

251 AA

0,

2000US-0246528 2000US-0246532 2000US-0246609 2000US-0246610 2000US-0246611 2000US-0246613 2000US-0246613

23-AUG-2002 ABP47870;

(first entry)

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31-JAN-2000; 2000US-179065P.
04-FEB-2000; 2000US-18062BP.
28-JUN-2000; 2000US-214886P.
07-JUL-2000; 2000US-216847P.
07-JUL-2000; 2000US-21749FP.
11-JUL-2000; 2000US-21749FP.
11-JUL-2000; 2000US-21749FP.
14-JUL-2000; 2000US-217496P.
14-JUL-2000; 2000US-20963P.
26-JUL-2000; 2000US-224518P.
14-AUG-2000; 2000US-224518P.
14-AUG-2000; 2000US-224518P.
                                                                   26-JUL-2000;
26-JUL-2000;
14-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae; group A streptococcus; Streptococcus; orange, antiinflammatory; infection; vaccine; meningitis; gene therapy.
                                                                                              27-OCT-2000; 2000GB-0026333.
24-NOV-2000; 2000GB-0028727.
07-MAR-2001; 2001GB-0005640.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptococcus polypeptide SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                     29-OCT-2001; 2001WO-GB04789.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptococcus agalactiae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABP30505;
                                                                                                                                                                                                                                                                                                                                                                           WO200234771-A2
(CHIR-) CHIRON SPA. (GENO-) INST GENOMIC RES.
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Ö 10186.

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The invention relates to novel genes (ABQ66521-ABQ66785) and proteins CC (ABP47846-ABP48110) useful for preventing, treating or ameliorating CC (ABP47846-ABP48110) useful for preventing, treating or ameliorating CC medical conditions e.g. by protein or gene therapy. The genes are CC isolated from a range of human tissues disclosed in the specification. CC The nucleic acids, proteins, antibodies and (ant) agonists are useful CC in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital; CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune cC namelytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative (c) cardiovascular disorders such as myocardial ischaemias; (c) cardiovascular disorders such as myocardial ischaemias; (c) dispersy; and (f) infectious diseases such as viral, bacterial, fungal cand parasitic infections.

CC Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at sequence.html?DocID=999909764870.
                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 11; SEQ ID NO 300; 235pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New nucleic acid encoding human proteins, useful for diagnosis, treatment and prevention of e.g. osteoporosis, also related polypeptides and antibodies -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-470713/50
N-PSDB; ABQ66545.
02-JUL-2002 (first entry)
                                                                              ABP30505 standard; Protein;
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(RUBE/)
(BARA/)
                                                                                                                                                                                                                 167 KPTPTPP 173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ) ROSEN C A.
) RUBEN S M.
) BARASH S C.
                                                                                                                                                                                    KPTPTPP 217
                                                                                                                                                                                                                                                                                                                                               251 AA;
                                                                                                                                                                                                                                                              2.2%; Score 7; DB ilarity 100.0%; Pred. No. 2e Conservative 0; Mismatches
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                                                                                                                                                                                                                                                       DB 23; bc.,
No. 2e+02;
                                                                                                                                                                                                                                                                                                      Length 251;
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RESULT 36
ABB08497
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Best Local S
Matches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the treatment or prevention of infection or disease caused by Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes. Nucleic acids encoding (I) are used to detect Streptococcus in a biological sample. (I) is used to determine whether a compound binds to (I). A composition comprising (I) or a nucleic acid encoding (I), may be used as a vaccine or diagnostic composition. The disease caused by Streptococcus that is prevented or treated may be meningitis. Nucleic acid encoding (I) may be used to recombinantly produce (I) and may be used in gene therapy. Antibodies to (I) are used for affinity chromatography, immunoassays, and distinguishing/identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Telford J, F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a protein (ABP25413-ABP30895) from group B streptococcus/GBS (Streptococcus againstiae) or group A streptococcus/GAS (Streptococcus spanishing one of 5483 sequences (S1), given in the specification. The proteins have antibacterial and antiinflammatory activity. (I), nucleic acids encoding (I), ABN66044-AEN71526 and antibodies that bind (I) are used in the manufacture of medicaments for
STABILISED RECOMBINANT ANIMAL CELL LINE OF HCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                chromatography, immunoass
Streptococcus proteins..
                                                                                                                                                                                                                                                                                                                                                                                       ABB08497 standard; Protein; 300 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New Streptococcus protein for the treatment or prevention of infection or disease caused by Streptococcus bacteria, such as meningitis, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-352536/38.
N-PSDB; ABN71136.
                                        N-PSDB; ABL41548.
                                                   WPI; 2000-144176/13.
                                                                                                                                                                 30-JUL-1994;
                                                                                                                                                                                             30-APR-1998
                                                                                                                                                                                                                                                 Unidentified.
                                                                                                                                                                                                                                                                           Envelope 2 protein;
                                                                                                                                                                                                                                                                                                      Envelope 2 protein of HCV
                                                                                                                                                                                                                                                                                                                                   23-MAY-2002
                                                                                                                                                                                                                                                                                                                                                             ABB08497;
                                                                               Ryu W,
                                                                                                          (GLDS )
                                                                                                                                      30-JUL-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                for detecting a compound
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                                                                               Yang J,
                                                                                                          LG CHEM CO LID.
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                                                                                                                                      94KR-0018832
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                                                                                Cho
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100.0%; Pr
                                                                                                                                                                                                                                                                            HCV.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 23; Le
b. 2.3e+02;
ches 0;
            EXPRESSING ENVELOPE
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1 -
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Mismatches

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RESULT 37
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Best Local
                                                                                                    The present sequence is that of the LlaIIC gene product, an endonuclease, part of a Lactococcus lactis restriction/modification (R/M) system. The LlaII R/M system is similar to the MboI system which recognises the sequence 5'-GATC-3' and cleaves it before the guanine. A plasmid contg. the DNA (AAT30440) encoding the R/M system can confer phage resistance to a bacterium, such as providing resistance to phage-sensitive dairy cultures. The DNA and proteins can be used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This invention relates to stabilised recombinant animal cell line expressing envelope 2 protein of HCV. The present sequence represents the envelope 2 protein of HCV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                         Sequence
                                                                                                                                                                                                                                    DNA encoding restriction and modification confers phage resistance to bacteria, for
                                                                                                                                                                                                                                                                       N-PSDB; AAT30400.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LlaIIA; LlaIIB; LlaIIC; m6A-methyltransferase; endonuclease; restriction;
modification system; phage resistance; milk; dairy product;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-DEC-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 7; 8pp; Korean.
                                                                                                                                                                                                  Claim 2; Fig 4; 48pp;
                                                                                                                                                                                                                                                                                    WPI; 1996-333992/33.
                                                                                                                                                                                                                                                                                                            Moineau S,
                                                                                                                                                                                                                                                                                                                                                          19-APR-1995;
30-DEC-1994;
                                                                                                                                                                                                                                                                                                                                                                                              29-DEC-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lactococcus lactis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Endonuclease LlaIIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR98460 standard; Protein; 304
                                                                                          improving fermentation of a dairy prod. and
                                                                                                                                                                                                                           additive
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                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9621017-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           food additive
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                                                         304 AA;
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94US-0366480.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMQ-17
                     2.2%;
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                      Score 7;
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                                                                                                                                                                                                                                      enzymes from L. lactis use in milk and as a fo
                                                                                          proteins can be used as additives in food
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RESULT 39
ABP28875
ID ABP28
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AC ABP28
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DT 02-JU
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Best Local Similarity
7; Conserv
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(MADS/)
(NYEN/)
                         02-JUL-2002
                                                                                ABP28875;
                                                                                                                            ABP28875 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   virus resistance, more specificall strain used in cheese manufacture.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 65-66; 93pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Type II restriction-modification systems obtd. from Lactococcus lactis - for conferring phage resistance on lactic acid bacteria, useful as starter cultures for cheese and fermented milk prods.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1996-393404/39.
N-PSDB; AAT36391.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lactococcus lactis ssp. cremoris W9 restriction
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) MADSEN A.
) NYENGAARD N R.
) VOGENSEN F K.
                                                                                                                                                                                                                                                                         TVSKIAO 177
                                                                                                                                                                                                                                                                                                                             TVSKIAQ 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                304 AA;
                         · (first entry)
                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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Pred. No. 2.:
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 304;
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RESULT 40
AAG38356
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                                                                                                                                                                                                                                                                          Query Match
Best Local
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24-NOV-2000;
07-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New Streptococcus protein for the treatment or prevention of infection or disease caused by Streptococcus bacteria, such as meningitis, and for detecting a compound that binds to the protein -
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                                                                                      AAG38356;
                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 3855; 4525pp; English.
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N-PSDB; ABN69506.
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Tettelin H;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptococcus polypeptide SEQ ID NO 6926.
                         Arabidopsis thaliana protein fragment SEQ ID NO: 47308.
                                                       18-OCT-2000
                                                                                                                 AAG38356 standard; Protein; 337 AA
                                                                                                                                                                                                                                                                                                                                                      Streptococcus proteins.
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                                                                                                                                                                                                                                                          Similarity 7; Conserv
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2000GB-0028727.
2001GB-0005640.
                                                       (first entry)
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Protein identification; signal transduction pathway; metabolic pathway;

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	mapping; gene
	expression control;
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    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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RESULT 1
US-09-027-064-2
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GENERAL INFORMATION:
APPLICANT: SHABON, USMAN
APPLICANT: SHABON, DERK
TITLE OF INVENTION: A YAK-1 RELATED SERINE/THREONINE
TITLE OF INVENTION: PROTEIN KINASE-HTLAR33
NUMBER OF SEQUENCES: 6
NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/027,064
FILING DATE: 20-FEB-1998
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 60/053,924
FILING DATE: 20-FEB-1998
                                                                            TELEFAX: 610-407-0701
TELEX: 846169
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 557 amino acids
                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: PRESTIA, PAUL F
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GH-7
TELEPHONE: 610-407-0700
TELEPHONE: 610-407-0701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS
                  STRANDEDNESS: single TOPOLOGY: linear DLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: RATNER & PRESTIA
STREET: P.O. BOX 980
CITY: VALLEY FORGE
STATE: PA
                                                                 TYPE: amino acid
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USA
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US-08-480-750-41
US-08-53-501A-85
US-08-765-783A-104
US-08-765-783A-104
US-08-554-840-13
US-08-554-840-13
US-08-854-840-13
US-08-894-017-5
US-08-894-017-5
US-08-818-11-111
US-08-818-11-111
US-08-818-111-112
US-08-818-111-112
US-08-818-111-112
US-08-818-111-112
US-08-925-339-13
US-08-925-339-13
US-08-925-339-13
US-08-925-339-13
US-08-925-339-13
US-08-925-339-13
US-08-925-339-13
US-08-925-339-13
US-08-925-339-13
US-08-925-339-13
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85, Appli
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104, App
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1113, Appli
1114, Appli
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APPLICANT: SHABON, USMAN
TITLE OF INVENTION: A YAX-1 RELATED SERINE/THREONINE PROTEIN KINASE-HTLAR33
FILE REFERENCE: GH-70172-1
CURRENT APPLICATION NUMBER: US/09/271,815
CURRENT FILING DATE: 1999-03-18
EARLIER APPLICATION NUMBER: 09/027,064
EARLIER FILING DATE: 1999-07-20
PARLIER FILING DATE: 1999-07-28
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 557
TYPE: PRT
ORGANISM: Homo sapiens
US-09-271-815-2
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US-09-271-815-2
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ZIP: 94404

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/258,152
FILING DATE: 10-JUN-1994
FILING DATE: 10-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/09271815
Patent No. 6297036
PATENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 2.1
Best Local Similarity 100
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                          Bequered No. 568027.0N:
GENERAL INFORMATION:
GENERAL INFORMATION:
FINER, MITCHELL H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 2.5%;
Best Local Similarity 100.0%
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: FINER:
APPLICANT: ROBERTS
APPLICANT: DULL, T
APPLICANT: ZEBO,
                                                                                                                                                                                                           APPLICANT: QUALITY NO.

APPLICANT: QUALITY NO.

TITLE OF INVENTION: VIRUS AND HIT TITLE OF INVENTION: VIRUS AND HIT TITLE OF INVENTION: OF MANMALIAN NUMBER OF SEQUENCES: 32

CORRESSONDENCE ADDRESS: INC.

ADDRESSEB: CELL GENESYS, INC.

STREET: 322 LAKESIDE DRIVE

COTY: FOSTER CITY

CONTENT ON TOWNS
                                                                                                                                                                                  COUNTRY:
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                                                                                                                                                                                                   CALIFORNIA
                                                                                                                                                                                    USA
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DULL, THOMAS J.
ZSEBO, KRISZTINA M.
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100.0%; Pred. No. 20;
tive 0; Mismatches
                                                                                                                                                                                                                                                                              METHOD FOR PRODUCTION OF HIGH TITER VIRUS AND HIGH EFFICIENCY RETROVIRAL MEDIATED TRANSDUCTION OF MAMMALIAN CELLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 8; DB;
; Pred. No. 20
0; Mismatches
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Best Local Similarity 100.0%; P
Matches 7; Conservative 0;
                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: TIBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/076,299A
FILING DATE: 11-JUN-1993
CLASSIFICATION = 435
PRIOR APPLICATION = 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
APPLICATION NUMBER:
FILING DATE:
THEOREM TAPONATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 9, Application US/08076299A Patent No. 5834256
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INFORMATION FOR SEQ ID NO:
                                                                              TELEFAX: 415-349-7392 INFORMATION FOR SEQ ID NO:
                                                                                                           ATTORNEY AGENT INFORMATION:
NAME: KRUPEN, KAREN I.
REGISTRATION NUMBER: 34,647
REFERENCE/DOCKST NUMBER: CELL 13.0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-358-9600 X131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-358-9600 X131
TELEFAX: 415-349-7392
                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: ROBERTS, MARGO R. APPLICANT: DULL, THOMAS J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: QIN, LU FITLE OF INVENTION: FITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: US 08/076,299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: CELL GENESYS, INC.
STREET: 322 LAKESIDE DRIVE
CITY: FOSTER CITY
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: KRUPEN, KAREN I.
REGISTRATION NUMBER: 34,647
REFERENCE/DOCKET NUMBER: CE
    STRANDEDNESS:
                                       ENGTH:
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                      amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FINER, MITCHELL H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-JUN-1993
single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KRISZTINA M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VIRUS AND HIGH EFFICIENCY RETROVIRAL MEDIATED TRANSDUCTION OF MAMMALIAN CELLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 METHOD FOR PRODUCTION OF HIGH TITER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9:
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                                                                                            US-08-438-582-9
                                 Matches
                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER: US 08/258,152
APPLICATION NUMBER: US 08/258,152
FILING DATE: 10-JUN-1994
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/076,299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 9, App. ...
Sequence 9, App. ...
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                                                              Query Match
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                                                                                                                                                                                  TELEFAX: 415-349-7392
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                       STRANDEDNESS:
TOPOLOGY: lin
MOLECULE TYPE:
                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 08/07
FILING DATE: 11-JUN-93
ATTORNEY/AGENT INFORMATION:
NAME: KRUPEN, KAREN I
REGISTRATION NUMBER: 34,647
                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: CEL
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-358-9600 X131
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                               Local Similarity 
nes 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity hes 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/0
FILING DATE: 10-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                       ENGTH:
   41 STSGSGS 47
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T: 322 LAKESIDE DRIVE
FOSTER CITY
                                                                                                                                                  amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Application US/08438582
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                                                                                                                                                                     13 amino acids
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                                 Conservative
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                                                                                                                        linear
                                                                                                         peptide
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                                                                                                                                       single
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                                              2.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               METHOD FOR PRODUCTION OF HIGH TITER
VIRUS AND HIGH EFFICIENCY RETROVIRAL MEDIATED TRANSDUCTION
OF MANWALIAN CELLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                  US/08/438,582
                                                                                                                                                                                                                                                              CELL
                                               Score 7; DB 2; 
; Pred. No. 5.6;
                                 0,
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                                                              Length 13;
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                               0
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RESULT 7
US-08-479-737-44
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Best Local S
Matches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 415-349-7392
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                 Sequence 44, Application Patent No. 6319494
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION UNMBER: 08/517,488
FILING DATE: 21-AUG-1995
APPLICATION NUMBER: US 08/258,152
APPLICATION NUMBER: US 08/258,152
ETILING DATE: 10-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/076,299
ETILING DATE: 11-JUN-1993
ATTORNEY/AGENT INFORMATION:
ANAME: VEHERM LEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Flopp disk.
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-358-9600 X131
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PPLICANT: COOKE, KEEGAN

PPLICANT: COOKE, KEEGAN

PPLICANT: FARSON, DEBORAH A.

ITLE OF INVENTION: METHOD FOR PRODUCTION OF HIGH TITER

ITLE OF INVENTION: VIRUS AND HIGH EFFICIENCY RETROVIRAL MEDIATED TRANSDUCTION

FITLE OF INVENTION: OF MAMMALIAN CELLS

NUMBER OF SEQUENCES: 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: CALTEST

CALTY

CALTEST: 322 LAKESIDE DRIVE

CITY: FOSTER CITY

STATE: CALTEST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: KRUPEN, KAREN I.
REGISTRATION NUMBER: 34,647
REFERENCE/DOCKET NUMBER: CELL 13.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/09/266,596 FILING DATE:
                                                                                                                                                                                                                                                                                                           Match 2.2%; Score 7; DB (
Local Similarity 100.0%; Pred. No. 5.0
25 7; Conservative 0; Mismatches
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                                                                                                                          Application US/08479737
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FINER, MITCHELL H.
DULL, THOMAS J.
ZSEBO, KRISZTINA M.
COOKE, KEEGAN
ENEGEN, KEEGAN
                                                                                                                                                                                                                                                                                                                                                                                                                  single
linear
E:
Capon, Daniel J
Weiss, Arthur
Irving, Brian A
Roberts, Margo R
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RESULT 8
US-08-475-442A-44
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APPLICATION NUMBER: 08/238,405

FILING DATE: 05-MAX-1994

ATTORNEY/AGENT INFORMATION:

NAME: Mandel, Saralynn

REGISTRATION NUMBER: 31,853

REFERENCE/DOCKET NUMBER: Cell 5.3

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 358-9600

TELEPHONE: (415) 358-9600

TELEPHONE: (415) 358-9600

TELEPHONE: (415) 358-9600

INFORMATION FOR SEQ ID NO: 44:

SEQUENCE CHARACTERISTICS:

LENGTH: 13 anino acids

TYPE: mino acids

TYPE: mino acids

TYPE: mino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                    SENERAL INFORMATION:
                                                                                                                                                                                                  APPLICANT: WEISS, ARTHUR
APPLICANT: INVING, BRIAN A
APPLICANT: ROBERTS, MARGO R
APPLICANT: ZSEBO, KRISZTINA
TITLE OF INVENTION: CHIMERIC CHAINS FOR
TITLE OF INVENTION: RECEPTOR-ASSOCIATED
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                 COUNTRY:
ZIP: 944
                                                                                                         STREET: 322 LAKESIDE DRIVE CITY: FOSTER CITY STATE: CALIFORNIA COUNTRY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IEM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOTTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION DATA:

APPLICATION UNMER: US/08/479,737

FILING DATE: 07-Unn-1995

CLASSIFICATION: CUNknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: peptide SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zsebo, Krisztina
TITLE OF INVENTION: CHAMERIC CHAINS FOR RECEPTOR ASSOCIATED
SIGNAL TRANSDUCTION PATHWAYS
                                                                                                                                                                                                                                                                                                                                                                                                                            44, Application US/08475442A
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7; Conserv
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STATE: California
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
                                                                                                       USA
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322 Lakeside Drive
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                                                               Query Match
Best Local S
Matches 7
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EARLIER FILING DATE: 1996-09-04
NUMBER OF SEQ ID NOS: 19
SEQ ID NO 15
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 15, Appl
Patent No. 603079
                                                                                                                                                                                                                                                        APPLICANT: Saitch, Masao
APPLICANT: Miyazono, Kohei
APPLICANT: IChijo, Hidenori
TITLE OF INVENTION: NUCLEIC ACID MOLECULE ENCODING TGF RECEPTOR HAVING MODIFIED
TITLE OF INVENTION: GROWTH INHIBITION, AND ITS USE
FILE REFERENCE: L0461/7027
CURRENT APPLICATION NUMBER: US/09/029,424A
CURRENT FILING DATE: 1998-04-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (415)358-96(
TELEPAX: (415)349-7392
INFORMATION FOR SEQ ID NO:
                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                  LENGTH: 56
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: KRUPEN, KAREN I
REGISTRATION NUMBER: 34,647
REFERENCE/DOCKET NUMBER: CEI
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: PCT/US91/09431
FILING DATE: 12-DEC-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 07/627,643 FILING DATE: 14-DEC-1990 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/238,405
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,442A
                                                               Local Similarity nes 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 0 FILING DATE: 09-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
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                               41
35
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7; Conservative
STSGSGS 41
                               STSGSGS 47
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                                                              2.2%; Score 7; DB:
ilarity 100.0%; Pred. No. 21
Conservative 0; Mismatches
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100.0%; Pred. No. 5.0
ative 0; Mismatches
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                                                                                              Length 56;
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RESULT 11
US-09-193-931C-19
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US-09-103-478-19
                                                                                                                                                                                Sequence 19, Application US/09193931C Patent No. 6320102 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 19, Appl
Patent No. 623597
                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 2.2%; Score 7; Best Local Similarity .100.0%; Pred. No.
            APPLICANT: Harada, John
APPLICANT: Lotan, Tamar
APPLICANT: Ohto, Masa-aki
APPLICANT: Goldberg, Robert B.
APPLICANT: Fischer, Robert L.
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: LEAFY COTYLEDONI Genes and Their Uses
FILE REFERENCE: 023070-077620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
CURRENT APPLICATION NUMBER: US/09/193,931C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (415) 576-030 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 19-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 21-FEB-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 800
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 09/026,221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA: APPLICATION UNMBER: US/09/103,478 FILING DATE: 24-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PPLICANT: Goldberg, Robert B.
PPLICANT: Fischer, Robert L.
TIE OF INVENTION: LEAFY COTYLEDON1 Genes and Their Uses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Einhorn, Gregory P.
REGISTRATION NUMBER: 38,440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ENGTH:
                                                                                                                                                                                                                                                                                                                                                                  314 YVDPLTV 320
                                                                                                                                                                                                                                                                                                                            78 YVDPLTV 84
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Ohto, Masa-aki
                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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32;
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; LOCATION: (11...(90)
; OTHER INFORMATION: LEC1 HAP3 subunit of CCAAT box-binding factor
; OTHER INFORMATION: (CBF) protein B domain homolog
US-09-193-931C-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 2.2%; Score 7; DB 4; Best Local Similarity 100.0%; Pred. No. 32; Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 09/026,221
PRIOR TILING DATE: 1998-02-19
PRIOR APPLICATION NUMBER: US 08/804,534
PRIOR FILING DATE: 1997-02-21
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin Ver. 2.0
                                                         APPLICATION UNMEER: US 09/026,221
APPLICATION UNMEER: US 08/026,221
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/804,534
APPLICATION INFORMATION:
NAME: ELIHOOTH, Gregory P.
REGISTRATION NUMBER: 38,440
REFERENCE/DOCKET NUMBER: 023070-0776
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT FILING DATE: 1998-11-17
PRIOR APPLICATION NUMBER: US 09/103,478
PRIOR FILING DATE: 1998-06-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
TELEFAX: (415) 576-030
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/103,478
FILLING DATE: 24-JUN-1998
                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 800 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PLICANT: Lotan, Tamar
PLICANT: Ohto, Masa-aki
PLICANT: Goldberg, Robert B.
PLICANT: Fischer, Robert L.
TLE OF INVENTION: LEAFY COTYLEDON1 Genes and Their Uses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
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Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
                  5) 576-0300
576-0300
2:
                                                                                                                   023070-077611US
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FILE REFERENCE: 023070-077620

CURRENT APPLICATION NUMBER: US/09/193,931C

CURRENT FILING DATE: 1998-11-17

PRIOR APPLICATION NUMBER: US 09/103,478

PRIOR APPLICATION NUMBER: US 09/026,221

PRIOR FILING DATE: 1998-02-19

PRIOR FILING DATE: 1998-02-19

PRIOR PILING DATE: 1998-02-19

PRIOR APPLICATION NUMBER: US 08/804,534

PRIOR FILING DATE: 1997-02-21

NUMBER OF SEQ ID NOS: 29

SEQ ID NO 2

SEQ ID NO 2

LENGTH: 208
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US-09-193-931C-2
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US-09-103-478-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT; ORGANISM: Arabidopsis thaliana US-09-193-931C-2
                                                                                                                                                                                                                                                                                RESULT 14
                                                                                                                                                                                                                                                                 US-08-424-641B-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence 2, Application US/09193931C Patent No. 6320102
GENERAL INFORMATION:
                                                                                                        APPLICANT: Sylvain Moineau, Shirley A. APPLICANT: Walker, Ebenezer R. Vedamuthu, APPLICANT: and Peter A. Vondenbergh TITLE OF INVENTION: Isolated DNA Encoding TITLE OF INVENTION: Enzyme For Phage TITLE OF INVENTION: Resistance NUMBER OF SEQUENCES: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TLE OF INVENTION: LEAFY COTYLEDON1 Genes and Their Uses
                                                                                         NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid TOPOLOGY: linear
COUNTRY: UZIP: 48864
                                                            STREET:
                                                                         ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    105 YVDPLTV 111
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                                           Okemos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ohto, Maga-aki
Goldberg, Robert B.
Fischer, Robert L.
The Regents of the University of California
                                                                                                                                                                                                                                                 Application US/08424641B
                             Michigan
                                                            E: Ian C. McLeod
2190 Commons Parkway
              USA
                                                                              C. McLeod
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0; Mismatches
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lo. 69;
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5. 69;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb

CURRENT APPLICATION DATA:

SOFTWARE:

Wordperfect 5.1

COMPUTER: Acer
OPERATING SYSTEM: MS-DOS

EDIUM TYPE:

storage

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US-08-820-980-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patent No. 592538
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/424,64
FILING DATE: April 19, 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: NO. 5824523e INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ENERAL
                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb
MEDIUM TYPE: storage
COMPUTER: Acer
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: MT 4.1-151
TELECOMMUNICATION INFORMATION:
TELEPHONE: (517) 347-4100
TELEFAX: (517) 347-4103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Ian C. McLeod
REGISTRATION NUMBER: 20,931
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STREET: 21.
Okemos
"10hig
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APPLICATION NUMBER: 08/366,480
FILING DATE: December 30, 1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                      TYPE: Amino Acid
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                                                                                                            FILING DATE:
                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                       COUNTRY: USA
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                                                                                                                                                                                                                                                                                                      Michigan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Sylvain Moineau, Shirley A.
Walker, Ebenezer R. Vedamuthu,
and Peter A. Vandenbergh
TVENTION: Isolated DNA Encoding
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                                                                                                                                                                                                                                                                                                                                                                                                               Resistance
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                                                                                                                             US/08/820,980
                                                         08/424,641
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Query Match
Best Local Similarity
Matches 7; Conserva
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APPLICANT: Sylvai
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                                                                                               TELEPHONE: (517) 347-4103
TELEFAX: (517) 347-4103
TELEX: NO. 5972673e
INFORMATION FOR SEQ ID NO: '
                                                                                                                                                                                                                                         CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION UNBER: 08/424,
FILING DATE: April 19, 1995
CLASSIFICATION: 530
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                COMPUTER: Acer
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/826,439
                                                                                                                                               REFERENCE/DOCKET NUMBER: Quest 4.1-155
TELECOMMUNICATION INFORMATION:
TELEPHONE: (517) 347-4100
                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Ian C. McLeod
REGISTRATION NUMBER: 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Sylvain Moineau, Shirley A.
APPLICANT: Walker, Ebenezer R. Vedamuthu,
APPLICANT: and Peter A. Vandenbergh
TITLE OF INVENTION: Isolated DNA Encoding
TITLE OF INVENTION: Enzyme For Phage
TITLE OF INVENTION: Resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS
LENGTH: 304 Amino Acid
                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 20,931
REFERENCE/DOCKET NUMBER: QUITELECOMMUNICATION INFORMATION:
TOPOLOGY: L
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                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                     FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: Sir
TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (517) 347-41
TELEFAX: (517) 347-4103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: Amino Acids
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                                                              ENGTH:
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                                              R: 304 Amino Acids
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                 Linear
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                             Single
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                                                                                                                                                                                              20,931
                                                                                                 4:
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Pred. No.
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RESULT 18
US-09-147-236-11
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Best Local S
Matches
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Best Local
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Patent No. 6300109
                                                                                             APPLICANT: TONOUGHI, Naoto
APPLICANT: TONOUGHI, Takayasu
APPLICANT: TONOUGHIDA, Takayasu
APPLICANT: YOSHINAGA, Fumihiro
APPLICANT: TAHARA, Naoki
APPLICANT: THARAR, Naoki
APPLICANT: HAYASHI, Takahisa
TITLE OF INVENTION: NOVEL GENE, GROUP OF GENES, AND NOVEL BETA-GLUCOSIDASE
TILE REFERENCE: 6537-011-0PCT
CURRENT APPLICATION NUMBER: US/09/147,236A
CURRENT FILING DATE: 1999-04-08
EARLIER APPLICATION NUMBER: PCT/JP97/03633
EARLIER FILING DATE: 1997-10-09
NUMBER OF SEQ ID NOS: 12
SOPTWARE: PATENTH ONS: 12
SOPTWARE: PATENTH ONS: 12
SOPTWARE: PATENTH ONS: 12
ILD NO 11
                                                                                                                                                                                                                                                                                                                                                                           equence 11, Application US/09147236A atent No. 6316251
                               ORGANISM: Acetobacter xylinum FEATURE:
OTHER INFORMATION: n at positions 15741 and 15767 may be a, OTHER INFORMATION: {\tt t}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: DK 01
FILING DATE: 17-FEB-1995
NFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                       ENGTH: 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 304 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 1
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
RRENT APPLICATION DATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Match 2.2%;
Local Similarity 100.0%;
es 7; Conservative
                                                                                                                                                                                                                                                                                                                                                          INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     171 TVSKIAQ 177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80 TVSKIAQ 86
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Similarity 100.0%;
7; Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plasmid-derived type II restriction-modification systems from Lactococcus lactis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Release #1.0, Version #1.30 (EPO)
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Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 304;
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US-08-909-828-2
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US-08-909-828-1
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Best Local S
Matches
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Best Local Similarity 100.0%;
Matches 7; Conservative
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                                                                       APPLICATION NUMBER: US/08/909,828
FILING DATE:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US
FILING DATE:
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPONENTING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA RE-lease #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                   TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
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TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                      UMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 350 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                           STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ENGTH:
                                                          ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        159 TPPVVVV 165
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                                                                                                                                                                                                                                                                                                                 INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                          81 TPPVVVV 87
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                                          amino acids
TYPE:
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         ss: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                               Tolerance of Trichothecence Mycotoxins in Plants and Animals Through the Modification of the Peptidyl Transferase Gene
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Pred. No.
                                                                                                                                                     Version
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40. 1.1e+02;
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                                                                                                                                                      #1.30
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                                                                                                                                                      (EPO)
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Best Local Similarity
""" hes 7; Conserve
                                                                                                                                        APPLICANT: Gimeno, Ruth E.
APPLICANT: Gimeno, Ruth E.
APPLICANT: Tartaglia, Louis A.
TITLE OF INVENTION: FATTY ACID TRANSPORT PROTEINS
FILE REFERENCE: WHI97-21p3MB
CURRENT APPLICATION NUMBER: US/09/232,200A
CURRENT FILING DATE: 1999-01-14
EARLIER APPLICATION NUMBER: 60/071,374
EARLIER APPLICATION NUMBER: 60/093,491
EARLIER FILING DATE: 1998-01-20
EARLIER FILING DATE: 1998-07-20
EARLIER FILING DATE: 1998-07-20
EARLIER APPLICATION NUMBER: 60/110,941
EARLIER APPLICATION NUMBER: 60/110,941
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Patent No. 6284487
GENERAL INFORMATION:
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                                                                                SEQ ID NO 4
LENGTH: 3
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 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/232,191
CURRENT FILING DATE: 1999-01-14
EARLIER APPLICATION NUMBER: 60/071,374
EARLIER FILING DATE: 1998-01-15
EARLIER APPLICATION NUMBER: 60/093,491
EARLIER FILING DATE: 1998-07-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Stahl, Andreas
APPLICANT: Hirsch, David J.
APPLICANT: Lodish, Harvey F.
TITLE OF INVENTION: Fatty Acid Transport Proteins
FILE REFERENCE: WHI97-21p3ME
                                                                                                                NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EARLIER APPLICATION NUMBER: 60/110,941
EARLIER FILING DATE: 1998-12-04
                                                                                                                                                                                                                                                                                                                                             APPLICANT: Hirsch, David J.
APPLICANT: Lodish, Harvey F.
                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Stahl, Andreas
                                                                                                                                                                                                                                                                                                                                                                                                           quence 4, Application US/09232200A
                                       TYPE: PRT ORGANISM: Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Saccharomyces cerevisiae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                145 TEAPFAT 151
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Score 7;
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5. 1.1e
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Length 356;
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Query Match
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; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-09-232-197-4
; ORGANISM: Saccharomyces cerevisiae
US-09-232-201-4
                                                                                                                                   FILE REFERENCE: WHI97-21D3MC

CURRENT APPLICATION NUMBER: US/09/232,201A

CURRENT FILING DATE: 1999-01-14

EARLIER APPLICATION NUMBER: 60/071,374

EARLIER FILING DATE: 1998-01-15

EARLIER APPLICATION NUMBER: 60/093,491

EARLIER FILING DATE: 1998-07-20

EARLIER APPLICATION NUMBER: 60/110,941

EARLIER FILING DATE: 1998-07-04

EARLIER FILING DATE: 1998-12-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-232-201-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EARLIER APPLICATION NUMBER: 60/071,374
EARLIER FILING DATE: 1998-01-15
EARLIER APPLICATION NUMBER: 60/09,491
EARLIER FILING DATE: 1998-07-20
EARLIER APPLICATION NUMBER: 60/110,941
EARLIER FILING DATE: 1998-12-04
NUMBER OF SEQ 1D NOS: 105
SOFTMARE: FastSEQ for Windows Version 3.0
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US-09-232-197-4
                                                                            NUMBER OF SEQ ID NOS: 105
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4, Application US/09232201A Patent No. 6348321
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Patent No. 630009
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Stahl, Andreas
APPLICANT: Hirsch, David J.
APPLICANT: Lodish, Harvey F.
APPLICANT: Gimeno, Ruth B.
APPLICANT: Tartaglia, Louis A.
TITLE OF INVENTION: FATTY ACID TRANSPORT PROTEINS
                                                                                                                                                                                                                                                                                                                    ENERAL INFORMATION:
APPLICANT: Stahl, Andreas
APPLICANT: Hirsch, David J.
APPLICANT: Lodish, Harvey F.
APPLICANT: Gimeno, Ruth E.
APPLICANT: Tartaglia, Louis A.
APPLICANT: Gameno, Rath E.
APPLICANT: Gameno, Ruth E.
                                      LENGTH: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/232,197A CURRENT FILING DATE: 1999-01-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 186 TEAPFAT 192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%;
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Sequence 15, Patent No. 5

INFORMATION:

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TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 501
TYPE: antino acid
STRANDEDNESS:
                                         Sequence 15, Application US/08317847
Patent No. 5547854
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 2.2%; Score 7; DB 4; Ler Best Local Similarity 100.0%; Pred. No. 1.1e+02; Matches 7; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                            Query Match 2.2%; Score 7; DB Best Local Similarity 100.0%; Prod. No. 1. Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: "U.S.A.
COUNTRY: "U.S.A.
COUNTRY: "U.S.A.

COUNTRY: 02110-2804

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 555X
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WOXIGNERIECT (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/149,105
FILING DATE: MS-DOS (VERSION 5.1)
PRIOR APPLICATION NUMBER: 08/029,673
APPLICATION NUMBER: 08/029,673
APPLICATION NUMBER: 07/853,396
FILING DATE: MS-Ch 11, 1993
APPLICATION NUMBER: 07/853,396
FILING DATE: MS-Ch 18, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Clark, PSul T.
REGISTRATION NUMBER: 00786/211001
TELEPHONE: (617) 542-5070
TELEPHONE: (617) 542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Donahoe, Patricia K.
APPLICANT: Gustafson, Michael
APPLICANT: He, Wei W.
APPLICANT: He, Wei W.
APPLICANT: Wang, Xiao-Fan
TITLE OF INVENTION: TGF- TYPE I
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
  APPLICANT: Donahoe, Patricia K. APPLICANT: Gustafson, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Massachusetts
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                                                                                                                                                                                                                                                                                                    DB 1; Length 501;
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COUNTRY:
COUNTRY:
ZIP: 02110-2804

ZIP: 02110-2804

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 1BM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: W5-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/317,847
FILING DATE: March 11, 1993
APPLICATION NUMBER: 08/029,673
FILING DATE: March 18, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T
REGISTRATION NUMBER: 00786/127002
REFERENCE/DOCKET NUMBER: 0786/127002
REFERENCE/DOCKET NUMBER: 0786/127002
TELECOMOUNICATION INFORMATION:
TELEPAN: 200154
INFORMATION TOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 501
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-382-256-8
                                                                                                                                                                                                                                                                                                                                                                                Sequence 8, Application US/09382256A Patent No. 6207814
GENERAL INFORMATION:
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Best Local :
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TITLE OF INVENTION: FOU
TITLE OF INVENTION: FAN
NUMBER OF SEQUENCES: 1.7
CORRESPONDENCE ADDRESSE
ADDRESSEE: Fish & Ric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                               APPLICANT: MIYAZONO, Kohei
TEN DIJKE, Peter
FRANZEN, Petra
YAMASHITA, Hidetoshi
HELDIN, CATI-Henrik
TITLE OF INVENTIN: ACTIVIN RECEPTOR LIKE KINASES, PROTEINS
HAVING SERIME THREONINE KINASE DOMAINS,
                                                                                   NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSES: Fulbright & Jaworski L.L.P.
STREET: 666 Fifth Avenue
CITY: New York
STRIE: New York
CHARLES New York
COUNTRY: USA
ZIP: 10103
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.25 inch, 1.44mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    187 STSGSGS 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41 STSGSGS 47
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225 Franklin Street
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ilarity 100.0%;
Conservative
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1.5e+02;
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RESULT 26 US-08-317-847-15

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187 ŚrŚGŚGŚ 193

41 STSGSGS 47

; TOPOLOGY: linear US-08-149-105-15

OPERATING SYSTEM: PC-DOS

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US-09-382-256-16
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Patent No. 6207814
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: MIYAZONO, Kohei
TEN DIJKE, Peter
FRANZEN, Petra
YAMASHITA, Hidetoshi
HELDIN, Carl-Henrik
TITLE OF INVENTION: ACTIVIN RECEPTOR LIKE KINASES,
HAVUNG SERINE THREONINE KINASE
AND THEIR USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: No. 6207814man D. Hanson
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5298.1
ZIP: 10103

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette,
COMPUTER: IBM PS/2
                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              187 STSGSGS 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41 STSGSGS 47
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APPLICATION NUMBER: GB 9304680.3
FILING DATE: March 8, 1993
APPLICATION NUMBER: 9311047.6
FILING DATE: May 28, 1993
APPLICATION NUMBER: 9311763.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity 7; Conserv
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APPLICATION NUMBER: 9316099.2
FILING DATE: August 3, 1993
APPLICATION NUMBER: 321344.5
FILING DATE: October 15, 1993
                                                                                                                                                                                                       ADDRESSEE: Fulbright & Jaworski L.L.P. STREET: 666 Fifth Avenue CITY: New York City STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/09/382,256A
FILING DATE: 24-Aug-1999
CLASSIFICATION: 514
APPLICATION DATA:
                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (212) 752-5958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: PCT/GB93/02367
FILING DATE: No. 6207814ember 17,
APPLICATION NUMBER: GB 9224057.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (212) 318-3000
                                       3.25 inch, 1.44mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 4; Length 505; . 1.6e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 16:
                                              COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Diskette,
                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                             APPLICANT: Miyazono, APPLICANT: Franzen, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 9316099.2
FILING DATE: August 3, 1993
APPLICATION NUMBER: 321344.5
FILING DATE: October 15, 1993
ATTORNEY/AGENT INFORMATION:
NAME: No. 6207814man D. Hanson
REGISTRATION NUMBER: 30,946
                                                                                                                                                                                                        ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
                                                                                                                                                                       STATE: Ne
ZIP: 1002
                    APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity les 7; Conserv
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 16:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41 STSGSGS 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: PCT/GB93/02367
FILING DATE: NO. 6207814ember 17, 1993
APPLICATION NUMBER: GB 9224057.1
FILING DATE: No. 6207814ember 17, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/09/382,256A FILING DATE: 24-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (212) 318-30
TELEFAX: (212) 752-5958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: LUD 5298.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: May 28, 1993
APPLICATION NUMBER: 9313763.6
FILING DATE: July 2, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 5:
                                                                                                                                                                                          New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PILING DATE: March 8, 1993
APPLICATION NUMBER: 9311047.6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ILING DATE: March 8, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2.2%;
ilarity 100.0%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CATION NUMBER:
                                                                                                                                                                                                                                                                                                           Having Serine Threonine Kinase Domains And Their Use
                                                                                                                                                                                                                                                                                                                               Activin Receptor-Like Kinase,
                                                                                                                                                                                                                                                                                                                                               Petra; Yamashita,
                                                                                                                                                                                                                                                                                                                                                                   Kohei; Dijke,
                                  us/09/395,115
                                                                                                                               3.5 inch, 360 kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 7;; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        <u>,</u>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                     Peter Ten;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 4; Len
lo. 1.6e+02;
                                                                                                                                                                                                                                                                                                                                               Hidetoshi; Heldin, Carl-Henrik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 505;
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PLICATION NUMBER

30-October-1995

US/08/436,265

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RESULT 30
US-09-395-115-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TOPOLOGY: linear; MOLECULE TYPE: protein US-09-395-115-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 2.2%; Score 7; DB 4; Length 505; Best Local Similarity 100.0%; Pred. No. 1.6e+02; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRICE APPLICATION DATA:

APPLICATION NUMBER: 9311047.6

FILING DATE: 28-May-1993

PRIOR APPLICATION NUMBER: 9313763.6

APPLICATION NUMBER: 9313763.6

FILING DATE: 9313763.6
                                                                                                                                                                                                                                                                 APPLICANT: MIYAZONO,
APPLICANT: MIYAZONO,
APPLICANT: Franzen,
TITLE OF INVENTION: H
TITLE OF INVENTION: H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (212) 838-386 (INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 505 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 922405...
APPLICATION 17-NO. 6271365emb
ETLING DATE: 17-NO. 6271365emb
PRIOR APPLICATION DATA:
9304677.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: LUTELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 9136099.2
FILING DATE: 3-August-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9321344.5
FILING DATE: 15-October-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
Application variation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 930467
FILING DATE: 8-March-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
FILING DATE: 8-Marc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Kohlei, Vineet
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                               ence 16, Application US/09395115
                                                     OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PPLICATION NUMBER
                                                                                                                                    TATE: New York
                                                                                                                                                                                                           DDRESSEE:
                                                                                                                                                                                                                               RESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LING DATE: 17-NO.
R APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               187 STSGSGS 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41 STSGSGS 47
WARE: Wordperfect
| APPLICATION DATA:
| ICATION NUMBER: US/09/395,115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid
                                                                                                                                                                   SEE: Felfe & Lynch
F: 805 Third Avenue
New York City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MBER: 9224057.1
17-No. 6271365ember-1992
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17-No. 6271365ember-1993
                                                                                         Diskette, 3.5 inch, 360 kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    838-3884
                                                          PC-DOS
                                                                                                                                                                                                                                                                   , Kohei; Dijke, Peter Ten;
Petra; Yamashita, Hidetosh
Activin Receptor-Like Kina
Having Serine Threonine Ki
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Like Kinase, Proteins
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; TOPOLOGY: linear; MOLECULE TYPE: protein US-09-395-115-16
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US-08-123-934A-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 505 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: JUD 5298
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEPAX: (212) 688-9200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:

PRIOR APPLICATION NUMBER: 9311047.6
APPLICATION NUMBER: 99193
PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER
APPLICATION NUMBER

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 30-ON APPLICATION NUMBER FILING DATE: 17-NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                ADDRESSEE: Genet
STREET: 87 Cambridge
                                                                                                                                                        MBER OF SEQUENCES:
DRRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 9224057.1
FILING DATE: 17-No. 6271365ember-1992
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PPLICATION NUMBER: US/08/436,265
PILING DATE: 30-October-1995
                                                  COUNTRY: US
                                                                                                                                                                                             TLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                            187 STSGSGS 193
                                                                                                                                                                                                                                                                                                                                                                                                                                              41 STSGSGS 47
                                                                                                                                                                                                                                                                                   INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid
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CATION DATA:
9304677.9
                                                                                                                  E: Genetics Institute Inc.- Legal Affairs
87 CambridgePark Drive
                                                                  USA
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15-October-1993
                                                                                                                                                                                             No. 6291206oru
RECEPTOR PROTEINS
                                                                                                                                                                                                                                                Anthony J.
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6271365ember-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
                                                                                                                                                                   APPLICATION NUMBER: 9224057.1
FILING DATE: 17-No. 6316217ember-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB93/02367
FILING DATE: 17-No. 6316217ember-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 30-Octobe:
CLASSIFICATION: 435
              PRIOR APPLICATION DATA:
                                                               PRIOR APPLICATION DATA:
                                                                                                                  PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: NC. 10022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: 617 876 1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
                                  APPLICATION NUMBER: FILING DATE: 28-May
                                                                               APPLICATION NUMBER: 93046 FILING DATE: 8-March-1993
                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
                                                                                                                                    APPLICATION NUMBER: FILING DATE: 8-Marc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: LAZAR, Steven R
REGISTRATION NUMBER: 32,618
REFERENCE/DOCKET NUMBER: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
les 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   505 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Miyazono, Kohei; Dijke, Peter Ten;
Franzen, Petra; Yamashita, Hidetoshi; Heldin, Carl-Henrik
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                                                                                                                                UMBER: 9304677.9
8-March-1993
                                                                                                                                                                                                                                                                                                                                                                                                                  Diskette, 3.5 inch, 360 kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-SEP-1993
                                                                                                                                                                                                                                                                                                             MBER: US/08/436,265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2.2%; Score 7; DB 4; Length 505; 100.0%; Pred. No. 1.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Activin Receptor-Like Kinase, Proteins
Having Serine Threonine Kinase Domains And Their Use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PC-DOS/MS-DOS
n Release #1.0, Version #1.25
                                                 9311047.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US/08/123,934A
                                                                                                  9304680.3
9313763.6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                          APPLICATION NUMBER: PCT/GB93/02367
FILING DATE: 17-No. 6316217ember-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9224057.1
FILING DATE: 17-No. 6316217ember-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM
OPERATING SYSTEM: PC-DA
SOFTWARE: WORDERFECT
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Miyazono,
APPLICANT: Franzen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 15-October-
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
               RIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                FILING DATE: 30 CLASSIFICATION:
                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/436,265
                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 505 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 37,003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 9136099.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                   10022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New York City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                     New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Application US/08436265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Miyazono,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Felfe & Lynch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                8-March-1993
                                                                               8-March-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (212)
                                28-May-1993
                                                                                                                                                                                                                                                                                                   30-October-1995
                                                                                                                                                                                                                                                                                                                                                                                                  Diskette, 3.5 inch, 360 kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-October-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3-August-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , Kohei; Dijke, Peter Ten;
Petra; Yamashita, Hidetoshi; Heldin, Carl-Henrik
Activin Receptor-Like Kinase, Proteins
Having Serine Threonine Kinase Domains And Their Use
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9313763.6
                                                                                               9304680.3
                                                9311047.6
                                                                                                                                                9304677.9
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s; Pred. No. 1.6
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LUD 5298
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No. 1.6e+02;
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9136099.2
FILING DATE: 3-AUGUST-1993
PRIOR APPLICATION DATA:

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; MOLECULE TYPE: protein
US-08-436-265-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 9321344.5

PILING DATE: 15-October-1993

ATTORNEY/AGENT INFORMATION:

NAME: KOhlei Vineet

REGISTRATION NUMBER: 37,003

REFERENCE/DOCKET NUMBER: LUD 5298

TELEPHONE: (212) 688-9200

TELEPHONE: (212) 888-3884

INFORMATION FOR SEQ ID NO: 16:

SEQUENCE CHARACTERISTICS:

LENGTH: 505 amino acids

TYPE: amino acid

TYPE: amino acid
                                                                                                                 CURRENT APPLICATION DATA:

APPLICATION UNMER: US/09/679,187

APPLICATION UNMER: US/09/679,187

FILING DATE: 03-OCT-2000

PRIOR APPLICATION NUMBER: US/08/436,265

PRIOR APPLICATION NUMBER: US/08/436,265

PRIOR APPLICATION NUMBER: PCT/CB93/02367

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/CB93/02367

FILING DATE: 17-No. 6331621ember-1993

PRIOR APPLICATION NUMBER: 9224057.1

FILING DATE: 17-No. 6331621ember-1992

PRIOR APPLICATION NUMBER: 9304677.9

PRIOR APPLICATION NUMBER: 9304677.9

PRIOR APPLICATION NUMBER: 9304670.3

PRIOR APPLICATION NUMBER: 9304670.3

PRIOR APPLICATION DATA: 9304680.3
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PRIOR APPLICATION NUMBER: 9304680.3
APPLICATION NUMBER: 9304680.3
FILING DATE: 8 March-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9311047.6
APPLICATION NUMBER: 28-May-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Miyazono, Kohei; Dijke, Peter Ten;
APPLICANT: Franzen, Petra; Yamashita, Hidetoshi;
TITLE OF INVENTION: Activin Receptor-Like Kinase,
TITLE OF INVENTION: Having Serine Threonine Kinas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Match 2.2%; Score 7; DB Local Similarity 100.0%; Pred. No. 1. es 7; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PC-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 4; 1.6e+02; 0;
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RESULT 35
US-09-679-187-16
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NUMBER OF SEQUENCES: 29

CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 360 kb
COMPUTER: 1BM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/679,187
FILING DATE: 03-CCT-2000
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: PCT/GB93/02367
FILING DATE: 17-No. 6331621ember-1993
PRIOR APPLICATION NUMBER: 9224057.1
FILING DATE: 17-No. 6331621ember-1993
PRIOR APPLICATION NUMBER: 9304677.9
FILING DATE: 18-March-1993
PRIOR APPLICATION NUMBER: 9304680.3
FILING DATE: 8-March-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9304680.3
FILING DATE: 8-March-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9311047.6
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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LENGTH: 505 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTUNIONAL CONTROL OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROP
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FILING DATE: 15-October-1993
ATTORNEY/AGENT INFORMATION:
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FILING DATE: 3-August-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Miyazono,
APPLICANT: Franzen,
TITLE OF INVENTION:
TITLE OF INVENTION:
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FILING DATE: 2-July-1993
RIOR APPLICATION DATA:
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Petra; Yamashita, Hidetoshi; Heldin,
Activin Receptor-Like Kinase, Proteir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9136099.2
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o. 1.6e+02;
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PRIOR APPLICATION DATA:

APPLICATION NUMBER: 9313 FILING DATE: 2-July-1993

9313763.6

RIOR APPLICATION DATA:

28-May-1993

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PCT-US94-10080-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 8, Application PC/TUS9410080 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein 1-09-679-187-16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (212) 688-92
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO:
                                                                 TELEFAX: (617) 876-58
NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acids
TOPOLOGY: 1:--
OLECTIF
SEQUENCE CHARACTERISTICS:
LENGTH: 505 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: LAZAR, Steven R
REGISTRATION NUMBER: 32,618
REFERENCE/DOCKET NUMBER: 52
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/123,934
FILING DATE: 17-SEP-1993
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: GENETICS INSTITUTE, INC.
TITLE OF INVENTION: RECEPTOR PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 15-October-
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 100.0%; Pred. No. 1. hes 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 87 Cambi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Kohlei, Vineet
REGISTRATION NUMBER: 37,003
REFERENCE/DOCKET NUMBER: LUD
                                                                                                 TELEPHONE:
                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 9136099.2
                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B: Genetics Institute Inc.- Legal Affairs87 CambridgePark Drive
                                                                                 (617)
                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
                                                                                                 (617) 498-8260
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RESULT 38

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                                                                  Matches
                                                                                              Query Match
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                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (415) 576-03
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: PatentIn Release #1.0, Ver.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,412A
PILING DATE: 05-UN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 543 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Garrett-Mackowski, Bugenia
REGISTRATION UNMBER: 37,330
REFERENCE/DOCKET NUMBER: 015280-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                             LOCATION: 1..543
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PPLICANT: Sgouras, Dionyssios N. ITLE OF INVENTION: The ERF Genetic Locus and Its Products
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 94111-3834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: San Francisco
STATE: California
                                                                                                                                                                                                                 NAME/KEY:
                                                                                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                   ropology:
398 SGSGGLA 404
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                               51 SGSGGLA 57
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                                                                                 Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mavrothalassitis, George J
                                                                                                                                                                                                                 Protein
                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                protein
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) 576-0300
- MO: 7:
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                                                             2.2%; Score 7; DB:
100.0%; Pred. No. 1.
tive 0; Mismatches
                                                                                                                                              /note= "murine ERF amino acid sequence
(first 8 amino acids from first exon not
included)"
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US-09-021-715-7
; Sequence 7, Application US/09021715
; Patent No. 6194547
; GENERAL INFORMATION:
APPLICANT: Mavrothalassitis, George J.
Blair, Donald G.
Robert J.
                                                                                                                                                                                                                                                                                                                              밁
                                                                                                                                                                                                                                       US-09-232-200-89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE DESCRIPTION: SEQ ID NO: 7: US-09-021-715-7
                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                           Sequence 89, Appl
Patent No. 628821
                              APPLICANT: Stahl, Andreas
APPLICANT: Hirsch, David J.
APPLICANT: Lodish, Harvey F.
APPLICANT: Gimeno, Ruth E.
APPLICANT: Tartaglia, Louis A.
TITLE OF INVENTION: FATTY ACID TRANSPORT PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Garrett-Wackowski, Eugenia
REGISTRATION NUMBER: 37,330
REFERENCE/DOCKET NUMBER: 015280-229000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0300
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Beal Jr., Gregory J.
Athanasiou, Meropi A.
Sgouras, Dionyssios N.
TITLE OF INVENTION: The ERF Genetic Locus and Its Products
NUMBER OF SEQUENCES: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTMARE: PATENTIA Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE
                                                                                                                                                                         INFORMATION:
                                                                                                                                                                                                                                                                                                                              398 SGSGGLA 404
APPLICATION NUMBER: US/09/232,200A
                                                                                                                                                                                                                                                                                                                                                                     51 SGSGGLA 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 543 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/09/021,715 FILING DATE: 10-Feb-1998 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IOCARTION: 1..543

OTHER INFAMATION: /note= "murine ERF amino acid sequence (first 8 amino acids from first exon not included)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: Protein LOCATION: 1..543
                                                                                                                                                                                                                  Application US/09232200A
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ilarity 100.0%;
Conservative (
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Pred. No. 1.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 543
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Search completed: July 8, Job time : 42 secs

2003, 11:22:01

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APPLICANT: Stahl, Andreas
APPLICANT: Hirsch, David J.
APPLICANT: Hirsch, David J.
APPLICANT: Hirsch, David J.
APPLICANT: Hirsch, David J.
APPLICANT: Gimeno, Ruth E.
APPLICANT: Tartaglia, Louis A.
APPLICANT: Tartaglia, Louis A.
APPLICANT: Tartaglia, Louis A.
APPLICANT: Tartaglia, Louis A.
APPLICANTON: MIJOT-21D3MB
CURRENT FILING DATE: 1999-01-14
EARLIER APPLICATION NUMBER: 60/071,374
EARLIER APPLICATION NUMBER: 60/093,491
EARLIER APPLICATION NUMBER: 60/10,941
EARLIER APPLICATION NUMBER: 60/110,941
EARLIER APPLICATION NUMBER: 60/110,941
EARLIER APPLICATION NUMBER: 60/110,941
EARLIER APPLICATION NUMBER: 60/110,941
EARLIER APPLICATION NUMBER: 60/110,941
EARLIER FILING DATE: 1998-012-04
NUMBER OF SEQ ID NOS: 105
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Saccharomyces cerevisiae US-09-232-200-89
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                                                                                                                                                                                 ; ORGANISM: Saccharomyces cerevisiae US-09-232-200-98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT FILING DATE: 1999-01-14
EARLIER APPLICATION UNMBER: 60/07
EARLIER APPLICATION UNMBER: 60/09
EARLIER APPLICATION UNMBER: 60/09
EARLIER FILING DATE: 1998-07-20
EARLIER FILING DATE: 1998-12-04
EARLIER FILING DATE: 1998-12-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 105
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 2.2%; Sometime 100.0%; Best Local Similarity 100.0%; Matches 7; Conservative 0;
                                                                                     Query Match 2.2%;
Best Local Similarity 100.0%;
Matches 7; Conservative
                                                                                                                                                                                                                                                    SEQ ID NO 98
LENGTH: 623
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TYPE: PRT
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398 TEAPFAT 404
                                             186 TEAPFAT 192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TEAPFAT 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Application US/09232200A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACID TRANSPORT PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60/093,491
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                                                                                                                DB 4; Le
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b. 1.9e+02;
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Title:
Perfect score:
Sequence:
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Maximum DB seq length: 2000000000
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322
1 MTVTIAINSQNQKP
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Match
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Gapop 60.0 ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
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                                                                                                                                                                                                                                                                                                                                        Length
      GenCore version 5.1.6 (c) 1993 - 2003 Compugen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gapext 60
                                                                                                                                                                                                                                                                                                                                                                                                                     of results predicted by chance to have a qual to the score of the result being printed, sis of the total score distribution.
        US-09-738-626-3830
US-09-944-411-9
US-09-759-352-44
US-09-533-029-70
US-10-286-264-72
US-10-286-264-72
US-10-180-775-195
US-09-771-161A-109
US-10-156-761-18098
US-10-156-761-18098
US-10-156-761-13366
US-10-98-71-161A-200
US-09-771-161A-200
US-09-771-161A-200
US-09-903-068-8
US-09-93-686-16
US-09-93-686-16
US-09-93-686-8
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 Sequence 3830, Ap
Sequence 9, Appli
Sequence 44, Appl
Sequence 70, Appl
Sequence 72, Appl
Sequence 195, App
Sequence 109, App
Sequence 300, App
Sequence 300, App
Sequence 400, App
Sequence 14239, A
Sequence 8098, Appli
Sequence 212, Appli
Sequence 212, Appli
Sequence 212, Appli
Sequence 21366, A
Sequence 213, Appli
Sequence 214, Appli
Sequence 8, Appli
Sequence 8, Appli
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Sequence 8, Appli
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US-09-978-303-25
US-09-934-455-22
US-09-915-242-12713
US-09-915-242-12713
US-09-915-242-12713
US-09-915-086-7
US-09-956-086-7
US-09-956-087-7
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US-09-864-761-45-99
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956 957 959 959 960 960 962 963 964 965 966 5 1.66 1.66 1.66 1.66 1.66	944 944 944 944 954 955 955 955 955 955		915 916 917 918 918 919 919 919 919 919 919	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,
956 5 1.6 25 9 958 5 1.6 25 9 958 5 1.6 25 9 959 5 1.6 25 9 960 5 1.6 25 1 961 5 1.6 25 1 963 5 1.6 25 1 964 5 1.6 25 1 966 5 1.6 26 9 967 5 1.6 26 9 968 5 1.6 26 9	945 946 5 1.6 23 9 947 5 1.6 23 9 948 5 1.6 24 9 950 5 1.6 24 9 951 5 1.6 24 9 952 5 1.6 24 1 955 1.6 24 1	5 1.6 20 1 1 6 21 9 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	915 5 1.6 20 9 917 5 1.6 20 9 918 5 1.6 20 9 919 5 1.6 20 9 920 5 1.6 20 9 922 5 1.6 20 9 923 5 1.6 20 9 925 5 1.6 20 9 926 5 1.6 20 9 927 5 1.6 20 9 928 5 1.6 20 9 928 5 1.6 20 9 929 5 1.6 20 9	5 5 1 . 6 6 1 18 9 9 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5
956 5 1.6 25 9 958 5 1.6 25 9 958 5 1.6 25 9 959 5 1.6 25 9 960 5 1.6 25 1 961 5 1.6 25 1 963 5 1.6 25 1 964 5 1.6 25 1 966 5 1.6 26 9 967 5 1.6 26 9 968 5 1.6 26 9	945 946 5 1.6 23 9 947 5 1.6 23 9 948 5 1.6 24 9 950 5 1.6 24 9 951 5 1.6 24 9 952 5 1.6 24 1 955 1.6 24 1	5 1.6 20 1 1 6 21 9 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	915 5 1.6 20 9 917 5 1.6 20 9 918 5 1.6 20 9 919 5 1.6 20 9 920 5 1.6 20 9 922 5 1.6 20 9 923 5 1.6 20 9 925 5 1.6 20 9 926 5 1.6 20 9 927 5 1.6 20 9 928 5 1.6 20 9 928 5 1.6 20 9 929 5 1.6 20 9	5 11.6 118 5 11.6 118 5 11.6 118 5 11.6 118 5 11.6 118 5 11.6 118 5 11.6 119 5 11.6 119 1.6 119

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US-09-738-626-3830
US-09-738-626-3830
US-09-738-626-3830

Sequence 3830, Application US/09738626

PUBLICANT: NO US20020197605A1

APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: MIZOGUCHI, KEIKO
APPLICANT: HAYASHI, MIKIRO
APPLICANT: TATELSHI, NAOKO
APPLICANT: TATELSHI, NAOKO
APPLICANT: SENOH, AKHHIRO
APPLICANT: SENOH, MASATO
APPLICANT: OZAKI, AKI
APPLICANT: OZAKI, AKI
APPLICANT: DOLYNUCLEOTIDES
FILE REFERENCE: 249-125

FURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 90/159162
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOCTMARE: Patentin ver: 3.0

SEQ ID NO 3830
LENGTH: 223
TYPE: PATE
Query Match 2.5%; Score 8; DB 9; Best Local Similarity 100.0%; Pred. No. 23; Matches 8; Conservative 0; Mismatches
                                                                                                                                                ORGANISM: Corynebacterium glutamicum -09-738-626-3830
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10 US-09-864-761-41159
10 US-09-864-761-413426
10 US-09-921-397-35
10 US-09-921-397-35
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10 US-09-964-761-40237
10 US-09-864-761-46273
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13 US-09-939-724-8
14 US-09-931-397-1
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15 US-09-946-761-48468
16 US-09-935-291A-28
17 US-09-935-291A-28
18 US-09-935-291A-39
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12-17
                                                                          Length 223;
            Indels
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            0;
            Gaps
            0
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ADDRESSEE: CELL GENESIDE DRIVE
STREET: 322 LAKESIDE DRIVE
CITY: FOSTER CITY
STATE: CALIFORNIA
COMPUTER READABLE FORM:
MEDIUM TYPE: 10APY
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: BATESITION PC-COMPATION
PERICATION NUMBER: US/09/944,411
FILING DATE: 04-Sep-2001
CLASSIFICATION NUMBER: US/09/944,411
FILING DATE: O4-Sep-2001
PRIOR APPLICATION NUMBER: US/09/944,411
FILING DATE: UNKNOWN-
APPLICATION NUMBER: US/09/944,411
FILING DATE: UNKNOWN-
APPLICATION NUMBER: US/08/258,152
FILING DATE: 10-UNN-1994
APPLICATION NUMBER: US/08/258,152
FILING DATE: 11-UNN-1993
ATTORNEY/AGENT INFORMATION:
NAME: KRUPEN, KAREN I
REGISTRATION INFORMATION:
NAME: KRUPEN, KAREN I
REGISTRATION INFORMATION:
TELEPHONE: 415-358-9600 X131
TELEPHONE: 415-358-9600 X131
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TELEPHONE: 415-358-9600 X131
TELEPHONE: 415-358-9600 X131
TELEPHONE: 41
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US-09-944-411-9
J Sequence 9, Application US/09944411
J Sequence 9, Sequence 9, Sequence 9, Papel I Sequence 9, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Seque
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    RESULT 3
US-09-759-352-44
; Sequence 44, Application US/09759352
; Patent No. US20020111474A1
                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 7; Conserv
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CORRESPONDENCE ADDRESS:
ADDRESSEE: CELL GE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF
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                                                                                                                                                                                                                                                                            41 STSGSGS 47
                                                                                                                                                                                                                                                                                                                                                                   2.2%; Score 7; DB ilarity 100.0%; Pred. No. 15 Conservative 0; Mismatches
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INVENTION: METHOD FOR PRODUCTION OF HIGH TITER
VIRUS AND HIGH EFFICIENCY RETROVIRAL MEDIATED TRANSDUCTION
OF MAMMALIAN CELLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZSEBO, KRISZTINA M. COOKE, KEEGAN FARSON, DEBORAH A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 13; .
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US-09-533-029-70
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                                                                                                                                                                                                                                                                                                                                                                                                                     ; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 44:
US-09-759-352-44
                                                                                                                                                                                                                                                                                                                                Query Match 2.:
Best Local Similarity 100
Matches 7; Conservative
                                                                                       GENERAL INFORMATION:
                                                                                                         Sequence 70, Application US/09533029 Publication No. US20030046723A1
                                       APPLICANT: Heard, Jacqueline APPLICANT: Broun, Pierre
                  PPLICANT: Riechmann, Jose-Luis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
PPLICANT: Keddie, James
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: CAPON,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: KRUPEN, KAREN I
REGISTRATION NUMBER: 34,647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPUTER: DOS MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 08/567,393
FILING DATE: 01-DEC-1995
APPLICATION NUMBER: US 08/475,442
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/238,405
FILING DATE: 05-MAY-1994
APPLICATION NUMBER: US 07/988,194
FILING DATE: 09-DEC-1992
APPLICATION.NUMBER: US 07/627,643
FILING DATE: 13-DEC-1990
APPLICATION NUMBER: WO PCT/US91/09431
FILING DATE: 112-DEC-1991
APPLICATION NUMBER: WO PCT/US91/09431
FILING DATE: 112-DEC-1991
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STREET: 322 LAKESIDE DRIVE
CITY: FOSTER CITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (415)358-96
TELEFAX: (415)349-7392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/09/759,352 FILING DATE: 16-Jan-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INVENTION: CHIMERIC CHAINS FOR RECEPTOR-ASSOCIATED SIGNAL TRANDUCTION PATHWAYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ROBERTS, MARGO R
ZSEBO, KRISZTINA
                                                                                                                                                                                                                                                                                                                                2.2%; Score 7; DB:
100.0%; Pred. No. 15;
tive 0; Mismatches
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BRYAN A
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5. 15;
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Query Match
Best Local Similarity
Thes 7; Conserve
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                                                                                             ORGANISM: Arabidopsis thaliana; FEATURE:
OTHER INFORMATION: G620
US-10-286-264-72
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; OTHER INFORMATION: G620
US-09-533-029-70
                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 165
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 70
LENGTH: 208
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Best Local :
                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/125,814 PRIOR FILING DATE: 1999-03-23
                                                                                                                                                                                                                                                                               FILE REFERENCE: MBI-008
CURRENT APPLICATION NUMBER: US/10/286,264
CURRENT FILING DATE: 2002-11-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: MBI-010
CUTRENT APPLICATION NUMBER: US/09/533,029
CURRENT FILING DATE: 2000-03-22
EARLIER APPLICATION NUMBER: 60/125,814
EARLIER FILING DATE: 1999-03-23
NUMBER OF SEQ ID NOS: 121
                                                                                                                                                                                                                                                                                                                             APPLICANT: Rouber, Lynne
APPLICANT: Pilgrim, Marsha
APPLICANT: Samaha, Raymond
TITLE OF INVENTION: POLYNUCLEOTIDES FOR SEED TRAIT ALTERATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Yu, Guo-Liang
APPLICANT: Ratcliffe, Oliver
APPLICANT: Pilgrim, Marsha
APPLICANT: Jiang, Cai-Zhong
APPLICANT: Reuber, Lynne
TITLE OF INVENTION: DISEASE-INDUCED POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Ver. 2.1
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                                                                                                                                                           TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
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ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                LENGTH:
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314 YVDPLTV 320
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Zhang, James
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Heard, Jacqueline
                                                                                                                                                                                                                                                                                                                                                                                                 Broun, Pierre
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Ratcliffe, Oliver
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                               Conservative
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                                         Score 7; L.
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                               0; Mismatches
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o. 1.7e+02;
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o. 1.7e+02;
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                             Gaps
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105 YVDPLTV 111

Application US/10180375 b. US20030126638A1

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RESULT 6
US-10-180-375-195

// Sequence 195, Application US/101803.
// Publication No. US20030126638A1
// GENERAL INFORMATION:
// APPLICANT: Allen William B.
// APPLICANT: Famodu, Omolayo O.
// APPLICANT: Harvell, Leslie T.
// APPLICANT: Helentjaris, Timothy
// APPLICANT: Li, Changjiang
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                                                                                                                                                                                                                                                                                                          APPLICANT: LEVINE, et al.

TITLE OF INVENTION: VARIANTS Of PROTEIN KINASES
FILLE REFERENCE: 802620-2005.1
CURRENT APPLICATION NUMBER: US/09/771,161A
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 09/724,676
PRIOR APPLICATION NUMBER: 03/724,676
PRIOR PILING DATE: 2000-011-28
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-04-12
PRIOR FILING DATE: 2000-04-12
PRIOR FILING DATE: 2000-04-12
PRIOR FILING DATE: 2000-04-12
PRIOR FILING DATE: 2000-04-12
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PRIOR FILING DATE: 2000-04-12
PRIOR FILING DATE: 2000-04-12
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US-09-771-161A-109
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; NAME/KBY: misc_feature
; LOCATION:
; OTHER INFORMATION: gi 6552738
US-10-180-375-195
                                                                                                                                                            ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-771-161A-109
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TITLE OF INVENTION: Alteration Of Oil Traits In Plants
FILE REFERENCE: BB1458 US NA1
CURRENT APPLICATION NUMBER: US/10/180,375
CURRENT FILING DATE: 2002-06-26
NUMBER OF SEQ ID NOS: 222
SOFTWARE: Microsoft Office 97
SEQ ID NO 195
LENGTH: 208
TYPE: PRT
ORGANISM: Arabidopsis thaliana
FRATURE.
                                                                                                                                                                                                                                SOFTWARE: PatentIn
SEQ ID NO 109
LENGTH: 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 109, Application US/09771161A Patent No. US20020110811A1 GENERAL INFORMATION:
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Best Local Similarity 100.0%; Pred. No. 1.7e+02
Matches 7; Conservative 0; Mismatches 0
                                                    Query Match 2.2%; Score 7; DB 10; Le Best Local Similarity 100.0%; Pred. No. 1.7e+02; Matches 7; Conservative 0; Mismatches 0;
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e, Keith
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                                                          Indels
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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Rosen et al.

APPLICANT: Rosen et al.

FILE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

FILE REFERENCE: PTZ14C1

CURRENT APPLICATION NUMBER: US/10/125,540

CURRENT APPLICATION NUMBER: US/10/125,540

CURRENT FILLNG DATE: 2002-04-19

Frior Application removed - See File Wrapper or Palm

NUMBER OF SEQ ID NOS: 646

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 300

LENGTH: 251

TYPE: PRT

ORGANISM: Homo sapiens

US-10-125-540-300
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US-10-125-540-300
US-10-125-540-300
; Sequence 300, App
; Publication No. 1
; Publication No. 1
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US-10-156-761-14239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT; ORGANISM: Homo sapiens US-09-764-870-300
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US-09-764-870-300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 300, Application US/09764870
PATENT NO US20020042386A1
GENERAL INFORMATION:
APPLICANT: ROSen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PTZ14
CURRENT APPLICATION NUMBER: US/09/764,870
CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 646
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 300
LENGTH: 251
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Best Local Similarity 100.0%;
Matches 7; Conservative
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T: SAKAKI, YOSHIYUKI
T: HATTORI, MASAHIRA
INVENTION: NOVEL POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Application US/10125540 o. US20030059875A1
                                                                            ISHIKAWA, JUN
HORIKAWA, HIROSHI
                                                                                                                                                                                Application US/10156761
US20030119018A1
                                                                                                                       HARUO
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Best Local Similarity luu.
Thes 7; Conservative
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SEQ ID NO 14239
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Best Local Similarity
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                                                                                                                                                                                        Sequence 8098, Application US/10156761
Publication No. US20030119018A1
                                                                                    APPLICANT:
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Patent No. US20020106733A1
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CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: JP 2001-272697 PRIOR FILING DATE: 2001-08-02
CURRENT APPLICATION NUMBER: US/10/156,761
                           APPLICANT: SHEBA, TADAYOSHI
APPLICANT: SHEBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR FILING DATE: 1998-12-04
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSEQ for Windows Version 3.0
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CURRENT FILING DATE: 2001-08-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Hirsch, David J.
APPLICANT: Lodish, Harvey F.
TITLE OF INVENTION: Fatty Acid Transport Proteins
FILE REFERENCE: WHI97-21p3ME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ENERAL INFORMATION:
                                                                                                                                                         APPLICANT: OMURA, SATOSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Saccharomyces cerevisiae
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TYPE: PRT
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APPLICATION NUMBER: 09/232,191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 1999-10-14
                                                                                                                                                                         INFORMATION:
                                                                                                                                                                                                                                                                                                                                 186 TEAPFAT 192
                                                                                                                                                                                                                                                                                                145 TEAPFAT 151
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ISHIKAWA, JUN
HORIKAWA, HIROSHI
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100.0%; Pred. No. 2.6e+02;
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Pred. No.
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No. 2.7e+02;
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US-10-156-761-13366
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Best Local Similarity 100.
Conservative
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Best Local Similarity 100.
Thes 7; Conservative
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PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR PELING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 8098
LENGTH: 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 13366
LENGTH: 490
                                                                                                                                                                                                                   Sequence 212, Appropriate Publication No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 13366, Application US/10156761
Publication No. US20030119018A1
GENERAL INFORMATION:
                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Callen, Walter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEC_ID NOS: 15109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: OMURA, SATOSHI APPLICANT: IKEDA, HARUO
     APPLICANT: Frey, Gerhard
APPLICANT: Short, Jay M.
APPLICANT: Mathur, Eric J.
APPLICANT: Gray, Kevin A.
APPLICANT: Kerovuo, Janne S.
APPLICANT: Slupska, Malgorzata
APPLICANT: Slupska, Malgorzata
TITLE OF INVENTION: ENZYMES HAVING ALPHA AMYLASE ACTIVITY
TITLE OF INVENTION: AND METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
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ILE REFERENCE: 09010-108001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PPLICANT: SAKAKI, YOSHIYUKI
PPLICANT: HATTORI, MASAHIRA
TILE OF INVENTION: NOVEL POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                   179 APVAPPV 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     176 GTATVAG 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       215 GTATVAG 221
                                                                                                                                                                                                                                                                                                                              38 APVAPPV 44
                                                                                                                                                           Richardson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ISHIKAWA, JUN
HORIKAWA, HIROSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SHIBA, TADAYOSHI
                                                                                                                                                                                                                                    Application US/10081872
                                                                                                                                                                                                                     US20030125534A1
                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2.2%; Score 7; DB 100.0%; Pred. No. 2.1 tive 0; Mismatches
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100.0%; Pred. No. 3.
1ve 0; Mismatches
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No. 3.6e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 490;
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APPLICANT: LEVINE et al.

TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
FILE REFERENCE: 802620-2005.1
CURRENT APPLICATION NUMBER: US/09/771,161A
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 09/724,676
PRIOR FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: 136776
PRIOR APPLICATION NUMBER: 136776
PRIOR APPLICATION NUMBER: 136776
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 135619
PRIOR FILING DATE: 2000-04-12
NUMBER OF SEQ ID NOS: 273
SOFTWARE: PATENTIAN OF SEQ ID NOS: 273
SOFTWARE: PATENTIAN OF SEQ ID NOS: 273
SOFTWARE: PATENTIAN OF SEQ ID NOS: 273
SOFTWARE: PATENTIAN OF SEQ ID NOS: 273
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SOFTWARE: PATENTIAN OF SEQ ID NOS: 273
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CURRENT FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: US 60/270,495
PRIOR FILING DATE: 2001-02-21
PRIOR FILING DATE: 2001-02-21
PRIOR FILING DATE: 2001-05-14
PRIOR FILING DATE: 2001-05-14
VUMBER OF SEQ ID NOS: 321
SECTION APPLICATION NUMBER: US 60/291,122
PRIOR FILING DATE: 2001-05-14
VUMBER OF SEQ ID NOS: 321
SECTION APPLICATION NUMBER: US 60/291,122
PRIOR FILING DATE: 2001-05-14
VUMBER OF SEQ ID NOS: 321
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Best Local Similarity
Matches 7; Conserva
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US-09-771-161A-200
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; ORGANISM: Environmental
US-10-081-872-212
                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-903-068-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Homo sapiens
US-09-771-161A-200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 2.2%; Score 7; DB Best Local Similarity 100.0%; Pred. No. 3. Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                   Sequence 8, Application US/09903068
Patent No. US20020123139A1
GENERAL INFORMATION:
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LENGTH: 496
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THERAL INFORMATION:
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atent No. US20020110811A1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
                                                                                                                                                                                         APPLICANT: Miyazono, Kohei; Dijke, Peter Ten;
Franzen, Petra; Yamashita, Hidetoshi; Heldin, Carl-Henrik
TITLE OF INVENTION: Activin Receptor-Like Kinase, Proteins ...
Having Serine Threonine Kinase Domains And Their Use
                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              167 NNLNSSY 173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41 STSGSGS 47
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llarity 100.0%; Pred. No.
Conservative 0; Mismatc
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RESULT 17
US-09-903-068-16
; Sequence 16, Application US/09903068
; Patent No. US20020123139A1
; GENERAL INFORMATION:
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Best Local Similarity 100.0%; P
Matches 7; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEPHAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OCHECULAR: LIPY
OCERATING SYSTEM: PC-DOS
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/903,068
FILING DATE: 11-Jul-2001
PRIOR APPLICATION NUMBER: 09/679,187
FILING DATE: -Unknown-
APPLICATION NUMBER: PCT/GB93/02367
APPLICATION NUMBER: PCT/GB93/02367
FILING DATE: 17-No. US20020123139A1ember-1993
APPLICATION NUMBER: 9304677.9
FILING DATE: 8-March-1993
APPLICATION NUMBER: 9304677.9
FILING DATE: 8-March-1993
APPLICATION NUMBER: 9311047.6
FILING DATE: 8-May-1993
APPLICATION NUMBER: 9313763.6
FILING DATE: 3-AUGUST-1993
APPLICATION NUMBER: 913609.2
FILING DATE: 3-AUGUST-1993
APPLICATION NUMBER: 9321344.5
FILING DATE: 1-October-1993
APPLICATION NUMBER: 9321344.5
FILING DATE: 1-October-1993
APPLICATION NUMBER: 9321344.5
FILING DATE: 1-October-1993
APPLICATION NUMBER: 37,003
REFERENCE/DOCKET NUMBER: 100 5298
TREFCOMMINICATION INDOCKET NUMBER: 100 5298
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 505 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
                                                                                                                                                                                                                                                                             APPLICANT: Miyazono, Kohei; Dijke, Peter Ten;
Franzen, Petra; Yamashita, Hidetoshi; Heldin,
TITLE OF INVENTION: Activin Receptor-Like Kinase, Proteir
Having Serine Threonine Kinase Domair
                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                187 STSGSGS 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41 STSGSGS 47
OPERATING SYSTEM: PC-DOS
                                               TER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch,
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; Pred. No. 3.'
0; Mismatches
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                                                     360 kb storage
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US-09-874-628-8
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Patent No. US20020137133A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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APPLICATION NUMBER: 931047.6

FILING DATE: 28-May-1993

APPLICATION NUMBER: 9313763.6

FILING DATE: 2-July-1993

APPLICATION NUMBER: 9136099.2

FILING DATE: 3-August-1993

APPLICATION NUMBER: 931344.5

FILING DATE: 15-October-1993

APPLICATION NUMBER: 931344.5

APPLICATION NUMBER: 937003

APPLICATION NUMBER: 17.003

REGISTRATION NUMBER: 17.003

REGISTRATION NUMBER: 17.003

REGISTRATION INFORMATION:

TELEPHONE: (212) 688-9200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 100.0%; Pred. No. 3.7 nes 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: protein
                                ZIP: 02140

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                         APPLICANT: WOZNEY, John
CELESTE, Anthony J.
THIES, R. Scott
THIES, R. SCOTT
THIES, NO. US20020137133A10ru
TITLE OF INVENTION: RECEPTOR PROTEINS
NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE DESCRIPTION: SEQ ID NO: 16:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                         CURRENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA
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                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                   CITY: Cambridge
STATE: MA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/09/903,068 FILING DATE: 11-Jul-2001
                                                                                                                                                                                                                                          ADDRESSEE: Genetics Institute Inc.- Legal Affairs
APPLICATION NUMBER: US/09/874,628
                                                                                                                                                                            COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (212)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ENGTH: 505 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PPLICATION NUMBER: PCT/GB93/02367
PILING DATE: 17-No. US20020123139Alember-1993
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ILING DATE: 17-No. US2002012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PLICATION NUMBER: 9304680.3
LING DATE: 8-March-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LING DATE: 17-No. US20020123139Alember-1992
LICATION NUMBER: 9304677.9
ING DATE: 8-March-1997
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                                                                                                                                US-09-738-626-5890
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                                                                                                                                                                                               SOFTWARE: PatentIn ver. SEQ ID NO 5890
                                                                Matches
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                                                                            Query Match
Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 5890, Application US/09738626
Publication No. US20020197605A1
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                                                                                                                                                                                                                              PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
                                                                                                                                                                                                                                                                                                                                                 APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: NAKAGAWA, SATOSHI APPLICANT: MIZOGUCHI, HIROS
                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
                                                                                                                                           LENGTH: 806
TYPE: PRT
ORGANISM: Corynebacterium glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                                      PPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity nes 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/123,934
FILING DATE: 17-SEP-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein SEQUENCE DESCRIPTION: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 505 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION: TELEPHONE: 617 876 1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
631 WESGRDG 637
                               230 WFSGRDG 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          187 STSGSGS 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION:
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                                                              Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                 YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKIHIRO
IKEDA, MASATO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: LAZAR, Steven R
REGISTRATION NUMBER: 32,618
REFERENCE/DOCKET NUMBER: 520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 05-Jun-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HAYASHI, MIKIRO
OCHIAI, KEIKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 617 876 5851
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Conservative
                                                                Conservative
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                                                                              100.0%;
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                                                              Score 7; DB 9; Pred. No. 5.5
                                                                0
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                                                                              DB 9; Le
o. 5.5e+02;
                                                                0; Indels
                                                                                            Length 806;
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RESULT 20

US-09-978-303-25

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Samaha, Raymond

FILE REFERENCE: MBI-009
CURRENT APPLICATION NUMBER: US/10/278,173
CURRENT APPLICATION NUMBER: US/09/533,392
PRIOR APPLICATION NUMBER: US/09/533,392
PRIOR FILING DATE: 2000-03-22
PRIOR FILING DATE: 1999-03-23
NUMBER OF SEQ ID NOS: 177
SOFTWARE: PAtentin Ver. 2.1
SEQ ID NO 128
LERGTH: 1336
TYPE: PRTO

ORGAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION DAVID J.

APPLICANT: Unlius, David J.

APPLICANT: Caterina, Michael J.

APPLICANT: Brake, Anthony J.

APPLICANT: Brake, Anthony J.

TITLE OF INVENTION: uncleic acid sequences encoding TITLE OF INVENTION: capsaicin receptor and capsaicin rITLE OF INVENTION: polypeptides and uses thereof FILE REFERENCE: UCALO84CON

CURRENT APPLICATION NUMBER: US/9/978,303

CURRENT APPLICATION NUMBER: 09/235,451

PRIOR APPLICATION NUMBER: 60/072,151

PRIOR APPLICATION NUMBER: 60/072,151

PRIOR APPLICATION NUMBER: 09/235,461

PRIOR APPLICATION NUMBER: 08/915,461

PRIOR APPLICATION NUMBER: 08/915,461

PRIOR APPLICATION NUMBER: 08/915,461

PRIOR FILING DATE: 1997-08-20

INUMBER OF SEQ ID NOS: 48

SOFTWARE: FastESEQ for Windows Version 4.0

SEQ ID NO 25

LENGTH: 843

TYPE: PRI

ORGANISM: Chicken

US-09-978-303-25

2.2%; Score 7; DB 9; Len

TOTAL TO SEC ID NOS: 48

SOFTWARE: SCORE T; DB 9; Len

ORGANISM: Chicken
                                       ; FEATURE:
; OTHER INFORMATION: G987
US-10-278-173-128
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Best Local Similarity
7; Conserv
Query Match
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lication No. US20
ERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Riechmann, Jose-Luis
Pineda, Omaira
Zhang, James
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       iang, Cai-Zhong
Broun, Pierre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Application US/10278173 b. US20030061637A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2.2%; Score 7;
larity 100.0%; Pred. N
Conservative 0; Misma
2.2%; Score 7;
DB 9;
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Length 1336;
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RESULT 23
US-09-815-242-12713
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CURRENT APPLICATION NUMBER: US/09/934,455
CURRENT APPLICATION NUMBER: US/09/934,455
CURRENT FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/227439
PRIOR FILING DATE: 2000-08-22
PRIOR PPLICATION NUMBER: MBI-0022
PRIOR FILING DATE: 2001-11-16
PRIOR FILING DATE: 2001-04-17
NUMBER OF SEQ ID NOS: 516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn version 3.1
SEQ ID NO 22
LENGTH: 1336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 100.0%; Matches 7; Conservative 0;
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Best Local
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                         APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/191,078
                                                                                                                                                                                                                     HENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith I
APPLICANT: Wall, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Match 2.2%;
Local Similarity 100.0%;
es 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 QVITDSQ 67
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INVENTION: Genes for Modifying Plant Traits IV
                                                                                                                                                                                                                 Ohlsen, Kari L.
Zyskind, Judith W.
Wall, Daniel
CATION NUMBER: 60/206,848
                                                                                                                                                                                                    rawick, John D.
                                                                                                                                                                                                                                                                                                                                 Application US/09815242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         i, Jacqueline
y, Cai-Zhong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mann, Jose Luis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   im, Marsha
iffe, Oliver
                                                                                                                                                                                                                                                                                                                  061569A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arnold
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 7; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pred. No. 8.5e+02;

mismatches 0;
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No. 8.5e+02;
0;
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FILING DATE:

2000-05-23

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PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-0-023
PRIOR PILING DATE: 2000-10-23
PRIOR RELING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR PILING DATE: 2001-02-16
PRIOR PILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12713
LENGTH: 2344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
                                                                                                                                                                                                                                                                            US-09-712-363-246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Mycobacterium bovis
US-09-870-759-114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-12713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-870-759-114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/870,759
CURRENT FILING DATE: 2002-01-14
PRIOR APPLICATION NUMBER: US 60/208,128
PRIOR FILING DATE: 2000-05-30
NUMBER OF SEQ ID NOS: 166
SOFTWARE: Patentin version 3.1
SEQ ID NO 114
LENGTH: 2796
                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 114, Application Patent No. US20020177551A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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Best Local (
                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                APPLICANT: Eisenberg, David
APPLICANT: Rotstein, Sergio H.
APPLICANT: Marcotte, Edward M.
APPLICANT: MARCOTTEN BY COMPARATIVE ANALYSIS
TITLE OF INVENTION: INVERACTIONS OF PROTEINS BY COMPARATIVE ANALYSIS
FILE REFERENCE: 07419-032001
CURRENT APPLICATION NUMBER: US/09/712,363
CURRENT FILLING DATE: 2000-11-13
PRIOR APPLICATION NUMBER: PCT/US00/02246
PRIOR PILING DATE: 2000-01-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: TERMAN, David S
TITLE OF INVENTION: COMPOS
                                                                                                                                                                                                                                                           equence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: 870759
                                                                                                                                                                                                                                    equence 246, Application US/09712363
etent No. US20020164588A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                          2088 IHIKDAQ 2094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2088 STSGSGS 2094
                                                                                                                                                                                                                                                                                                                                                                                 272 IHIKDAQ 278
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                                                                                                                                                                                                                                                                                                                                                                                                                                100.08; --
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60/179,531
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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o. 1.6e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FOR TREATMENT OF NEOPLASTIC DISEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 2796;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 2344;
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Query Match
Best Local Similarity
Matches 7; Conserve
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US-09-956-086-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 7, Application US/09956086 Patent No. US20020155498A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 60/134,093
PRIOR FILING DATE: 1999-05-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 3069
                                                                                      APPLICATION NUMBER: US/09/956,086
FILING DATE: 20-Sep-2001
CLASSIFICATION: <URNOwn>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/069,821
FILING DATE: <UNKnown>
APPLICATION NUMBER: US 60/063,074
FILING DATE: 27-OCT-1997
APPLICATION NUMBER: US 60/050,472
FILING DATE: 23-UN-1997
APPLICATION NUMBER: US 60/050,472
FILING DATE: 23-UN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 60/165,124
FILING DATE: 1999-11-12
APPLICATION NUMBER: 60/165,086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 60/134,092 FILING DATE: 1999-05-14
                              APPLICATION NUMBER: US 60/044,449 FILING DATE: 30-APR-1997 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESSE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C
STREET: 1100 NEW YORK AVE., NW, SUITE 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: SINGLE-CHAIN ANTIGEN-BINDING PROTEINS
CAPABLE OF GLYCOSYLATION, PRODUCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 60/118,206
FILING DATE: 1999-02-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 2000-02-01
APPLICATION NUMBER: 60/117,844
                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 60/126,593
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: FILPULA, DAVID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 272 IHIKDAQ 278
                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: US
ZIP: 20005
                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: DC
REGISTRATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WANG, MACLIANG SHORR, ROBERT
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o. 1.8e+03;
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TELEPHONE:

)371-2540

REFERENCE/DOCKET NUMBER: 0977.2280003

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Sequence ... US20020157120A1
Patent No. US20020157120A1
GENERAL INFORMATION:
APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
APPLICANT: Tsien, Roger Y.
APPLICANT: Baird, Geoffrey
TITLE OF INVENTION: CHROULARLY PERMUTED FLUORESCENT PROTEIN INDICATORS
FILE REFERENCE: REGEN1470-1
CURRENT APPLICATION NUMBER: US/09/99,745
CURRENT FILING DATE: 2001-10-23
PRIOR APPLICATION NUMBER: 09/316,920
PRIOR APPLICATION NUMBER: 09/316,920
PRIOR TLING DATE: 199-05-21
NUMBER OF SEQ ID NOS: 67
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                  RESULT 28
US-09-999-745-60
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US-09-999-745-58
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SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-956-086-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Linker moiety US-09-999-745-58
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Best Local S
Matches 6
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Best Local Similarity 100.0%; P
Matches 6; Conservative 0;
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SOFTWARE: PatentIn version 3.0.
SEQ ID NO 58
LENGTH: 14
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GENERAL INFORMATION: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
APPLICANT: Teien, Roger Y.

APPLICANT: Baird, Geoffrey
TITLE OF INVENTION: CIRCULARLY PERMUTED FLUORESCENT PROTEIN INDICATORS
FILE REPERENCE: REGEN1470-1
CURRENT APPLICATION NUMBER: US/09/999,745
CURRENT FILING DATE: 2001-10-23
PRIOR APPLICATION NUMBER: 09/316,920
PRIOR FILING DATE: 1999-05-21
                                                                                                                                                                                                                                                                                                                                       Sequence 60, Application US/09999745
Patent No. US20020157120A1
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TYPE: PRT
TYPE: PRT
ORGANISM: Artificial Sequence
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SEQUENCE CHARACTERISTICS:
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o..US20020157120A1
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TYPE: amino acid
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.00.0%; Pred. No. 1.3e+0;
.ve 0; Mismatches (
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US-09-956-087-7
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Patent No. US20020161201A1
GENERAL INFORMATION:
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Best Local
Query Match
Best Local Similarity
                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)371-2600
TELEPAX: (202)371-2540
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYDE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 14
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/956,087
FILING DATE: 20-Sep-2001
                                                                                                                                                                                                                                                                                                PRIOR APPLICATION UNMEER: 09/069,821

PRILING DATE: 1998-04-30

APPLICATION UNMEER: US 60/063,074

PRILING DATE: 27-0CT-1997

APPLICATION UNMEER: US 60/050,472

FILING DATE: 23-JUN-1997

APPLICATION NUMBER: US 60/044,449

PILING DATE: 33-APR-1997

APPLICATION NUMBER: US 60/044,449

FILING DATE: 30-APR-1997

APPLICATION UNMEER: US 60/044,449

FILING DATE: 30-APR-1997

ATTORNEY/AGENT INFORMATION:

NAME: KIM, JUDITH U.

REFERENCE/DOCKET NUMBER: 0977.2280003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.9%;
Local Similarity 100.0%;
es 6; Conservative 0
                                                                             STRANDEDNESS: single TOPOLOGY: not relevant MOLECULE TYPE: peptide . SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESSE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVE., NW, SUITE 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: SINGLE-CHAIN ANTIGEN-BINDING PROTEINS
CAPABLE OF GLYCOSYLATION, PRODUCTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 1100 NEW CITY: WASHINGTON STATE: DC
                                                                                                                                                              TYPE: amino acio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILPULA, DAVID WANG, MAOLIANG SHORR, ROBERT
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  1.9%; Score 6; DB 9; Le 100.0%; Pred. No. 1.3e+02;
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Pred. No.
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                  Length 14;
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; OTHER INFORMATION:
US-09-554-000-42
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                                                                                                          Query Match
Best Local S
Matches 6
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LENGTH: 14
TYPE: PRT
                                                                                                                                                                                                                                                                                    SOFTWARE: FASTSEQ for Windows Version 4.0 SEQ ID NO 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patent No. US20020165364A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 44,
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                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Tsien, Roger Y.
APPLICANT: Miyawaki, Atsushi
TITLE OP INVENTION: FLUORESCENT PROTEIN SENSORS FOR
TITLE OP INVENTION: DETECTION OF ANALYTES
FILE REFERENCE: 07257/042001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Miyawaki, Atbushi
TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS
TITLE OF INVENTION: DETECTION OF ANALYTES
FILE REFERENCE: 07257/042001
CURRENT APPLICATION NUMBER: US/09/554,000
CURRENT FILLING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: 08/618,252
PRIOR PILING DATE: 1997-03-14
NUMBER OF SEQ ID NOS: 56
                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/554,000 CURRENT FILING DATE: 2000-04-20
                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 08/818,252
PRIOR FILING DATE: 1997-03-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Tsien, Roger Y.
APPLICANT: Miyawaki, Atsu
                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 56
                                                                                                                                                                                              OTHER INFORMATION: Linker moiety
                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                     TYPE: PRT
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                                                                                                                         Local Similarity
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                                                                       STSGSG 46
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                                                                                                        1.9%; Score 6; lilarity 100.0%; Pred. No. Conservative 0; Mismatci
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                                                                                                                                          DB 9;
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                                                                                                                                                           RESULT 34
US-10-158-238-9
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US-09-792-793A-6
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US-09-792-793A-4
           Sequence 9, Application US/10158238
Publication No. US20030040604A1
GENERAL INFORMATION:
APPLICANT: Immunex Corporation
APPLICANT: Dirk, Anderson M.
APPLICANT: Marken, John S.
TITLE OF INVENTION: SIGLEC-12 POLYPEPTIDES,
FILE REFERENCE: 3290-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 6, Application US/09792793A
Patent No. US20020168370A1
GENERAL INFORMATION:
APPLICANT: McDonald, John R.
APPLICANT: COggins, Philip
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE
TITLE OF INVENTION: OTHER INFLAMMATORY CONDITIONS AND DISORDERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 6; Conser
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: 25020-601D
CURRENT APPLICATION NUMBER: US/09/792,793A
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 93
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APPLICANT: COGGINS, PAILIP
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
TITLE OF INVENTION: OTHER INFLAMMATORY CONDITIONS AND DISORDERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT FILING DATE: 20
NUMBER OF SEQ ID NOS: 93
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CURRENT APPLICATION NUMBER: US/10/158,238
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ORGANISM: homo sapien
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
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Pred. No. 1.3e+02;
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                                   POLYNUCLEOTIDES,
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                                   AND METHODS OF USE THERE
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RESULT 35
US-10-247-279-3
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US-10-052-942-6
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; OTHER INFORMATION: Linker
US-10-247-279-3
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Best Local Similarity
Conser
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PRIOR APPLICATION NUMBER: US 60/294,199
PRIOR FILING DATE: 2001-05-29
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn version 3.1
SEQ ID NO 9
LENGTH: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: PCTUS 01/08946
PRIOR FILING DATE: 2001-03-19
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 14
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Best Local S
Matches 6
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Publication No. US20030086928A1
GENERAL INFORMATION:
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Publication No. US20030104402A1
GENERAL INFORMATION:
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APPLICANT: Wagner, Brandee
APPLICANT: Wagner, Brandee
TITLE OF INVENTION: COMPOSITIONS ASSOCIATED WITH COMPLEX
TITLE OF INVENTION: FORMATION AND METHODS OF USE THEREOF
FILE REFERENCE: SALKIMS.036CP1
CURRENT APPLICATION NUMBER: US/10/247,279
CURRENT FILING DATE: 2002-09-17
PRIOR APPLICATION NUMBER: 60/190,705
PRIOR APPLICATION NUMBER: DETTIC 01/00046
APPLICANT: Zaudezer, Maurice
APPLICANT: Smith, Ernest
APPLICANT: Wei, Chungwen
TITLE OF INVENTION: Methods of Producing or Identifying Intrabodies in
FILE REFERENCE: 1821.0090004
CURRENT APPLICATION NUMBER: US/10/052,942
CURRENT FILING DATE: 2002-01-23
CURRENT FILING DATE: 2002-06-15
PRIOR APPLICATION NUMBER: 60/298,095
PRIOR APPLICATION NUMBER: 60/271,422
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ORGANISM: Artificial Sequence
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100.0%; Pred. No. 1.
tive 0; Mismatches
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APPLICANT: WILEY, Steven R.
APPLICANT: WILEY, Steven R.
TITLE OF INVENTION: TWEAK RECEPTOR
TITLE OF INVENTION: TWEAK RECEPTOR
TITLE OF INVENTION: TWEAK RECEPTOR
CURRENT FILING DATE: 2001-06-18
PRIOR APPLICATION NUMBER: US 60/172,878
PRIOR APPLICATION NUMBER: US 60/203,347
PRIOR APPLICATION NUMBER: US 60/203,347
PRIOR FILING DATE: 2000-05-10
PRIOR FILING DATE: 2000-12-19
PRIOR PRIOR FILING DATE: 2000-12-19
PRIOR PRIOR PRIOR DATE: 2000-12-19
PRIOR PRIOR DATE: 2000-12-19
PRIOR PRIOR PRIOR DATE: 2000-13-19
PRIOR PRIOR PRIOR DATE: 2000-13-19
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 13
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; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Linker Molety
US-09-883-777-13
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US-09-987-456-11
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PRIOR FILING DATE: 2001-01-23
NUMBER OF SEQ ID NOS: 154
SOFTWARE: Patentin version 3.0
SEQ ID NO 6
LENGTH: 14
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Best Local Similarity
6; Conser
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Sequence 11, Application US/09987456
Patent No. US20020123057A1
GENERAL INFORMATION:
APPLICANT: University of Rochester
APPLICANT: Zauderer, Maurice
APPLICANT: Ernest S. Smith
TITLE OF INVENTION: In Vitro Methods Of Producing And Selecting
TITLE OF INVENTION: Immunoglobulin Molecules In Eukaryotic Cells
FILE REFERENCE: 1821.0070004
CURRENT APPLICATION NUMBER: US/09/987,456
CURRENT FILING DATE: 2001-11-14
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Best Local
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Conservative (
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Pred. No.
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APPLICATION NUMBER: 60/271,424
FILING DATE: 2001-02-27
APPLICATION NUMBER: 60/262,067
FILING DATE: 2001-01-18

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RESULT 40
US-09-883-777-15
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US-09-883-777-14
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; TYPE: PRT
; GRGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: linker peptide
US-09-987-456-11
                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Linker Moiety US-09-883-777-14
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PRIOR FILING DATE: 1999-12-20
PRIOR PPLICATION NUMBER: US 60/203,347
PRIOR FILING DATE: 2000-05-10
PRIOR APPLICATION NUMBER: PCT/US00/34755
PRIOR APPLICATION NUMBER: PCT/US00/34755
PRIOR FILING DATE: 2000-12-19
PRIOR PPLICATION NUMBER: US 09/742,454
PRIOR FILING DATE: 2000-12-19
NUMBER OF SEQ ID NOS: 16
                   Sequence 15, Application US/09883777
PATENT NO. US20020110853A1
GENERAL INFORMATION:
APPLICANT: Wiley, Steven R.
TITLE OF INVENTION: TWEAK RECEPTOR
FILE REFERENCE: 2968-C
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Best Local Similarity 100.0%; P
Matches 6; Conservative 0;
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PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/249,268
PRIOR FILING DATE: 2000-11-17
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CURRENT FILING DATE: 2001-06-18
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APPLICANT: Wiley, Steven R.
TITLE OF INVENTION: TWEAK RECEPTOR
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URRENT APPLICATION NUMBER: US/09/883,777
                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 16
TYPE: PRT
ORGANISM: Artificial sequence
PEATURE:
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US20020110853A1
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.00.0%; Pred. No. 1.5e+02; 
.ve 0; Mismatches 0; Indels
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CURRENT FILING DATE: 2001-06-18

PRIOR APPLICATION NUMBER: US 60/172,878

PRIOR FILING DATE: 1999-12-20

PRIOR APPLICATION NUMBER: US 60/203,347

PRIOR APPLICATION NUMBER: US 60/203,347

PRIOR FILING DATE: 2000-05-10

PRIOR FILING DATE: 2000-05-10

PRIOR APPLICATION NUMBER: US 09/742,454

PRIOR FILING DATE: 2000-12-19

PRIOR FILING DATE: 2000-12-19

NUMBER OF SEQ ID NOS: 16

SOFTWARE: Patentin version 3.1

SEQ ID NO 15

LENGTH: 16

TYPE: PRI
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Linker Moiety

US-09-883-777-15

Query Match
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 0; Gaps

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Search completed: July 8, 2003, i1:30:23
Job time : 74 secs

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Result
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DB seq length: 2000000000
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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
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6 1.9 580 581	6 1.9 579 2 6 1.9 579 2 6 1.9 580 2	6 1.9 577 2 6 1.9 578 2	6 1.9 574 2	6 1.9 570 2	6 1.9 568 2	6 1.9 568 1 6 1.9 568 2	6 1.9 566 2	6 1.9 562 2 6 1.9 564 2	6 1.9 562 2	6 1.9 560 1 6 1.9 562 1	6 1.9 559 2	6 1.9 555 2	6 1.9 554 2	6 1.9 554 2	6 1.9 553 2	6 1.9 553 1	6 1.9 551 2	6 1.9 550 2	6 1.9 550 2	6 1.9 549 2	6 1.9 548 2	6 1.9 548 2	6 1.9 547 2	6 1.9 546 2	6 1.9 546 2	6 1.9 544 2	6 1.9 541 2	6 1.9 540 2	6 1.9 540 2	6 1.9 538 2	6 1.9 538 2	6 1.9 536 2	6 1.9 535 2	6 1.9 531 2	6 1.9 531 2	6 1.9 530 2	6 1.9 530 2	6 I.9 529 2	6 1.9 525 2	6 1.9 525 2	6 1.9 525 1	6 1.9 525 1	6 1.9 525 1	6 1.9 524 2	6 1.9 524 2	6 1.9 523 2	6 1.9 523 2	6 1.9 523	6 1.9 523 1	6 1.9 521 2 T456	6 1.9 521	6 1.9 521 2 S365	
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6 1.9 580 2 D86426 6 1.9 581 1 ERADP5 6 1.9 581 2 G83189	6 1.9 579 2 A86851 6 1.9 579 2 G84583 6 1.9 580 2 AB0994	6 1.9 577 2 T40297 6 1.9 578 2 T38775	6 1.9 574 2 T00245	6 1.9 570 2 197738	6 1.9 568 2 B86364	6 1.9 568 1 HNNZ41 6 1.9 568 2 D90525	6 1.9 566 2 T45162	6 1.9 562 2 C71473 6 1.9 564 2 S36637	6 1.9 562 2 AH2084	6 1.9 560 1 JX0153 6 1.9 562 1 HMIV2	6 1.9 559 2 T22179	6 1.9 555 2 TZ6413	6 1.9 554 2 ACO760	6 1.9 554 2 A56111	6 · 1.9 553 2 T45596	6 1.9 553 1 T02139	6 1.9 551 2 T22121	6 1.9 550 2 E84484	6 1.9 550 2 G95359	6 1.9 549 2 S37914	6 1.9 548 2 T36881	6 1.9 548 2 B46101	6 1.9 547 2 B96530	6 1.9 546 2 T19139	6 1.9 546 2 AC2368	6 1.9 544 2 841626	6 1.9 541 2 A87595	6 1.9 540 2 AC2353	6 1.9 540 2 T47858	6 1.9 538 2 A57624	6 1.9 538 2 AG3295	6 1.9 536 2 B46230	6 1.9 535 2 A46101	6 1.9 531 2 A95918	6 1.9 531 2 A98287	6 1.9 530 2 T43089	6 1.9 530 2 D82412	6 1.9 529 2 T35966	6 1.9 525 2 AF3649	6 1.9 525 2 T48824	6 1.9 525 1 JUUZ72 6 1.9 525 2 249601	6 1.9 525 1 VHNZMH	6 1.9 525 1 A48556	6 1.9 524 2 T06021	6 1.9 524 2 \$46007	6 1.9 523 2 C84753 hv	6 1.9 523 2 A38101 pc	6 1.9 523 2 F71302 as	6 1.9 523 1 VHNZMV	6 1.9 521 2 T45608	6 1.9 521 2 A43319	6 1.9 521 2 S36571	
6 1.9 580 2 D86426 6 1.9 581 1 ERADP5 6 1.9 581 2 G83189	6 1.9 579 2 A86851 6 1.9 579 2 G84583 6 1.9 580 2 AB0994	6 1.9 577 2 T40297 6 1.9 578 2 T38775	6 1.9 574 2 T00245	6 1.9 570 2 197738	6 1.9 568 2 B86364	6 1.9 568 1 HNNZ41 6 1.9 568 2 D90525	6 1.9 566 2 T45162	6 1.9 562 2 C71473 6 1.9 564 2 S36637	6 1.9 562 2 AH2084	6 1.9 560 1 JX0153 6 1.9 562 1 HMIV2	6 1.9 559 2 T22179	6 1.9 555 2 TZ6413	6 1.9 554 2 ACO760	6 1.9 554 2 A56111	6 · 1.9 553 2 T45596	6 1.9 553 1 T02139	6 1.9 551 2 T22121	6 1.9 550 2 E84484	6 1.9 550 2 G95359	6 1.9 549 2 S37914	6 1.9 548 2 T36881	6 1.9 548 2 B46101	6 1.9 547 2 B96530	6 1.9 546 2 T19139	6 1.9 546 2 AC2368	6 1.9 544 2 841626	6 1.9 541 2 A87595	6 1.9 540 2 AC2353	6 1.9 540 2 T47858	6 1.9 538 2 A57624	6 1.9 538 2 AG3295	6 1.9 536 2 B46230	6 1.9 535 2 A46101	6 1.9 531 2 A95918	6 1.9 531 2 A98287	6 1.9 530 2 T43089	6 1.9 530 2 D82412 chaperon	6 1.9 529 2 T35966 probable	6 1.9 525 2 AF3649 multidru	6 1.9 525 2 T48824	6 1.9 525 1 JUUZ72 6 1.9 525 2 249601	6 1.9 525 1 VHNZMH	6 1.9 525 1 A48556	6 1.9 524 2 T06021	6 1.9 524 2 \$46007	6 1.9 523 2 C84753 hv	6 1.9 523 2 A38101 potassium	6 1.9 523 2 F71302 asparagin	6 1.9 523 I VHNZMV nucleocapi	6 1.9 521 2 T45608 hypothetic	6 1.9 521 2 A43319 chromaffin	6 1.9 521 2 S36571	
6 1.9 580 2 6 1.9 581 1 6 1.9 581 2	6 1.9 579 2 A86851 6 1.9 579 2 G84583 6 1.9 580 2 AB0994	6 1.9 577 2 T40297 6 1.9 578 2 T38775	6 1.9 574 2 T00245	6 1.9 570 2 197738	6 1.9 568 2 B86364	6 1.9 568 1 HNNZ41 6 1.9 568 2 D90525	6 1.9 566 2 T45162	6 1.9 562 2 C71473 6 1.9 564 2 S36637	6 1.9 562 2 AH2084	6 1.9 560 1 JX0153 6 1.9 562 1 HMIV2	6 1.9 559 2 T22179	6 1.9 555 2 TZ6413	6 1.9 554 2 ACO760	6 1.9 554 2 A56111	6 · 1.9 553 2 T45596	6 1.9 553 1 T02139	6 1.9 551 2 T22121	6 1.9 550 2 E84484	6 1.9 550 2 G95359	6 1.9 549 2 S37914	6 1.9 548 2 T36881	6 1.9 548 2 B46101	6 1.9 547 2 B96530	6 1.9 546 2 T19139	6 1.9 546 2 AC2368	6 1.9 544 2 841626	6 1.9 541 2 A87595	6 1.9 540 2 AC2353	6 1.9 540 2 T47858	6 1.9 538 2 A57624	6 1.9 538 2 AG3295	6 1.9 536 2	6 1.9 535 2 A46101	6 1.9 531 2 A95918	6 1.9 531 2 A98287	6 1.9 530 2 T43089	6 1.9 530 2 D82412 chaperon	6 1.9 529 2 135966 probable se	6 1.9 525 2 AF3649 multidrug r	6 1.9 525 2 T48824 hypothetica	6 1.9 525 1	6 1.9 525 1 VHNZMH nucleocapsi	6 1.9 525 1 A48556 nucleocapsi	6 1.9 524 2 T06021 hypothetica	6 1.9 524 2 S46007 hypothetica	6 1.9 523 2 C84753 hypothetical	6 1.9 523 2 A38101 potassium	6 1.9 523 2 F71302 asparagin	6 1.9 523 I VHNZMV nucleocapi	6 1.9 521 2 T45608	6 1.9 521 2 A43319 chromaffin	6 1.9 521 2 S36571	

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Conserved hypothetical protein ykuD - Bacillus subtilis
CySpecies: Bacillus subtilis
CySpecies: Bacillus subtilis
CySpecies: Bacillus subtilis
CySpecies: A69865
CyAccession: A69865
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C; Bron, S.; Brouellet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chc
A; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
R;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuel,
Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Porretelle
R;eger, M.; Tamakoshi, A.; Tanaka, T.; Teopstra, P.; Tognoni, A.; Sadaie, Y.; Sato, T.; Senion,
A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.; Tosato, V.; Uchiyama,
A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A;Seatus: preliminary; nucleic acid sequence not shown; translation not shown
A;Esteus: DNA
A;Residues: 1-164 < KUN's
A;Esteus: Strain 168
C:Genetics:
hypothetical protein BH3888 [imported] - Bacillus halodurans (strain C-125) C;Species: Bacillus halodurans C;Species: Bacillus halodurans C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001 C;Accession: H84135
                                                           RESULT
H84135
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Best Local Similarity
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5883
5887
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5991
5998
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%; Pred. No. 5.5
0; Mismatches
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A98112
A96955
AC1644
AC1644
T45618
T456972
T51712
S50972
T51712
C83650
D71391
D71391
D783540
AB12366
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hypothetical prote
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ABC transporter (A
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RESULT 4
T52340
cell wall-plasma membrane linker protein homolog [imported] - Arabidopsis thaliana (;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Accession: T52340
R;Goo, J.H.; Park, A.R.; Park, W.J.; Park, O.K.
Plant Mol. Biol. 41, 415-423, 1999
A;Title: Selection of Arabidopsis genes encoding secreted and plasma membrane prot A;Reference number: Z25437; MUID:20064977; PMID:10598107
A;Reference number: Z25437; MUID:20064977; PMID:10598107
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                            A;Cross-references:
C;Genetics:
A;Note: CWLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R; Pauley, A.

R; Pauley, A.

Rubmitted to the EMBL Data Library, November 1994
A; Description: The sequence of S. cerevisiae cosmid 8003.
A; Reference number: $50366
A; Accession: $50385
A; Molecule type: DNA
A; Residues: 1-244 < PAUD
A; Cross-references: EMBL:U17243; NID:g596030; PIDN:AAB67346.1;
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Gene: MIPS:YLR301w
A;Cross-references: SGD:S0004292
A;Map position: 12R
C;Superfamily: Saccharomyces cer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 3

$50385

hypothetical protein YLR301w - yeast (Saccharomyces cerevisiae)
hypothetical protein t8003.2

N;Alternate names: hypothetical protein L8003.2

C;Species: Saccharomyces cerevisiae

C;Date: 13.40n-1995 #sequence_revision 20-Feb-1995 #text_change

C;Accession: $50385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hiran Nucleic Acids Res. 28, 4317-4331, 2000

A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and c A;Recession: H84135

A;Accession: H84135

A;Accession: H84135

A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-227 <STOo
A;Cross-references: GB:AP001520; GB:BA000004; NID:g10176401; PIDN:BAB07607.1; GSPDB:GN00.
A;Experimencal source: strain C-125
            Query Match
Best Local S
Matches 8
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A;Gene: BH3888
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Matches 8
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       Similarity 100
8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Saccharomyces cerevisiae hypothetical protein YLR301w
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ilarity 100.0%;
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2.5%; Scu
100.0%; Pr
~ 've 0;
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       Score 8; DB 2;
Pred. No. 9.4;
0; Mismatches
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; Pred. No. 7.
0; Mismatches
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0; Mismatches
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A;Resloues: 020-200 A;Rross-references: EMBL:Z71519
A;Cross-references: EMBL:Z71519
A;Experimental source: strain S288C
R;Holtzman, D.A.; Yang, S.; Drubin, D.G.
J. Cell Biol. 122, 635-644, 1993
A;Title: Synthetic-lethal interactions identify two novel
A:Peference number: A40673; MUID:93328765; PMID:8335689
                                                                                                                                                                          A;Cross-references: GB:Z22811; NID:g311412; PIDN:CAA80464.1; PID:g311413 R;Yoon, H.; Donahue, T.F. submitted to the EMBL Data Library, March 1994 A;Description: DNA sequence of ufg1 gene in yeast. A;Reference number: S61932 A;Accession: S61932
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Biol. 31, 771-781, 1996 A;Title: Transcripts of a gene encoding a putative cell wall-plasma membran. A;Reference number: S71558, MUID:96400032; PMID:8806408 A;Accession: S71558 A;Molecule type: DNA A;Paccession: S71558 A;Molecule type: DNA A;Paccession: S71558 DNA A;Paccession: S71558 DNA A;Paccession: S71558 DNA A;Paccession: S71558 DNA A;Paccession: S71558 DNA A;Paccession: S71558 DNA A;Paccession: S71558 DNA A;Paccession: S71558 DNA A;Paccession: S71558 DNA A;Paccession: S71558 DNA A;Paccession: S71558 DNA A;Paccession: S71558 DNA A;Paccession: S71558 DNA A;Paccession: S71558 DNA A;Paccession: S71558 DNA A;Paccession: S71558 DNA A;Paccession: S71558 DNA A;Paccession: S71558 DNA A;Paccession: S71558 DNA A;Paccession: S71558 DNA A;Paccession: S71558 DNA A;Paccession: S71558 DNA A;Paccession: S71558 DNA A;Paccession: S71558 DNA A;Paccession: S71558 DNA A;Paccession: S71558 DNA A;Paccession: S71558 DNA A;Paccession: S71558 DNA A;Paccession: S71558 DNA A;Paccession: S71558 DNA A;Paccession: S71558 DNA A;Paccession: S71558 DNA A;Paccession: S71558 DNA A;Paccession: S71558 DNA A;Paccession: S71558 DNA A;Paccession: S71558 DNA A;Paccession: S71558 DNA A;Paccession: S71558 DNA A;Paccession: S71558 DNA A;Paccession: S71558 DNA A;Paccession: S71558 DNA A;Paccession: S71558 DNA A;Paccession: S71558 DNA A;Paccession: S71558 DNA A;Paccession: S71558 DNA A;Paccession: S71558 DNA A;Paccession: S71558 DNA A;Paccession: S71558 DNA A;Paccession: S71558 DNA A;Paccession: S71558 DNA A;Paccession: S71558 DNA A;Paccession: S71558 DNA A;Paccession: S71558 DNA A;Paccession: S71558 DNA A;Paccession: S71558 DNA A;Paccession: S71558 DNA A;Paccession: S71558 DNA A;Paccession: S71558 DNA A;Paccession: S71558 DNA A;Paccession: S71558 DNA A;Pa
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N;Alternate names: MOP2 protein; protein N1102; protein YNL243w; UFG1 protein
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C;Superfamily: hydroxyprollne-rich glycoprotein
F;1-27/Domain: signal sequence #status predicted <SIG>
F;28-376/Product: probable cell wall-plasma membrane linker protein PRP #sta
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A;Residues: 1-343,'A',345-968 <HOL>
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A;Accession: B40673
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A;Residues: 820-968 <PAN>
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A; Residues: 1-968 <SAI>
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type: DNA
: 327-343,'A',345-559,'R',561-886,'NTVP',891,'MLPMHAEVWVTTSW',904 <YOO>
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A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis sspa; Reference number: A86625; MUID:21235186; PMID:11337471 A;Accession: H86885
                                                                                                                                                                                                                                                                                                                                                                                                         50S ribosomal protein L24 [imported] - Lactococcus lactis subsp. lactis (st C;Species: Lactococcus lactis subsp. lactis C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001 C;Accession: H86885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yeast 12, 1071-1076, 1996
A;Title: The DNA sequence of cosmid 14-5 from chromosome XIV reveals
A;Reference number: S72073; MUID:97051596; PMID:8896273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: DNA
A;Residues: 820-968 <PAW>
A;Residues: 820-968 <PAW>
A;Cross-references: EMBL: 269381; NID:g1183970; PIDN:CAA93355.1; PID:e221951; PID:g1183971
a;Cross-references: EMBL: 269381; NID:g1183970; Valle, G.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-51, 'A', 53-343, 'A', 345-968 <NAS>
A; Residues: 1-51, 'A', 53-343, 'A', 345-968 <NAS>
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J. Biol. Chem. 270, 6815-6823, 1995
A;Title: MOP2 (SLA2) affects the abundance of the plasma membrane
A;Reference number: S64652; MUID:95204480; PMID:7896828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Keywords: transmembrane protein
F;771-787/Domain: transmembrane #status predicted
                                                                                          C; Superfamily: Escherichia coli ribosomal protein
                                                                                                                                                                      A; Experimental source: strain
                                                                                                                                                                                                                                                                                                                                                                 Genome Res. 11,
                                                                                                                                                                                                                                                                                                                                                                                   R; Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Map position:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Gene: SGD:SLA2; UFG1; END4; MOP2
A;Cross-references: MIPS:YNL243w;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:Z69381; NID:g1183970; PIDN:CAA93355.1; PID:e221951; PID:g1183971
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1996
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A;Experimental source: strain 117-8A
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                                                                                                                                             Genetics:
                                                                                                                                                                      ;Cross-references: GB:AE005176; PID:g12725141; PIDN:AAK06186.1; 
;Experimental source: strain IL1403
                                                                                                                                                                                                                                                               Status: preliminary
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                                             Query Match
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                                                                                                                                                                                                                 1-101 <STO>
Similarity 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                               731-753,
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                      Score 7;
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                                             Length 101;
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279 VKTGDTV 285

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A; Map position: 1L
C; Genetics: <RP2>
A; Gene: SPCC1322.11
A; Map position: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ribosomal protein L17 - fission yeast (Schizosaccharomyces pombe)
N/Alternate names: 60s ribosomal protein
C;Species: Schizosaccharomyces pombe
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 20-Jun-2000
C;Accession: T11639; T40942
S;Mood, V; Barrell, B.G.; Rajandream, M.A.
Submitted to the EMBL Data Library, December 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Barrell, B.G.
submitted to the EMBL Data Library, August 1994
A;Reference number: S47445
A;Accession: S69849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:AL021046
R;Lucas, M.; Gaillardin, C.; Lyne, M.; Rajandream, M.A.; Barrell, submitted to the EMBL Data Library, January 1999
A;Reference number: Z21959
A;Accession: T40942
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C;Species: Saccharomyces cerevisiae
C;Dace: 23-Aug-1996 #sequence_revision 06-Sep-1996 #text_change 26-Aug-1999
C;Accession: S69849
                                                                                                                                                                                                                                                                                                                                                      A;Residues: 1-139 <LUC>
A;Cross-references: EMBL:AL035259; PIDN:CAA22864.1; GSPDB:GN00068; SPDB:SPCC1322.
A;Experimental source: strain 972h-; cosmid c1322
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A; Accession: T11639
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;Residues: 1-139 <WOO>
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Residues: 1-115 <BAR>
                                                                                                                                                                            ;Superfamily: Escherichia coli ribosomal protein
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                                                                                         Matches
                                                                                                        Query Match
Best Local
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  132 ASNAGTV 138
                                         241 ASNAGTV 247
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                                                                                      Similarity 7; Conserv
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                                                                                 2.2%; Score 7; DB 2; ilarity 100.0%; Pred. No. 46; Conservative 0; Mismatches
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o. 39;
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RESULT

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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-141 <DUZ>
A;Residues: 1-141 <DUZ>
A;Cross-references: EMBL:U80445; PIDN:AAB37800.1; GSPDB:GN00019; CESP:C50F2.7
A;Experimental source: strain Bristol N2; clone C50F2
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Gene: CESP:Y47D3A.20
A;Introns: 42/1; 55/1; 83/2; 122/1
C;Superfamily: Caenorhabditis elegans hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Molecule type: DNA A;Residues; 1-561 <WILL A;Cross-references: EMBL:AL117202; PIDN:CAB55080.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Matthews, L. submitted to the EMBL Data Library, October 1999 A;Reference number: Z21043
A;Accession: T31531
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submitted to the EMBL Data Library, November 1996
A;Description: The sequence of C. elegans cosmid C50F2.
A;Reference number: Z20684
A;Accession: T29781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein Y47D3A.20 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 18-Aug-2000
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                                      A;Status: preliminary; translated from A;Molecule type: DNA A;Residues: 1-177 <WILD
                                                                                                      submitted to the EMBL Data Library, October 1998 A;Reference number: Z20319 A;Accession: T27153
                                                                                                                                                                                                hypothetical protein Y54E2A.4 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Decies: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change C;Accession: T27153
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A;Cross-references: EMBL:AL032646; PIDN:CAA21686.1; GSPDB:GN00019; CESP:Y54E2A.4
A;Experimental source: clone Y54E2A
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Best Local Similarity
7; Conserv
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se: clone Y47D3A
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Pred. No. 46;
0; Mismatches
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A; Cross references: GB: U23797; NID:g1143815; PIDN:AAC44000.1; PID:g1143817
A; Cross references: GB: U23797; NID:g1143815; PIDN:AAC44000.1; PID:g1143817
C.; Brom, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chd A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E. Rature 390, 249-256, 1997
A; Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler 1ech, J.; Harwood, C.R.; Henaut, A.; Hibbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F. Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetell Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sakowska, A.; Seror akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, A.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.
                                                                                                                                                                                                                                                                                                                                                                                         R,Dartois, V.; Djavakhishvili, T.; Hoch, J.A.
J. Bacteriol. 178, 1178-1186, 1996
A;Title: Identification of a membrane protein involved in A;Reference number: JC6024; MUID:98165276; PMID:8576055
A;Accession: JC6024
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barr.
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A;Introns: 13/1; 86/3
C;Superfamily: Caenorhabditis elegans hypothetical
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C;Superfamily:
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A; Residues: 1-189 < KUR>
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A; Residues: 1-198 < DAR>
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Date: 31-Dec-1996 #sequence_revision 31-Dec-1996 #text_change 15-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Accession: JC6024; F69647
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                                                  A;Status: preliminary; nucleic acid sequence not
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  Molecule type: DNA
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Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J., Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, Rer, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arab A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: G86352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A;Reference number: A65580; MUID:98044033; PMID:9384377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Gene: kbaA
C;Keywords: membrane protein
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Science 277, 1453-1462, 1997

A;Title: The complete genome sequence of Escherichia coli A;Reference number: A64720; MUID:97426617; PMID:9278503 A;Accession: H65003
                                                                              R; Blattner, F.R.; Plunkett III, A.; Rose, D.J.; Mau, B.; Shao,
                                                                                                                                                                                                      RESULT
XMECDD
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                                                                                                                      Species: Escherichia coli;Date: 31-Dec-1988 #sequence_revision 17-Oct-1997 #text_change 01-Mar-2002;Date: 31-Dec-1988 #sequence_revision 17-Oct-1997 #text_change 01-Mar-2002;Accession: H65003; E29803
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                                                                                                       Burland, V.; Riley,
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.S.; Maiti, R.;
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: Dewar, K.;
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shown; translation

not

shown

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conserved hypothetical protein AF0441 - Archaeoglobus fulgidus
(;Species: Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #sequence-revision 05-Dec-1997 #text_change 22-Oct-1999
C;Accession: A69305
C;Accession: A69305
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C; Superfamily: dedD pro
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J. Biol. Chem. 262, 12209-12217, 1987
A;Title: The hisT-purf region of the Escherichia coli K-12 chromosome. Identification of A;Reference number: A29803; MUID:87308226; PMID:3040734
A;Accession: E29803
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R;Seeger, K.J.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajisubmitted to the EMBL Data Library, July 1999
A;Reference number: Z21567
A;Accession: T35071
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A;Residues: 'V',2-211 <NON>
C;Comment: This protein is encoded
                                                                                                                                           A;Molecule type: DNA
A;Residues: 1-225 <K
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Best Local S
Matches 7
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;Residues: 1-211 <SEE>
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                                                                                                                                                                                                  Status: preliminary; nucleic acid sequence not shown; translation
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       Similarity
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larity 100.0%;
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                                                                                                     GB:AE001074;
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       2.2%;
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                                                                                                 GB:AE000782; NID:g2689397; PIDN:AAB90793.1; PID:g26501
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RESULT 21
C84340
ABC transport protein [imported] - Halobacterium sp. NRC-1
ABC transport protein sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: C64340
R;Ng, W.V.; Kennedy, S.D.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; R;Ng, W.V.; Kennedy, S.D.; Mahairas, G.G.; Berquist, B.; Pan, M.; Maddocks, D.G.; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.
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RESULT 19
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C;Species: Methanobacterium thermoformicicum plasmid pFV1

C;Species: Methanobacterium thermoformicicum plasmid pFV1

C;Species: Methanobacterium thermoformicicum

C;Species: Methanobacterium thermoformicicum

C;Date: 17-Apr-193 #sequence_revision 17-Apr-1993 #text_change 22-Oct-1999

C;Accession: $30305; $26440

R,Nocelling, J.; van Beden, F.J.M.; Eggen, R.I.L.; de Vos, W.M.

Nucleic Acids Res. 20, 6501-6507, 1992

N,Title: Modular organization of related Archaeal plasmids encoding different restriction

A;Title: Modular organization of related Archaeal plasmids encoding different restriction

A;Reference number: $30302; MUID: 93126090; PMID: 1336177

A;Accession: $30305
                                                                                                                                                                                                                                                                                                                                        R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; chardson, D.; Ermolaeva, M.D.; Vamathevan, J.J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P. 1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
A;Recession: H82435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                conserved hypothetical protein VCA0634 [imported] - Vibrio cholerae (strain N16961 serogate; Vibrio cholerae
C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C;Accession: H82435
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H82435
                                                                                                                                                                                                                                   A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-241 <HEI>A;Cross-references: GB:AE004393;
A;Experimental source: serogroup
                                                                                                                                                                    A;Gene: VCA0634
A;Map position: 2
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;Residues: 1-227 <N
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                                                                                                          Query Match
Best Local
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                                                                                Similarity 7; Conserv
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ilarity 100.0%;
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O1; strain N16961; biotype
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Pred. No.
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Mismatches
                                                                                     ore 7; DB 2; red. No. 74; Mismatches
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                                                                                                                         Length 241;
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                                                                                                                                                                                                                                      PIDN:AAF96535.1;
El Tor
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                                                                                   Gaps
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D.G.;

Lasky, S G.; Jablor

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R; anonymous, The C. elegans sequencing various R; anonymous, The C. elegans sequence 282, 2012-2018, 1998
A; Title: Genome sequence of the nematode C. elegans: a particle genome at 2000; MUID: 99069613; PMID: 9851916
A; Rote: see websites genome. wustl.edu/gsc/C_elegans/ and A; Note: published errata appeared in Science 283, 35, 1: A, Accession: F89455
A, Accession: F89455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rroc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, A;Title: Genome sequence of Halobacterium species NRC-1.
A;Reference number: A84160; MUID:20504483; PMID:11016950
A;Accession: C84340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Recession: C70151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein F55A4.4 [imported] - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 10-May-2001 | sequence_revision 10-May-2001 | C;Accession: F89455
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Experimental source: strain B31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Residues: 1-259 <KLE>
A;Cross-references: GB:AE001146; GB:AE000783; NID:92688312; PIDN:AAC66791.1; PID:9268833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein BB0412 -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-249 <STO>
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                                                                              Cross-references:
                                                                                               Residues:
                                                                                                            Molecule
                                                                                                                                                                                                                                                                Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Nov-2001
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                                                                                                                                                                                                                                                                                                                                                                                       109
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                                                                                                            type: DNA
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                                                                        1-269 <STO>
erences: GB:chr_X;
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                                                                           PIDN:AAB07562.1; PID:g1519659; GSPDB:GN00028;
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 Score
 7;
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76;
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o. 79;
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35, 1999; Science 283, 2103, 1999; and
Length
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                                                                             CESP: F55A4.
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C;Species: Methanobacterium thermoautotrophicum
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change
C;Accession: D69184
                                                  RESULT 26
D69184
UTP-glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) MTH634 [similarity]
                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:AB007317; PIDN:AAL0042: C;Genetics: A;Gene: ABC-MSP C;Superfamily: maltose transport protein malG
                                                                                                                                                                                                                                                                                                                                                                                                                          A;Accession: H98073
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; A;Title: Genome of the Bacterium Streptococcus pneumoniae S.A;Reference number: A97872; MUID:21429245; PMID:11544234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein ABC-MSP [imported] - Streptococcus pneumoniae (strain C;Species: Streptococcus pneumoniae C;Species: Streptococcus pneumoniae C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 02-Nov-2001 C;Accession: H98073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: A;Map position: 10R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Rose, M.; Koetter, P.; Entian, K.D. submitted to the Protein Sequence Dat A;Reference number: $56848
A;Accession: $57134
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N;Alternate names: hypothetical prot
C;Species: Saccharomyces cerevisiae
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A; Residues: 1-283 < ROS>
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C;Accession:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: EMBL:Z49611; NID:g1015825; PIDN:CAA89641.1; PID:g1015826; GSPDB:GN00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteriol. 183,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    skins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.; .; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; .; Sun, P.M.; Winkler, M.B. acteriol. 183, 5709-5717, 2001
                                                                                                                                                      181
                                                                                                                                                                                         254 MDGASIV 260
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                                                                                                                                                      MDGASIV 187
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100.0%; Pred. No.
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   Mismatches
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03-Jun-2002

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C;Accession: S28264
R;Raz, R., Jose, M.; Moya, A.; Martinez-Izquierdo, J.A.; Puigdomenech, P. A;Title: Different mechanisms generating sequence variability are revealed in distinct A;Recession: S28264
A;Recession: S28264
A;Recession: S28264
A;Recession: S28264
A;Residues: 1-303 <RAZ>
A;Cross-references: EMBL:X63134; NID:922332; PIDN:CAA44844.1; PID:922333
C;Superfamily: hydroxyproline-rich glycoprotein
C;Keywords: glycoprotein; hydroxyproline
                                                                                                                                                                                                                                                                             hydroxyproline-rich glycoprotein - maize
C;Species: Zea mays (maize)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 24-Sep-1999
C;Accession: S28264
R;Raz, R.; Jose, M.; Moya, A.; Marring, i...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Genome: plasmid
C;Superfamily: probable pheromone-responsive protein
C;Keywords: plasmid replication
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-288/Product: hypothetical 30.5K protein #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 27
JH0204
hypothetical 30.5K protein precursor - Enterococcus faecalis plasmid pAM-beta-1
C;Species: Enterococcus faecalis
C;Date: 31-Dec:-1990 #sequence_revision 31-Dec:-1990 #text_change 21-Jul-2000
C;Accession: JH0204
R;Swinfield, T.J.; Oultram, J.D.; Thompson, D.E.; Brehm, J.K.; Minton, N.P.
A;Title: Physical characterisation of the replication region of the Streptococcus A;Reference number: PH0201; MUID:90236302; PMID:2110101
A;Accession: JH0204
A;Molecule type: DNA
A;Residues: 1-288 cSWI>
A;Cross:-reference. EMBI. V17003. NTD.-202041. ETDN.-202044.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A:Cross references: EMBL:X17092; NID:g3023041; PIDN:AAC38600.1; PID:g3023044
C:Comment: A number of structural features of this protein suggest a localization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.0%; Fred. No.
Matches 7; Conservative 0; Mismatc.
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C;Superfamily: Escherichia coli UTP-glucose-1-phosphate uridylyltransferase
C;Keywords: nucleotidyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:AE000844; GB:AE000666; NID:g2621707; PIDN:AAB85140.1; PID:g26217.
A;Experimental source: strain Delta H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-285 < MTH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ki, S.; Church, G.
J. Bacteriol. 179,
A; Title: Complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: func
A;Reference number: A69000; MUID:98037514; PMID:9371463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 2.2%; Score 7; Best Local Similarity 100.0%; Pred. No. Matches 7; Conservative 0; Mismatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Status: preliminary, nucleic acid sequence not shown, translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     191 ATGSSGV 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                            27 ATGSSGV 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 288;
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hypothetical protein Y44A6B.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
                                                                                                        RESULT
T26886
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                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary
A;Molecule type: DNA
A;Residuse: 1-315 <STO>
A;Cross-references: GB:AP00039
A;Experimental source: strain
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Matches
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Best Local
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A;Map position: I
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AE3325
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      167 KPTPTPP 173
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kinage [imported] - Buchnera sp. (strain APS)
C;Species: Buchnera sp.
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Mar-2001
C;Accession: G84936
R,Shigenobu, S; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.
Nature 407, 81-86, 2000
A;Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera
A;Accession: G84936
A;Accession: G84936
A;Accession: G84936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: Preliminary
A;Molecule type: DNA
A;Residues: 1-309 -KUR>
A;Cross-references: GB:AEE008917; PIDN:AAL51768.1; PID:g17982509;
A;Experimental source: strain 16M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    commi, competence lipoprotein [imported] - Brucella melitensis (strain 16M)

C;Becies: Brucella melitensis

C;Accession: AE3325

R,DelVecchio, V.G; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova

Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002

A;Title: The genome sequence of the facultative intracellular pathogen Brucella melite;

A;Scence, AB3253; PMID:1175688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.0%; Pred. No. 92;
Matches 7; Conservative 0; Mismatches
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         2.2%; Score 7; DB 2 ilarity 100.0%; Pred. No. 94; Conservative 0; Mismatches
                                                                                                                                   GB:AP000398; GSPDB:GN00144
ce: strain APS
                            DB 2;
o. 94;
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o. 91;
                                               Length 315;
       0; Indels
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Gaps
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A;Reference number: Z20280
A;Accession: T26886
                                                                                                                                                                                                  R;Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Volckaert, submitted to the EMBL Data Library, October 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: protein A; Residues: 27-43 < ST2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Stiefel, V.; Ruiz-Avila, L.; Raz, R.; Valles, M.P.; Gomez, J.; Pages, M.; Mar
Plant Cell 2, 785-793, 1990
A;Title: Expression of a maize cell wall hydroxyproline-rich glycoprotein gene
A;Reference number: JQ0985; MUID:93005673; PMID:2152127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R; Ainscough
                                   A;Cross-references: EMBL:AL031966; PIDN:CAA21450.1; GSPDB:GN00068; SPDB:SPCC1442.16c
                                                                                                            A; Molecule type: DNA
                                                                                                                                                      A; Accession: T40981
                                                                                                                                                                         A; Reference number: Z21961
                                                                                                                                                                                                                                                                                                              probable quinone oxidoreductase - fission yeast (Schizosaccharomyces pombe)
                                                                                                                                                                                                                                                                                                                                           T40981
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: DNA
A;Residues: 1-326 <WIL>
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                                                                                                                                                                                                                                                               Species: Schizosaccharomyces pombe
Date: 03-Dec-1999 #sequence_revision 03-Dec-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cross-references: GB:S45164; NID:g257040; PIDN:AAB23539.1; PID:g257041; Accession: PS0215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Molecule type: DNA
Residues: 1-328 <STI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Species: Zea mays (maize)
Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 24-Sep-1999
Accession: JQ0985; PS0215
                                                                                      Residues: 1-329 <LYN>
                                                                                                                              Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                               Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Experimental source: leaf Superfamily: hydroxyproline-rich glycoprotein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cross-references: EMBL:AL021491; PIDN:CAA16373.1; GSPDB:GN00023; CESP:Y44A6B.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
les 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
SPCC285.01c; SPDB:SPCC1442.16c
                                                                                                                                                                                                                                                                                                                                                                                                                               121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         167 KPTPTPP 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        221
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2.2%;
Similarity 100.0%;
7; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                               KPTPTPP 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   L.; Raz, R.; Valles, M.P.; Gomez, J.; Pages, M.; Martinez-Izo
                                                                                                                                                                                                Library,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 7; DB 2; Pred. No. 97; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
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RESULT 35
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A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallert lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.; Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A.; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel, Y., M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T. M.; Portetelle, Rieger, M.; Rivolta, C.; Rocha, B.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, A.; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror, A; Awthors: Schleich, S.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Wipat, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasunoto, K.; Yata, K.; Yoshida, K. A; Althors: Yoshikawa, H.; Zumanitein, E.; Yoshikawa, H.; Danchin, A. A; Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis. A, Reference number: A69580; MUID:98044033; PMID:9384377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: EMBL:D26185; NID:g467326; PIDN:BAA05224.1; PID:d1005766; PID:g467378
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1993
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Certer, C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chon, B.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Asture 390, 249-256, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mol. Microbiol. 6, 629-634, 1992
A;Title: Genes and their organization in the replication
A;Reference number: I40435; MUID:92204018; PMID:1552862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Bacillus subtilis
C;Species: Bacillus subtilis
C;Date: 12-Aug-1996 #sequence revision 12-Aug-1996 #text_change 21-Jul-2000
C:Accession: I40448; S66018; C70084; S18084
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                                                                                                                                                                                                                                                                A;Gene: yyaD
A;Start codon:
                                                                                                                                                                                                                                                                                                                                                                                       A;Residues: 1-338 <KUN>
A;Cross-references: GB:Z99124; GB:AL009126; NID:g2636442; PIDN:CAB16131.1; PID:g2636641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Title: Systematic sequencing of the 180 kilobase region of the Bacillus subtilis chrome A;Reference number: S65967; MUID:96051385; PMID:7584024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Accession: I40448; S66018; (R; Ogasawara, N.; Yoshikawa, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     문
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C;Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Status: preliminary; nucleic acid sequence not shown; translation not shown
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DNA Res. 1, 1-14, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         conserved hypothetical protein yyaD (replication origin region) - Bacillus subtilis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: DNA
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                                                                                                                                                                 Query Match
Best Local
                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                         Experimental source: strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Molecule type: DNA
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213 GLIFGVI 219
                                                               19 GLIFGVI 25
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                                                                                                                          Similarity 7; Conserv
                                                                                                                                                                                                                                                                   GTG
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ilarity 100.0%;
Conservative
                                                                                                                                 Conservative
                                                                                                                                                                 2.2%;
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Pred. No.
                                                                                                                                                                 Score 7; DB 2;
Pred. No. 1e+02;
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o. 97;
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                                                                                                                                                                                             Length 338;
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proline-rich protein TPRP-F1 - tomato
(;Species: Lycopersicon esculentum (tomato)
(;Date: 07-Apr-1994 #sequence revision 07-Apr-1994 #text_change 2
(;Date: 07-Apr-1994 #sequence revision 07-Apr-1994 #text_change 2
(;Accession: S19129; S16589; S16551
R;Salte, Y.; Keniggbuch, D.; Wachs, R.; Gruissem, W.; Barg, R.
Plant Mol. Biol. 18 407-409, 1992
A;Title: DNA bequence of the tomato fruit expressed proline-rich
A;Reference number: S19129; MUID:92119262; PMID:1731999
A;Accession: S19129
A;Molecule type: DNA
A;Residues: 1-346 <SAL>
A;Residues: 1-346 <SAL>
A;Residues: 1-346 <SAL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein C42D4.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change
A;Status: preliminary; translated A;Molecule type: DNA A;Residues: 1-339 < DUZ>
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R;Salts, Y.; Wachs, R.; Gruissem, W.; Barg, R.
Plant Mol. Biol. 17, 149-150, 1991
A;Title: Sequence coding for a novel proline-rich protein preferentially expressed
A;Reference number: S16589; MUID:91329722; PMID:1868217
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S19129
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A;Residues: 34-346 <SAW>
A;Residues: 34-346 <SAW>
A;Cross-references: EMBL:X57076; NID:g19520; PIDN:CAA40361.1;
A;Experimental source: cv. Arava; haplotype 2n
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Best Local S
Matches 7
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Accession: T34158
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Best Local (
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Gene: CESP:C42D4.6
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;Superfamily: hydroxyproline-rich glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                  ;Genetics:
;Gene: TPRP-F1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cross-references: EMBL:X61395; NID:g1669697; PIDN:CAA43666.1; Experimental source: cv. VFNT cherry
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                                                                                                                                                                                      190
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                                                                                                                                                                                                                        169 TPTPPVV 175
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                                                                                                                                                                                                                                                           2.2%; Score 7; DB:
llarity 100.0%; Pred. No. 1e-
Conservative 0; Mismatches
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/ 100.0%; Pr
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Pred. No. 1e.
0; Mismatches
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o. 1e+02;
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lo. 1e+02;
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Mol. Gen. Genet. 233, 252-259, 1992
A;Title: Different mechanisms generating sequence variability
A;Reference number: S22456; MUID:92293123; PMID:1603067
A;Reference: S22456
A;Molecule type: DNA
A;Residues: 1-350 <RAZ>
A;Residues: 1-350 <RAZ>
A;Cross-references: EMBL:X64173; NID:g22091; PIDN:CAA45514.1;
C;Keywords: glycoprotein; hydroxyproline
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AC0302
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A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
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AyVariety: strain J99
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AyVariety: strain J99
AyVariety: strain J99
AyVariety: strain J99
Bequence_revision 12-Feb-1999 #text_change 08-Oct-1999
C;Accession: G71958
Bequence_revision 12-Feb-1999 #text_change 08-Oct-1999
A;A;Accession: G71958
A;Accession: G71958
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C;Genetics:
A;Gene: YPO2474
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A; Residues: 1-351 < KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein jhp0220 - Helicobacter pylori (strain J99)
C;Species: Helicobacter pylori
                                                                                                                                      A;Gene:
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Best Local S
Matches 7
   Query Match
Best Local S
Matches 7
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Best Local Similarity 100.0%;
Matches 7; Conservative
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                                                                                                                                                                                                     ;Molecule type: DNA
;Molecule type: 1-355 ARN>
;Cross-references: GB:AE001460; GB:AE001439; NID:g4154733; PIDN:AAD05807.1;
;Experimental source: strain J99
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R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bradman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, I.Cry, S.; Olson, M.V.

Nature 406, 959-964, 2000

A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathological complex: A82950; MUID:20437337; PMID:10984043

A;Reference number: A82950; MUID:20437337; PMID:10984043

A;Accession: H83202

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-367 <STO>

A;Cross-references: GB:AE004775; GB:AE004091; NID:g9949692; PIDN:AAG06935.1; GSPDB:GN001

A;Experimental source: strain PA01
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Search completed: July 8, 2003, 11:21:37 Job time : 65 secs
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A;Gene: algL; PA3547
C;Superfamily: Pseudomonas aeruginosa poly(beta-D-mannuronate) lyase
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C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: H83202
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EDUCATION: THE CYS-148 OF THE PRIMARY SITE OF CANDALLY INVESTED THE PRIMARY SITE OF SUBSECUENCE FROM N.A.

2. Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.

2. I SUBMITTED (MAY-1999) to the EMBL/GenBank/DDBJ databases.

2. I SUBMITTED (MAY-1999) to the EMBL/GenBank/DDBJ databases.

2. I SUBMITION SYSTEM SITE ANTIOLIDARY WHICH CONSTITUTES AND TABALIZALS. CAN PROVIDE PROTECTION AGAINST SULFUR-CONTAINING OXIDATION SYSTEM BUT CONTAINING OXIDATION SYSTEM BUT CONTAINING OXIDATION SYSTEM BUT CONTAINING OXIDATION.

2. I SUBUNIT: HOMODIMER; DISULFIDE-LINKED, UPON OXIDATION.

2. I SUBCELLULAR LOCATION: CYCOPLASMIC.

2. I SUBCELLULAR LOCATION: CYCOPLASMIC.

3. I SUBCELLULAR LOCATION: CYCOPLASMIC.

3. I SUBCELLULAR LOCATION: CYCOPLASMIC.

3. I SUBCELLULAR LOCATION: CYCOPLASMIC.

4. (2) O(2), AND THE OXIDIZED CYS-48 (PROBABLY CYS-SOH) RAPIDLY REACTS WITH CYS-169-SH OF THE OTHER SUBUNIT TO FORM AN INTERMOLECULAR DISULFIDE. THIS DISULFIDE IS SUBSEQUENTLY REDUCED BY THIOREDOXIN.

3. INTERMOLECULAR DISULFIDE. THIS DISULFIDE IS SUBSEQUENTLY REDUCED BY THIOREDOXIN.
Query Match 2.5%; Score 8; DB Best Local Similarity 100.0%; Pred No. 1. Matches 8; Conservative 0; Mismatches
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Pro; IPR000866; AhpC-TSA.
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KV4A_MOUSE
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LYC_CHRAM
LYC_LOPLE
LYC_PAVCR
LYC_SYRRE
LYC_SYRRE
LYC_SYRSO
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RMI4 ACACA
UMP1 SCHPO
Y207 AERPE
BCCP STRMU
CLP1 DROME
YQJF ECOLI
AGSW YULUU
C79A LOCMI
                                                                                                                                                                                                                                                                                                                                                                                                                Saccharomycotina; Saccharomycetes; Saccharomycetales; Candida.
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           DB 1;
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                      Length 196;
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P01636
P01706
P00706
P124364
P128349
P14733
P817711
Q87556
Q9746767
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P129339
P42619
P455860
P45586
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pavo crista
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schizosacch
seropyrum p
streptococc
drosophila
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Z69381; CAA93355.1;

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RA Sgource J., Peat N., Hayles J., Baker S., Basham D., Bownan S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cromin A., Davis P., Feltwell T., Praser A.,
RA Gollins M., Connor R., Cromin A., Davis P., Feltwell T., Praser A.,
RA Gollins M., Connor R., Cromin A., Davis P., Feltwell T., Hodgson G.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA Holroyd S., Hornsby T., Howarth S., McDonald S., McDenald S.,
RA James K., Jones M., Leather S., McDonald S., McDenald S.,
RA James K., Jones M., Leather S., McDonald S., McDenald S.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Noutherford K., Rutter S., Saunders D., Geeger K., Sharp S.,
RA Rutherford K., Rutter S., Saunders D., Geeger K., Sharp S.,
RA Rutherford K., Rutter S., Saunders D., Geeger K., Sharp S.,
RA Rutherford K., Rutter S., Suares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Weltjens I., Volkaert G., Aert R., Robben J., Grymonprez B.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottler S.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottler S.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottler S.,
RA Gallbert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Morseno S., Armstrong J., Forsburg S.L.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RT "The genome sequence of Schizosaccharomyces pombe.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DR FTT FTT SQ
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60S ribbsomal protein L23.

(RPL23A OR RPL23 OR SPAC3G9.03) AND (RPL23B OR SPCC1322.11).

Schizosaccharomyces pombe (Fission yeast).

Schizosaccharomycetes;

Bukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RL23_SC
042867;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=21848401; PubMed=11859360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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Pfam; PF01608; I_LWEQ; 1.
ProDom; PD011820; ILWEQ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            L5-DEC-1998 (Rel. 37, Created)
L5-DEC-1998 (Rel. 37, Last sequence update)
L5-JUN-2002 (Rel. 41, Last annotation update)
50S ribosomal protein L23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Structural protein;
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InterPro; IPR001026; ENTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR002558; ILWEQ.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (RPL23A AND RPL23B).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rajandream M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              s; Pred. No. 7.4
0; Mismatches
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P -> A (IN REF. 2).

A -> R (IN REF. 4).

A -> R (IN REF. 3).
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TLKTAEMEQQVEILKLEQSLSNARKRLGEIRRHAYYNQDDD
-> NTVPKMLPMHAEVMVTTSWV (IN REF. 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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5. 7.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lyne M., Lyne R.,
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Best Local S
Matches 7
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Best Local Similarity
Matches 7; Conserv
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01-FEB-1996 (Rel. 3
15-JUL-1999 (Rel. 3
Hypothetical 18.6 k
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             _BUGGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YC67_EUGGR
P48337;
                                                             EMBL; Z11874; -; NOT_ANNOTATED_CDS.
EMBL; X70810; CAASO117.1; -
InterPro; IPR001700; RNA pol_A bac.
Pfam; PF01000; RNA pol_A bac; 1.
Chloroplast; Hypothetical protein.
SEQUENCE 161 AA; 18606 MW; 3779
                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentaties requires a license agreement (See http://www.isb-sib.ch/an or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                        Hallick R.B., Hong L., Drager R.G., Favreau M.R., Monfort Orsat B., Spielmann A., Stutz E.; "Complete sequence of Euglena gracilis chloroplast DNA."; Nucleic Acids Res. 21:3537-3544(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00238; Ribosomal_L14; 1.
ProDom; PD001093; Ribosomal_L14; 1.
PROSITE; PS00049; RIBOSOMAL_L14; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Euglenozoa;
NCBI_TaxID=3039;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chloroplast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ribosomal protein; Multigene family. SEQUENCE 139 AA; 14882 MW; D8C9F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AL021046; CAA15912.1; -. EMBL; AL035259; CAA22864.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -1- MISCELLANEOUS: THERE ARE TWO GENES FOR L23 IN S.POMBE.
-1- SIMILARITY: BELONGS TO THE L14P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 415:871-880(2002).
                                                                                                                                                                                                                                                                                                         -!- SIMILARITY: BELONGS TO THE YCF67 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=93347989; PubMed=8346031;
                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000218; Ribosomal_L14.
Local Similarity res 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 ASNAGTV 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              132 ASNAGTV 138
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 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    38,
kDa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
Last sequence update)
Last annotation update)
protein ycf67 (ORF161).
                  2.2%; Score 7;
100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Euglenida; Euglenales; Euglena.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 7; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         D8C9A8903225F4AD CRC64;
                                                                377944A5C814949C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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                                 DB 1;
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RX MEDLINE=98044033; PubMed=9384377;
RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A.M., Borchert S.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A.M., Borchert S.,
RA Borriss R., Boursler L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Borriss R., Boursler L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Fritz C., Fujita M., Dusterhoft A., Ebrilch S.D., Emmerson P.T.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galieron N.,
RA Guiseppi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,
Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Kurita K., Lapidus A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Noone D., O'Reilly M., Ogawa K., O'giwara A., O'dega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Parro V., Pohl T.M., Portetelle B., Rappoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
RA Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B S., Soldo B.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Sato T., Scanlan S., Valeiche T., Takahashi H., Takemaru K.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Tarkahashi H., Takemaru K.,
RA Winters P., Wipat A., Yamdenbol M., Vannier F., Vassarotti A.,
RA Winters P., Wipat A., Yamdenbol M., Vannier F., Vassarotti A.,
RA Winters P., Wipat A., Yamdenbol M., Vannier F., Vassarotti A.,
Ra Minters P., Wipat A., Yamden K., Vassarotti A.,
Ra Paro C., Charlet B., Rappoport G., Park R.,
Ra Kanda H., Charlet B., R
SEQUENCE OF 1-91 FROM N.A. STRAIN=168; MEDLINE=90257591; PubMed=2517635;
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01-OCT-1996
15-JUN-2002
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STRAIN=168 / JH642;

MEDLINE=96.165276; PubMed=8576055;

MEDLINE=96.165276; PubMed=8576055;

MEDLINE=96.165276; PubMed=10.10.1 A.;

"Identification of a membrane protein involved in activation wind pathway to sporulation in Bacillus subtilis.";

J. Bacteriol. 178:1178-1186 (1996)
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Yasumoto K., Liu H., Jeong S.M., Ohashi Y., Kakinuma S.
Tanaka K., Kawamura F., Yoshikawa H., Takahashi H.;
"Sequence analysis of a 50 kb region between spooth and Bacillus subtilis chromosome ", and the subtilis subtilius subtilis chromosome ", and the subtilius subtilius subtilius subtilius subtilius subtilius subtilius subtilius subtilius subtilius subtilius subtilius chromosome ", and subtilius subtilius subtilius chromosome ", and subtilius subtilius chromosome ", and subtilius subtilius chromosome ", and subtilius subtilius chromosome ", and subtilius subtilius chromosome ", and subtilius subtilius chromosome ", and subtilius subtilius chromosome ", and subtilius subtilius chromosome ", and subtilius subtilius chromosome ", and subtilius subtilius chromosome ", and subtilius subtilius chromosome ", and subtilius subtilius subtilius chromosome ", and subtilius subtilius subtilius subtilius subtilius subtilius subtilius subtilius subtilius subtilius subtilius subtilius subtilius subtilius subtilius subtilius subtilius subtilius subtilius subtilius subtilius subtilius subtilius subtilius subtilius subtilius subtilius subtilius subtilius subtilius subtilius subtilius subtilius subtilius subtilius subtilius subtilius subtilius subtilius subtilius subtilius subtilius subtilius subtilius subtilius subtilius subtilius subtilius subtilius subtilius subtilius subtilius subtilius subtilius subtilius subtilius subtilius subtilius subtilius subtilius subtilius subtilius subtilius subtilius subtilius subtilius subtilius subtilius subtilius subtilius subtilius subtilius subtilius subtilius subtilius subtilius subtilius subtilius subtilius subtilius subtilius subtilius subtilius subtilius subtilius subtilius subtilius subtilius subtilius subtilius subtilius subtilius subtilius subtilius subtilius subtilius subtilius subtilius subtilius subtilius subtilius subtilius subtilius subtilius subtilius subtilius subtilius subtilius subtilius subtilius subtilius subtilius subtilius subtilius subt
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STRAIN-K12 / MG1655;
MEDILINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A.
Riley M., Collado-Vides J., Glasner J.D.,
Gregor J., Davis N.W., Kirkpatrick H.A.,
MRu B., Shao Y.;
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01-MAR-1989
16-OCT-2001
16-OCT-2001
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STRALN=K12;
STRALN=K12;
MEDLINE=87308226; PubMed=3040734;
MODRET M.L., Marvel C.C., Tolan D.R.;
"The hisT-purf region of the Escherichia contentification of additional genes of the J., Biol. Chem. 262:12209-12217(1987).
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SEQUENCE FROM N.A.
STRAIN=K12;
MEDLINE=97349980; PubMed=9205837;
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Bacteria; Proteobacteria;
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DEDD OR B2314.
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"Cloning and sequencing of the gerb gene of Bacillus
J. Gen. Microbiol. 135:3431-3445(1989).
- I- FUNCTION: INVOLVED IN THE ACTIVATION OF THE KINB
OF SPORULATION.
- I- SUBCELLULAR LOCATION: Integral membrane protein.
                                                                                                                                                                                 Science
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                                                                                                                                                                            complete genome sequence
nce 277:1453-1474(1997).
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42 62 POTENTIAL.
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173 193 POTENTIAL.
198 AA; 22775 MW; 24917B51
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.D., Rode C.K., Mayhew
A., Goeden M.A., Rose I
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SEQUENCE
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STRAIN-DSM 3848 / THF;
MEDLINE=93126090; PubMed=1336177;
MODELLINE=93126090; PubMed=1336177;
Noelling J., van Beden F.J.M., Eggen R.I.L., de Vos W.M.;
"Modular organization of related Archaeal plasmids encoding restriction-modification systems in Methanobacterium
                                                                                                                               the European Bioinformatics Institute. The use by non-profit institutions as not removed. modified and this statement is not removed. entitles requires a license agreement (See lor send an email to license@isb-sib.ch).
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01-APR-1993 (Rel. 25, Last sequence update)
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Hypothetical 24.7 kDa protein (ORFSA).
Methanobacterium thermoformicicum.
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EMBL; AE000320; AAC75374.1; ALT INIT.
EMBL; D90862; BAA16162.1; ALT_INIT.
EMBL; D90863; BAA16170.1; ALT_INIT.
EMBL; D90863; KMECDD.
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"Construction of a contiguous 874-kb sequence of the Escherichia coli-
"Construction of a contiguous 80.0-68.8 min on the linkage map and -K12 genome corresponding to 50.0-68.8 min on the linkage map and panalysis of its sequence features.";
                                                                                   EMBL; X68366; CAA48429.1;
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Methanobacteriaceae; Methanothermobacter.
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Tagami H., Takahashi H., Takeda J.,
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Itoh T., Kimura S., Kitagawa M., Makino K., Miki T., Mitsuhashi N
Mizobuchi K., Mori H., Nakade S., Nakamura Y., Nashimoto H.,
Oshima T., Oyama S., Saito N., Sampei G., Satoh Y., Sivasundaram
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Best Local (
                                                                                                                                                            P50177;

01-OCT-1996 (Rel. 34, Created)

01-OCT-1996 (Rel. 34, Last sequence update)

16-OCT-2001 (Rel. 40, Last annotation update)

17ype II restriction enzyme LlaDCHI (EC 3.1.21

LLADCHI) (R.LLADCHI) (LlaII).

LLADCHIR OR LLAIIC.

Lactococcus lactis (subsp. cremoris) (Streptone Plasmid pSRQ700.

Bacteria; Firmicutes; Lactobacillales; Streptone Plasmid pSRQ700.
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Hypothetical
SEQUENCE 22
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01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Hypothetical 32.2 kDa protein in CPA2-NNF1 intergenic region
YJR111C OR J2009.
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Rose M., Koetter P., Entian K.D.;
Submitted (SEP-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
MEDLINE=95314272; PubMed=7793939; Moineau S., Walker S.A., Vedamuthu "Cloning and sequencing of LlaDCHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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                                                                            STRAIN=DCH-4
                                                                                              SEQUENCE FROM N.A.
                                                                                                                                               NCBI_TaxID=1359;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=4932;
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hetical protein; Plasmid.
NCE 227 AA; 24681 MW;
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                                                                                                                                                                                                                                                                                         ion update)
(EC 3.1.21.4)
  E.R., Vandenbergh P.A.; restriction/modification
                                                                                                                                                                                                                       (Streptococcus cremoris)
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P57168;
15-JUN-2002
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                                                                                                                                               EMBL; AP001118; BAB12783.1; -.
Interpro; IPR002173; PfkB.
Pfam, PP002294; pfkB; 1
PROSITE; PS00583; PFKB_KINASES_1; 1.
PROSITE; PS00584; PFKB_KINASES_2; FALSE_NEG.
PROSITE; PS00584; PFKB_KINASES; Kinase; Compleyothetical protein; Transferase; Kinase; Compleyothetical protein; Tansferase; Kinase; Compleyothetical protein; Tansferase; Kinase; Compleyothetical protein; Tansferase; Kinase; Compleyothetical protein; Tansferase; Kinase; Compleyothetical protein; Tansferase; Kinase; Compleyothetical protein; Tansferase; Kinase; Compleyothetical protein; Tansferase; Kinase; Compleyothetical protein; Tansferase; Kinase; Compleyothetical protein; Tansferase; Kinase; Compleyothetical protein; Tansferase; Kinase; Compleyothetical protein; Tansferase; Kinase; Compleyothetical protein; Tansferase; Kinase; Compleyothetical protein; Tansferase; Kinase; Compleyothetical protein; Tansferase; Kinase; Compleyothetical protein; Tansferase; Kinase; Compleyothetical protein; Tansferase; Kinase; Compleyothetical protein; Tansferase; Kinase; Compleyothetical protein; Tansferase; Kinase; Compleyothetical protein; Tansferase; Kinase; Compleyothetical protein; Tansferase; Kinase; Compleyothetical protein; Tansferase; Kinase; Compleyothetical protein; Tansferase; Kinase; Compleyothetical protein; Tansferase; Kinase; Compleyothetical protein; Tansferase; Kinase; Compleyothetical protein; Tansferase; Kinase; Compleyothetical protein; Tansferase; Kinase; Compleyothetical protein; Tansferase; Kinase; Compleyothetical protein; Tansferase; Kinase; Compleyothetical protein; Tansferase; Kinase; Compleyothetical protein; Tansferase; Kinase; Compleyothetical protein; Tansferase; Kinase; Compleyothetical protein; Tansferase; Kinase; Compleyothetical protein; Tansferase; Kinase; Compleyothetical protein; Tansferase; Compleyothetical protein; Tansferase; Compleyothetical protein; Compleyothetical protein; Compleyothetical protein; Compleyothetical protein; Compleyothetical protein; Compleyothetical protein; Compleyothetical protein; Compleyothetical pr
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Appl. Environ. Microbiol. 61:1193-2202 (1995).
-i- FUNCTION: RECOGNIZES THE DOUBLE-STRANDED UNMETHYLATED SEQUENCE GATC AND CLEAVES BEFORE G-1.
-i- CATALYTIC ACTIVITY: Endonucleolytic cleavage of DNA to give specific double-stranded fragments with terminal 5'-phosphates.
-i- SIMILARITY: TO R.DPNII AND R.MBOI.
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Shigenohy
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SEQUENCE 304 AA; 34670 MW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDILINE=20145173; PubMed=1093077;
Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;
"Genome sequence of the endocellular bacterial symbiont of aphids
Buchnera sp. APS.";
Nature 407:81-86(2000).
-!- SIMILARITY: BELONGS TO THE PFKB FAMILY OF CARBOHYDRATE KINASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Buchnera aphidicola
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            Similarity 7; Conser
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RA Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
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RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
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RA Chim S.Y., Glaser P., Goffeau A., Golighty E.J., Grandi G.,
RA Guiseppi G., Guy B.J., Haga K., Haicch J., Harwood C.R., Henaut A.,
RA Hibert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Hibert H., Koetter P., Koningstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
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None D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Persecott A.M.,
RA Persecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
RA Raperso V., Johl T.M., Portetelle D., Porwollik S., Park S., Soldo B.,
RA Schiguchi J., Secheska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
RA Schiguchi J., Takaja T., Takahashi H., Takemaru K.,
RA Yirit A., Wambutt R., Wedler E., Wedler H., Weitzenegger T.,
Willia K., Voshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.,
The Complete genome sequence of the Gram-positive bacterium Bacillus
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MEDLINE=96051385; PubMed=7584024;
MEDLINE=96051385; PubMed=7584024;
Ogassawara N., Nakai S., Yoshikawa H.;
"Systematic sequencing of the 180 kilobase region of the Bacillus subtills chromosome containing the replication origin.";
DNA Res. 1:1-14(1994).
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                     Nature 390:249-256(1997).
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STRAIN-CV. VENT (Cherry; TISSUE=Fruit;
MEDLINE=92119262; PubMed=1731999;
Salts Y., Wachs R., Kenigsbuch D., Gruissem W., Barg R.;
Salts Y., Wachs R., Kenigsbuch D., Gruissem W., Barg R.;
TONA sequence of the tomato fruit expressed proline-rich protein gene
TPRP-F1 reveals an intron within the 3 untranslated transcript.";
Plant Mol. Biol. 18:407-409(1992).
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EMBL; Z99124; CAB16131.1; -.

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a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tomato fruit.";
                                   2.2%; bu
100.0%; Pr
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37721 MW; 8E5DE922917BBEE4 CRC64;
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                      moved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
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                                                                 DB 1;
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STRAIN-ATCC 15692 / PAO1;

MEDLINE=20437337; PubMed=10984043;

MEDLINE=20437337; PubMed=10984043;

Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., La Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yu Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  006749; Q57292;
01-FEB-1995 (Rel. 31, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Alginate lyase precursor (EC 4.2.2.3) (Poly(beta-D-mannuronate) lyase)
                                                                                                                                                                                                                                                             between the Swiss Institute of Bioinformatics and the Extrement the European Bioinformatics Institute. There are no rest use by non-profit institutions as also content modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.isborsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=93328683; PubMed=8335634; Schiller N.L., Monday S.R., Boyd C.M., Keen N.T. "Characterization of the Pseudomonas aeruginosa (algL): cloning, sequencing, and expression in E.J. Bacteriol. 175:4780-4789(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PSEAE
                                                                                                                                           EMBL; L14597; AAA71990.1; -.
EMBL; U27829; AAA91127.1; -.
EMBL; AE004775; AAG06935.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Complete genome sequence of Pseudomonas aeruginosa opportunistic pathogen.";
Nature 406:959-964(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -I- FUNCTION: Depolymerizes alginate by cleaving the beta-1,4
glycosidic bond. May enhance the production of alginate by
controlling the length of the polymer chain during export.
-I- CATALYTIC ACTIVITY: Eliminative cleavage of polysaccharides
containing beta-D-mannuronate residues to give oligosaccharides
with 4-deoxy-alpha-L-erythro-hex-4-enopyranuronosyl groups at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. STRAIN=FRD1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gene 131:1-8(1993).
[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Sequence of the algL gene of Pseudomonas aeruginosa and of its alginate lyase product.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=93380656; PubMed=8370530;
Boyd A., Ghosh M., May T.B., Shinabarger D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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ALGL OR PA3547.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: Periplasmic.
SIMILARITY: BELONGS TO THE POLYSACCHARIDE LYASE FAMILY 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   their ends.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Keen N.T., Ohman D.E.;
eruginosa alginate lyase gene
ssion in Escherichia coli.";
                                                                                                                                                                                                                                                                                                                                                                                  There are no restrictions
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K., Lim R.M.,
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.J., Lagrou M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL outstation
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SIGNAL PIR; JN0777;

Signal;

Periplasmic;

Complete proteome POTENTIAL.
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Best Local S
Matches 7
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P14126; 008459;
01-JAN-1990 (Rel. 13, C
01-NOV-1997 (Rel. 35, L
15-DEC-1998 (Rel. 37, L
60S ribosomal protein I
                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=97279235; PubMed=9133743;
Walens M., Bohn C., Daignan-Fornier B., Dang V.,
"The sequence of a 54.7 kb fragment of yeast chro
the presence of two tRNAs and 24 new open reading
Yeast 13:379-390(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                               SEQURNCE OF 1-19.

MEDIINE-84038947; PubMed=6355773;

Otaka E., Higo K.I., Itoh T.;

"Yeast ribosomal proteins: VII. Cytoplasmic Schizosaccharomyces pombe.";

Mol. Gen. Genet. 191:519-524(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein)
                                                                                                                                                                                                                                                               SEQUENCE OF 1-9.
MEDLINE-92184799; PubMed-1544921;
Takakura H., Tsunasawa S., Miyagi M., V
"NH2-terminal acetylation of ribosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Schultz L.D., Friesen J.D.;
"Nucleotide sequence of the tcm1 gene
Saccharomyces cerevisiae.";
J. Bacteriol. 155:8-14(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RPL3 OR TCM1 OR MAKE OR YOR063W OR YOR29-14.
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota, Fungi, Ascomycota, Saccharomycotina, Sacch
Saccharomycetales, Saccharomycetaceae, Saccharomyces.
                                                                                                                                                                                                                          cerevisiae.";
J. Biol. Chem. 267:5442-5445(1992).
-i- FUNCTION: THE L3 PROTEIN IS A COMPONENT OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=83238226; PubMed=6305925;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                CYTOPLASMIC RIBOSOMES.
SUBCELLAUGAR LOCATION: Cytoplasmic.
MISCELLAUGAR LOCATION: Cytoplasmic.
MISCELLAUGAR MOTANT ALLELS OF TCM1 CONFERS RESISTANCE TO
MISCELLAUGAR AND ANTICHOTECENE TOXIN PRODUCED BY PLANT-PATHOGENIC
                                                                                                                                             SIMILARITY: BELONGS TO THE L3P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         109
 J01351; AAA88732.1; -. Z74971; CAA99256.1; -.
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367
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100.0%; Pr
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Pred. No.
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; EAA3FE30032AB3BA CRC64;
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Pred. No. 32;
Mismatches
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(Trichodermin
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l proteins of Saccharomyces
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ast chromosome XV reveals
reading frames.";
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Q03420;
01-OCT-1993
01-OCT-1993
15-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Geremia R.A., Goldman G.H., Jacobs D., Ardiles W., Vila S.B.,
van Montagu M., Herrera-Estrella A.;
"Molecular characterization of the proteinase-encoding gene, pri
related to mycoparasitism by Trichoderma harzianum.";
Mol. Microbiol. 8:603-613 (1993).

-i- FUNCTION: SERINE PROTEBASE, SECRETED SPECIFICALLY DURING THE
MYCOPATAGIEL PROCESS, MHICH IS INVOLVED IN THE DEGRADATION
PHYTOPATHOGEN CELL WALLS, MEMBRANES AND OF THE PROTEINS RELE
AFTER LYSIS OF THE HOST.

-I- SUBCELLULAR LOCATION: Secreted.
-I- INDUCTION: BY MYCELIA, FUNGAL CELL WALLS, AND CHITIN, BUT ON
IN THE ABSENCE OF GLUCOSE.
-I- SINILARITY: BELONGS TO PEPTIDASE FAMILY S8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL, 270678; CAA94548.1; --
PIR; S05843; RSD44E.
SGD; S000559; RPL3.
InterPro; IRR000597; Ribosomal_L3.
Pfam; PF00297; Ribosomal_L3; 1.
PROSITE; PS00474; RIBOSOMAL_L3; 1.
InterPro; IPR000209; Peptidase_S8.
Pfam; Pr00082; Peptidase_S9; 1.
PRINTS; PR00723; SUBTILASE ASP; 1.
PROSITE; PS00136; SUBTILASE ASP; 1.
PROSITE; PS00137; SUBTILASE_HIS; 1.
PROSITE; PS00138; SUBTILASE_SER; 1.
PROSITE; PS00138; SUBTILASE_SER; 1.
PROSITE; PS00138; SUBTILASE_SER; 1.
PROSITE; PS00138; SUBTILASE_SER; 1.
POTENTIAL.
PROPEP 21 120 POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A., AND PARTIAL SEQUENCE STRAIN=IMI 206040;
MEDLINE=93316857; PubMed=8326868;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Trichoderma harzianum.
Bukaryota; Fungi; Ascomycota; Pezizomycotina; Sor
Hypocreales; mitosporic Hypocreales; Trichoderma.
NCBI_TaxID=5544;
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INIT MET 0
CONFLICT 254
                                                                                                                                                                                                                                                EMBL; M87518; AAA34211.1; -.
EMBL; M87516; AAA34209.1; -.
PIR; S32905; S32905.
HSSP, Q99405; NIPT.
MEROPS; S08.UPA; -.
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386 AA;
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(Rel. 27, Last sequence update)
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steinase precursor (EC 3.4.21.-) (
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ilarity 100.0%;
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 Query Match
Best Local Similarity
                                              Nuclear protein.
ZN_FING 256
ZN_FING 310
DOMAIN 69
DOMAIN 130
DOMAIN 235
DOMAIN 315
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CARBOHYD
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
                                                                                                                                                                                                                             EMBL; S80425; AAA93491.1; -. HSSP; P17679; IGNF. ZFIN; ZDB-GENE-990415-82; gata3.
                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=96028520; PubMed=7547465;
Neave B., Rodaway A., Wilson S., Patient R., Holder N.;
"Expression of zebrafish GATA 3 (gta3) during gastrulation and merculation suggests a role in the specification of cell fate.";
"""
                                     SEQUENCE
                                                                                                                               SMART; SM00401; ZDF GATA; 2.

PROSITE; PS00344; GATA_ZN_FINGER_1; 2.

PROSITE; PS50114; GATA_ZN_FINGER_2; 2.

Transcription_regulation; Activator; DNA-binding;
                                                                                                                                                                                           InterPro; IPR000679; Znf GATA.
InterPro; IPR001164; hRIP like.
Pfam; PF00320; GATA; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                          neurulation suggests a role
Mech. Dev. 51:169-182(1995)
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SIMILARITY: CONTAINS 2 GATA-TYPE ZINC FINGERS.
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                                              GATA-TYPE 1.
GATA-TYPE 2.
POLY-PRO.
POLY-SER.
POLY-SER.
POLY-THR.
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 Score 7; |
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CHARGE RELAY SYSTEM (BY SIMILARITY).
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CHARGE RELAY SYSTEM (BY SIMILARITY).
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            Length 438;
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RESULT 18
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                                                                                                                                                                                                                                                                                    EMBL; AE000058; AAB96242.1; -.
InterPro; IPR000120; Amidase.
InterPro; IPR004412; GatA.
Pfam; PF01425; Amidase; I.
TIGRFAMB; TIGR00132; gatA; 1.
PROSITE; PS00571; AMIDASES; 1.
PROCEIN biosynthesis; Ligase; Co
SEQUENCE 478 AA; 53229 MW; F
KIR2_HUMAN STANDARD; PRT; 505 AA. P36896; Q15479; Q15480; Q15481; Q15482; Q1-JUN-1994 (Rel. 29, Created) Q1-JUN-1994 (Rel. 29, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Serine/threonine-protein kinase receptor R2 p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GATA_MYCPN P75534;
                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- FUNCTION: FURNISHES A MEANS FOR FORMATION OF CORRECTLY CHARGED
GLN-TRNA (GLN) THROUGH THE TRANSAMIDATION OF MISACYLATED GLU-
TRNA (GLN) IN ORGANISMS WHICH LACK GLUTAMINYL-TRNA SYNTHETASE. THE
REACTION TAKES PLACE IN THE PRESENCE OF GLUTAMINE AND ATP THROUGH
AN ACTIVATED GAMMA-PHOSPHO-GLU-TRNA (GLN) (BY SIMILARITY).
-!- CATALYTIC ACTIVITY: ATP + L-GLUTAMYL-TRNA (GLN) + L-GLUTAMINE = ADE
-!- CATALYTIC ACTIVITY: ATP + L-GLUTAMYL-TRNA (GLN) + L-GLUTAMINE = ADE
-!- SUBUNIT: HETEROTRIMER OF A, B AND C SUBUNITS (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE AMIDASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pneumoniae.";
Nucleic Acids Res. 24:4:
-!- FUNCTION: FURNISHES
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01-NOV-1997 (Rel. 35, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Glutamyl-tRNA(Gln) amidotransferase subunit A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=ATCC 29342 / M129;
MEDLINE=97105885; PubMed=8948633;
Himmelreich R., Hilbert H., Plage
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Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Complete sequence analysis of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Herrmann R.;
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                                                                                                                                                             ISRNGVY 193
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ISHES A MEANS FOR FORMATION OF CORRECTLY CHARGED
                                                                                                                                                                                                                                         2.2%;
                                                                                                                                                                                                                          Score 7; DB 1; Pred. No. 41; 0; Mismatches
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precursor

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EMBL; 222536; CAAA80258.1; -.
EMBL; U14722; AAA50246.1; -.
EMBL; L10125; AAA60555.1; -.
EMBL; L10126; AAA60556.1; -.
EMBL; L31848; AAA53349.1; -.
EMBL; L31848; AAA53350.1; -.
EMBL; L31848; AAA53350.1; -.
EMBL; B1848; AAA53351.1; -.
EMBL; B21848; AAA53351.1; -.
EMBL; B21848; AAA53351.1; -.
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EMBL; B21848; AAA53351.1; -.
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EMBL; B21848; AAA53351.1; -.
EMBL; B21848; B21843351.1; -.
EMBL; B21848; B21843351.1; -.
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EMBL; B21848; B218451.1; -.
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                                                                InterPro; IPR000472; Activin_rec.
InterPro; IPR000719; Euk_pkinase:
InterPro; IPR002290; Ser thr pkinase.
InterPro; IPR003605; TGFbeta_GS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=94254839, PubMed=8196624;
Carcamo J., Weis F.M., Ventura F., Wieser R., Wrana J.L.,
Attisano L., Massague J.;
"Type I receptors specify growth-inhibitory and transcriptional responses to transforming growth factor beta and activin.";
Mol. Cell. Biol. 14:3810-3821(1994).
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MEDLINE-93390967; PubMed-8397373;
ten Dijke p., Ichijo H.. Franzen P., Schulz P., Saras J.,
Toyoshima H., Heldin C.-H., Miyazono K.;
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"Activin receptors with predicted serine/threonine kinase activity.";
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ACVR1B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in
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Submitted
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Eukaryota; M
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Xu J., Matsuzaki K., McKeehan K.,
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NCBI_TaxID=9606;
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pkinase; 1.
Activin_recp; 1.
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Primates;
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SMART; SM00467; GS; 1.

PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.

PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

Receptor; Transferase; Serine/threonine-protein kinase; ATP-binding;

Receptor; Transferase; Serine/threonine-protein kinase; ATP-binding;
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01-OCT-1993 (Rel. 27, Last sequence update)
16-OCT-2090 (Rel. 40, Last annotation updat
Serine/threonine-protein kinase receptor R2
                                                                                                                                                                                                                                                     STRAIN-Sprague-Dawley; TISSUE-Urogenital ridge;
MEDLINE=93372378; PubMed=895914;
He W.-W., Gustafson M., Hirobe S., Donahoe P.;
"Developmental expression of four novel serine/threonine receptors homologous to the activin/transforming growth f type II receptor family.";
Dev. Dyn. 196:133-142(1993).
                          TISSUE=Pituitary;

MEDLINE=95113007; PubMed=7813622;

Takuni T., Moustakas A., Lin H.Y., Lodish H.F.;

Takuni T., Moustakas A., Lin H.Y., Lodish H.F.;

Teceptor characterization of a type I serine-threonine receptor for TGF-beta and activin in the rat pituitary tu line GH3.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACVRIB OR ACVRIK4.
Rattus norvegicus (Rat).
Eukaryota, Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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   Cell Res. 216:208-214(1995)
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YBALRVMGKMMRECWYANGAARLTALRKTLSQLSVQEDV
KI -> TELFCLCSYLPFQDAGSPKAVLLPPFFLQPVGCLL
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1SOFORM 3).
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-> VRSWPPAAPSA, (IN ISOPORM 2).
L -> V (IN DBSNB-928906).
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Sciurognathi; Muridae;
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16-OCT-2001 (Rel. 40, Last sequence up
15-JUN-2002 (Rel. 41, Last annotation
Maternal experantia protein.
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SMART; S
"Marcey D., Watkins W.S., Hazelrigg T.;
"The temporal and spatial distribution pattern of maternal exuperantia protein: evidence for a role in establishment maintenance of bicoid mRNA localization.";
EMBO J. 10:4259-4266(1991).
                                                                                                   Drosophila melanogaster (Pruit fly).
Eukaryota; Metazoa; Arthropoda; Mandibulata;
Insecta; Pterygota; Neoptera; Endopterygota;
Muscomorpha; Ephydroidea; Drosophilidae; Dros
NCBI_TaxID=7227;
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HSSP; P36897;
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                                                                SEQUENCE FROM N.A.
MEDLINE=92097546; PubMed=1756733;
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SUBCELLULAR LOCATION: Type I membrane protein.
TISSUE SPECIFICITY: UROSENITAL RIDGE, TESTIS, OVARY, BRAIN AN
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PF01064; Activin recp; 1.
m; PD000001; Euk pkinase; 1.
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PS00108; PROTEIN KINASE ST; 1.
PS50011; PROTEIN KINASE DOM; 1.
PTansferase; Serine/threonine-protein kinase; ATP-binding;
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IPRO00719; Euk_pkinase.
IPRO02290; Ser thr pkinase.
IPRO03605; TGFbeta_GS.
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Diptera; Brachycera;
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FlyBase; FBgn0000615; exa.

Developmental protein; RNA-binding.

DOMAIN 207 246 SER-RI

VARIANT 223 223 M -> I

VARIANT 339 339 R -> S

SER-RICH.
M -> I.
R -> S (IN PJ42 MUTANT,

LOSS OF EXU

EMBL; \$72757; AAB20673.1; -. EMBL; \$72363; AAB20670.1; -. EMBL; AE003791; AAM68399.1;

(See http://www.isb-sib.ch/announce/

and

for

commercia.

S18643; S18643. A41639; A41639.

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RA Brandon R.C., ROGERS Y.-H.C., Malazej R.C., Champe W., Chell L.A.,
RA Wan K.H., Doyle C., Baxcer E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Maril J.F., Agoyrs Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Ballew R.M., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C. Busam D.A., Butler H., Cadieu B., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.R.
RA Durbin K.J. Busangelista C.C., Perris C., Ferrisca S., Fleischmann W.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gabart W.M., Glasser K.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Harris N.I., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris M.I., Harvey D., Kraft C., Kravitz S., Kulp D., Lai Z.,
Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.-P., McPherson D.,
RA Meison D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Melson D.R., Nelson K.A., Saunders R.D.C., Scheeler F., Shen H.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong G., Zhao Q.A.,
Wei J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Mang Z.-Y., Wassaman D.A., Weinstock G.M., Wassamhan D.A., Weinstock G.M., Wassamhan G.C., Stapleton M., Strong G., Zhao Q., Mang Z.-Y., Wassaman C., Stapleton M., Strong G., Zhao Q., Mang Z.-Y., Wassaman D.A., Weinstock G.M., Stapski M.F., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong G., Zhao Q., Mang X.,
Wang Z.-Y., Wassaman D.A., Weinstock G.M., Weissenbach J.,
RA Yeng S., And Weissenbach J., Wassaman D., Strong S., Zhao Q., Smith H.O.,
RA Spier E., Spradling A.C., Stapleton M., Skupski M.F., Smith H.O.,
RA Shang S., Shang S., Shang S., Shang S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=20196006; Pubmed=10/31131,
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Adams M.D., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
Amanatides P.G., Scherer S.E., Richards S., Ashburner M., Henderson S.N.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RX MEDLINE=20.470413; PubMed=11586360;

RX MEDLINE=21470413; PubMed=11586360;

RA Parkhill J., Wren B W., Thomson N.R., Titball R.W., Holden M.T.G.,

RA Parkhill J., Sebaihia M., James K.D., Churcher C., Mungall K.L.,

RA Parkhill J., Sebaihia M., James K.D., Churcher C., Mungall K.L.,

RA Parkhill J., Sebaihia M., James K.D., Churcher C., Mungall K.L.,

RA Parkhill J., Sebaihia M., James K.D., Churcher C., Mungall K.L.,

RA Peltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,

RA Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,

RA Feltwell T., Hamlin N., Stevens K., Whitehead S., Barrell B.G.,

RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.,

RA Genome sequence of Yershnia pestis, the causative agent of plague.",

RI Mature 413:523-527(2001).

CC C. FUNCTION: Probably involved in periplasmic detoxification of copper by oxidizing Cu(I) to Cu(II) and thus preventing its uptake copper by oxidizing Cu(I) to Cu(II) and thus preventing its uptake copper by oxidizing Cu(I) to Cu(II) and thus preventing its uptake copper by oxidizing Cu(I) to Cu(II) and thus preventing its uptake copper by oxidizing Cu(I) to Cu(II) and thus preventing its uptake copper by oxidizing Cu(I) to Cu(II) and thus preventing its uptake copper by oxidizing Cu(I) to Cu(II) and thus preventing its uptake copper by oxidizing Cu(I) to Cu(II) and thus preventing its uptake copper by oxidizing Cu(I) to Cu(II) and thus preventing its uptake copper by oxidizing Cu(I) to Cu(II) and thus preventing its uptake copper by oxidizing Cu(I) to Cu(II) and thus preventing its uptake copper by oxidizing Cu(I) to Cu(II) and thus preventing its uptake copper by oxidizing Cu(I) to Cu(II) and thus preventing its uptake cu(II) and thus preventing its uptake cu(II) and thus preventing its uptake cu(II) and thus preventing its uptake cu(II) and thus preventing its uptake cu(II) and thus preventing its uptake cu(II) and thus preventing its uptake cu(II) and thus preventing its uptake cu(II) and thus preventing its uptake cu(I
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CUEO_YERPE
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Best Local S
Matches 7
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Q8ZBKO;
15-JUN-2002
15-JUN-2002
15-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15.-UN-2002 (Rel. 41, Created)
15.-UN-2002 (Rel. 41, Last sequence update)
15.-UN-2002 (Rel. 41, Last amotation update)
Blue copper oxidase cueO precursor (Copper efflux oxidase)
CUEO OR YPO3409.
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EMBL; AJ41417; CAC92639.1; ...
InterPro; IPRO01117; Cu-oxidase.
InterPro; IPRO0235; MultiCu_oxidse2.
Pfam; PP00394; Cu-oxidase; 1.
PROSITE; PS00080; MULTICOPPER OXIDASE2; 1.
Oxidoreductase; Copper; Metal-binding; Periplasmic;
                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=632;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN: The methionine-rich domain could provide binding sites exogenous copper ions. This methionine-rich region is probably important for copper tolerance in bacteria. SINILARITY: BELONGS TO THE FAMILY OF MULTICOPPER OXIDASES. SIMILARITY: CONTAINS 3 PLASTOCYANIN-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41 STSGSGS 47
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532 AA;
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176 K -> Q (IN REF. 1).
57974 MW; 50BD15B712A62C4E CRC64;
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100.0%; Pred. No. 45;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gamma
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lo. 45;
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Best Local S
Matches 7
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F_MOUSE
ERF_MOUSE
PF0459;
15-JUL-1998
15-JUL-1998
15-JUN-2002
                                                                                                                                                                                              STRAIN=129/SwJ;

MEDLINE=97282708; PubMed=9136988;

MEDLINE=97282708; PubMed=9136988;

Liu D., Pavlopoulos E., Modi W., Moschonas N., Mavrothalassitis G.J

"ERF: genomic organization, chromosomal localization and promoter

analysis of the human and mouse genes.";

Oncogene 14:1445-1451(1997).

-i- FUNCTION: POTENT TRANSCRIPTIONAL REPRESSOR THAT BINDS TO THE H1

-i- FUNCTION: POTENT TRANSCRIPTIONAL REPRESSOR THAT BINDS TO THE H1

-i- FUNCTION: POTENT TRANSCRIPTIONAL REPRESSOR THAT BINDS TO THE H1

-i- FUNCTION: POTENT TRANSCRIPTIONAL REPRESSOR THAT BINDS TO THE H1

-i- SUBCELLULAR PROLIFERATION (BY SIMILARITY).

-i- SUBCELLULAR LOCATION: Nuclear.

-i- PTM: PHOSPHORYLATED BY MULTIPLE KINASES INCLUDING PROBABLY ERK2

PHOSPHORYLATION REGULATES THE ACTIVITY OF ERF (BY SIMILARITY).
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SIGNAL
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                                                                                        This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Bh the European Bioinformatics Institute. There are no restruce by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-cr send an email to license@isb-sib.ch).
                        EMBL; U58533; AAC09474.1;
EMBL; U58534; AAC09474.1;
HSSP; Q01543; 1FLI.
MGD; MGI:109637; Erf.
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        324 LAIGSQV 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             56 LAIGSQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 (Rel. 36, Created)
8 (Rel. 36, Last sequence up
2 (Rel. 41, Last annotation
transcription factor ERF.
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533 AA;
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Rodentia;
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164
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PLASTOCYANIN-LIKE 1.
PLASTOCYANIN-LIKE 2.
PLASTOCYANIN-LIKE 3.
                                                                                                                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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45;
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IPR000418; ECS.
IPR002341; HSF_ETS

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FIXN_AZOCA
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Best Local
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DNA_BIND 27

DOMĀIN 166

DOMAIN 290

DOMAIN 362

DOMAIN 420

DOMAIN 420

MOD_RES 529
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01-FEB-1996
01-FEB-1996
15-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                               Mandon K., Kaminski P.A., Mougel C., Desnoues N., Elmerich C.;

"Role of the fixGHI region of Azorhizobium caulinodans in free-living and symbiotic nitrogen fixation.";

FEMS Microbiol. Lett. 114:185-189(1993).

-i- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. CO I IS THE CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN CYTOCHROME C OR A QUINOL ARE TRANSFERRED TO THE BIMETALLIC CENTER FORMED BY A HIGH-SPIN HEME AND COPPER B.

-i- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Azorhizobium caulinodans.
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Hyphomicrobium group; Azorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
MOD_RES
                                          EMBL; X74410; CAA52429.1; -. InterPro; IPR000883; COX1. InterPro; IPR004677; CcoN.
                                                                                                                                                                                     between the Swiss Institute of Bioinformatics
the European Bioinformatics Institute. There a
use by non-profit institutions as long as i
modified and this statement is not removed. Us
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                                                                                                                                           entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through
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PROSITE; PS00346; ETS_DOMAIN 2; 1.
PROSITE; PS50061; ETS_DOMAIN 3; 1.
Transcription regulation; Represso
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR00454; ETS; SMART; SM00413; ETS;
                                                                                                                                                                                                                                                                                                                                 SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                          PATHWAY: Respiratory chain; terminal step.
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
POTENTIAL TRANSMEMBRANE DOMAINS.
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7; Conserv
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(Rel. 33, Last sequence update)
(Rel. 41, Last annotation updat
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oxidase polypeptide I homolog (EC
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Pred. No.
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POLY-GLY.
POLY-SER.
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PHOSPHORYLATION
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0. 47;
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RESULT 25
SPPA_ECOLI
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Matches 7
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01-MAR-1989
01-MAR-1989
01-DEC-1992
SPPA_ECOLI STANDARD; PRT; 618 AA.
P08395; P77752; Q46723; Q46724; Q46725; Q46726;
01-AUG-1988 (Rel. 08, Created).
                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by ancentities requires a license agreement (See http://www.isb-cr send an email to license@isb-sib.ch).
                                                                                                                                                                                              EMBL; D10879; BAA016
EMBL; X14112; CAA323
PIR; G30084; WMBEW5.
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METAL
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SEQUENCE 580 AA; 62669 MW;
                                                                                                                                                                                                                                                                                                                                                                                   McGeoch D.J., Dairymple M.A., Davison A.J., Dolan A., McNab D., Perry L.J., Scott J.E., Taylor P.; "The complete DNA sequence of the long unique region
                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Herpes simplex virus (type 1 / strain 17).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Virion protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=88274327; PubMed=2839594;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alphaherpesvirinae;
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                                                                             167
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                                                                                                                     7;
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                                                                                               2.2%;
_arity 100.0%;
Conservative
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(Rel. 10, Last seq
(Rel. 24, Last ann
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                                                                                                                                                                                                         BAA01671.1; -.
CAA32317.1; -.
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                                                                                                                      0;
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ITON (LOW-SPIN HEME) (BY SIMI)
COPPER B (BY SIMILARITY).
COPPER B (BY SIMILARITY).
COPPER B (BY SIMILARITY).
IRON (HIGH-SPIN HEME) (BY SIMIIRON (BY SIMILARITY).
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EMBL; M13359; AAA24648.1; ...
EMBL; AE000271; AAC74836.1; -.
EMBL; D90820; BAA15557.1; -.
EMBL; U13772; AAA57008.1; -.
EMBL; U13773; AAA57009.1; -.
EMBL; U13774; AAA57010.1; -.
EMBL; U13775; AAA57011.1; -.
EMBL; U13776; AAA57012.1; -.
EMBL; U13776; AAA57013.1; -.
                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMPL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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16-OCT-2001
Protease IV
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STRAINELE;

MEDLINE-97251357; PubMed=9097039;

Alba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh

Alba H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M.,

Kasai H., Kashimoto K., Mori H., Mori T., Motomura K.,

Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,

Makade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Saito

Sampei G., Nakamura Y., Nashimoto H., Takeda J.,

Sampei G., Seki Y., Sivasundaram S., Tagami H., Takeda J.,

Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T.;

"A 570-kb DNA sequence of the Escherichia coli K-12 genome

corresponding to the 28.0-40.1 min region on the linkage map.";

[14]
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-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 110-433 FROM N.A.
STRAIN-VARIOUS ECOR STRAINS,
MEDLINE-95064015, PubMed-7973728;
Guttman D.S., Dykhuizen D.E.;
"Clonal divergence in Escherichia coli as a result not mutation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V Riley M., Collado-Vides J., Glasmer J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=86250892; PubMed=3522590; Ichihara S., Suzuki T., Suzuki M., Mizushima S., "Molecular cloning and sequencing of the sppA gene and characterization of the encoded protease IV, a signal peptidase, of Escherichia coli.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             peptidase).
SPPA OR B1766.
Escherichia coli.
Bacteria; Proteobacteria;
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STRAIN=K12 / MG1655;
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J. Biol. Chem. 261:9405-9411(1986)
[2]
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FUNCTION: DIGESTION OF THE CLEAVED SIGNAL PEPTIDE IS NECESSARY TO MAINTAIN PROPER SECRETION OF MATU ACROSS THE MEMBRANE.
SUBCUSIT: HOMOTETRAMER.
SUBCULTILAR LOCATION: Integral membrane protein.
(Probable).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complete genome sequence of Escherichia coli K-12."; nce 277;1453-1474(1997).
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: annotation update)
(Endopeptidase IV)
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TO 1-OCT-1994 (Rel. 30, Created)
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DT 16-OCT-2001 (Rel. 40, Last sequence update)
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EMBL; U1379; AAA57015.1; -.
EMBL; U13782; AAA57017.1; -.
EMBL; U13782; AAA57030.1; -.
EMBL; U1383; AAA57030.1; -.
EMBL; U1383; AAA57030.1; -.
EMBL; U1383; AAA57031.1; -.
EMBL; U1383; AAA57031.1; -.
PIR; A24813; PRECT4.
MEROPS; S49.001; -.
ECOGEne; EG10968; EDDA.
InterPro; IPR004635; SigPTase SpDA36.
InterPro; IPR004635; SigPTase SpDA67.
InterPro; IPR004635; SigPTase SDDA67.
Pfam, PP01343; Peptidase U7; 1.
TIGREPAMS; TIGR00706; SDDA 67K; 1.
TIGREPAMS; TIGR00706; SDDA 67K; 1.
TIGREPAMS; TIGR00706; SDDA dom; 1.
Hydrolase; Protease; Transmembrane; Inn.
Hydrolase; Protease; Transmembrane; Inn.
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POTENTIAL.
TRANSMEM 398 414
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SEQUENCE
           MEDLINE 97236810; PubMed=9079682;

Faergeman N.J., Dirusso C.C., Elberger A., Knudsen J., Black P.N.;

Faergeman N.J., Dirusso C.C., Elberger A., Knudsen J., Black P.N.;

Faergeman N.J., Dirusso C.C., Elberger A., Knudsen J., Black P.N.;

Fatty acid transport protein impairs uptake homologue to the murine fatty acid transport protein impairs uptake and growth on long-chain J. Biol. Chem. 272:8531-8538(1997).

J. Biol. Chem. 272:8531-8538(1997).

-! FUNCTION: MAY BE INVOLVED IN LONG-CHAIN FATTY ACIDS UPTAKE, AND PRIOR TO METABOLIC UTILIZATION. MAY PLAY AN IMPORTANT ROLE IN UPTAKE OF THESE HYDROPHOBIC COMPOUNDS UNDER CONDITIONS WHERE FAI ACID SYNTHESIS IS COMPROMISED.
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MORTON T.A., Runquist .....

Morton T.A., Runquist .....

A Wood H.G., Ljungdahl L.G.;

T "The primary structure of the subunits of carbon monox dehydrogenase/acetyl-CoA synthase from Clostridium the J. Biol. Chem. 266:23824-23828 (1991).

CC -i- FUNCTION: CATALYZES THE INTERCONVERSION OF CO AND SYNTHESIS OF ACETYL-COENZYME A. FROM THE METHYLATE CC SULTUR PROTEIN, CO, AND COENZYME A.

CC SULTUR PROTEIN.
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This SWISS-PROT entry the between the Swiss Institute of Bioinformatics Institute. There are no restitute by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.isb-rand an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                     Carbon monoxide dehydrogenase alpha subunit (EC 1.2.99.2) Moorella thermoacetica (Clostridium thermoaceticum). Bacteria; Firmicutes; Clostridia; Thermoanaerobacteriales; Thermoanaerobacteriaceae; Moorella group; Moorella.
                                                                                                                                                                                                                                                                      MEDLINE=92084676; PubMed=1748656; Morton T.A., Runquist J.A., Ragsdale S.W.,
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01-AUG-1992 (Rel.
16-OCT-2001 (Rel.
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PROSITE; PS00455; AMP_BINDING; 1.
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                                                                                                                           SUBUNIT: TETRAMER OF TWO ALPHA AND TWO BETA CHAINS.
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Pfam; PF03598; CdhC; 1.
TIGREAMs; TIGR00316; cdhC; 1.
Oxidoreductase; Nickel.
SEQUENCE 729 AA; 81725 MW;
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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
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B0285.7.
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Pfam; PF01433; Peptidase_M1; 1.
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                                                                                                                                                                                                                                             entities requires a license agreement (S or send an email to license@isb-sib.ch).
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RESULT 29

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Q02910;
Q1-OCT-1993
01-OCT-1993
01-FEB-1994
Calphotin.
CPN OR CAP.
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EMBL; LO211; AAA28405.1; -.

EMBL; LO211; AAA28405.1; -.

EMBL; FlyBase; FBgn0010218; Cpn.
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Eukaryota; Metazoa; Arthropoda; Mandibulata;
Insecta; Pterygota; Neoptera; Endopterygota;
Muscomorpha; Ephydroidea; Drosophilidae; Dros
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Ballinger D.G., Xue N., Harshman K.D.;

Ballinger D.G., Xue N., Harshman K.D.;

Ballinger D.G., Xue N., Harshman K.D.;

Proc. Natl. Acad. Sci. U.S.A. 90:1536-1540(1993).

-i- FUNCTION: MIGHT FUNCTION AS A CALCIUM-SEQUESTERING "SPONGE" TO REGULATE THE AMOUNT OF FREE CYTOPLASMIC CALCIUM. IT BINDS 0.3 MOLOF CAL2 PER MOL OF PROTEIN.

-i- SUBGULIT: HOMODIMER (PROBABLE).

-i- SUBCILILLAR LOCATION: CYTOPLASMIC; HYPODENSE COMPARTMENT.

-i- TISSUE SPECIFICITY: SOMA AND AXONS OF PHOTORECEPTOR CELLS OF COMPOUND EYES AND CCELLI.

DEVELOPMENTAL STAGE: EXPRESSED EARLY IN PHOTORECEPTOR CELL DEVELOPMENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=93165729; PubMed=8094559;
Martin J.H., Benzer S., Rudnicka M., Miller C.A.;
"Calphotin: a Drosophila photoreceptor cell calcium-binding protein.";
Proc. Natl. Acad. Sci. U.S.A. 90:1531-1535(1993).
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                                             APVAPPV 185
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I -> V (IN REF. 2).

T -> A (IN REF. 2).

P -> PP (IN REF. 2).

VQ -> AP (IN REF. 2).

I -> V (IN REF. 2).

S -> T (IN REF. 2).

A -> E (IN REF. 2).

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O -> E (IN REF. 2).

I -> T (IN REF. 2).

I -> T (IN REF. 2).

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Pred. No. 70;
0; Mismatches
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ota; Diptera; Brachycera;
Drosophila.
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HIRA_DROME
RC STRAINBECKeley; PubMed=10731132;
RC MEDLINBECKELEY; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Ashburner M., Henderson S.N.,
RA Adams M.D., Celniker S.E., Holt R.A., Ashburner M., Henderson S.N.,
RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Adams M.D., Celniker S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Iewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Barlaw R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Feiffer B.D.,
RA Abril J.F., Agbayani A., An H.-J., Andrews Ffannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Berriar C., Ferriar S., Fleischmann W.,
RA Glodek A., Gong F., Gorrell J.H., Galaar D., Harris M.,
RA Glodek A., Gong F., Gorrell J.H., Gollaar D., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Mount S.M., Melson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Alali M., Kallush F., Karpen G.H., Ke Z., Kennison J.A., Weitson D.L.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shan H.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shan H.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shan H.,
RA Mang Z.-Y., Wassarman D.A., Weitsinstock G.M., Weissenbach J.,
RA Yell S. R., Zhong F.N., Zhong W., Zhang S., Zhu X., Smith H.O.,
RA Yell S. R., Frector C., Tong W., Zhong S., Zhu X., Smith H.O.,

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Bukaryota, Metazoa; Arthropoda, Mandibulata; Pancrustacea;

Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brach

Muscomorpha; Ephydroidea; Drosophilade; Drosophila.

NCBI_TaxID=7227;
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MIDSULWE=9380288; PubMed=9712723;
Tlevadot R., Marques G., Pritchard M., Estivill X., Ferrus
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ProDom; PD000018; WH40; 3.

SMART; SM00320; WD40; 6.

PROSITE; PS00678; WD_REPEATS 1; 1.

PROSITE; PS50082; WD_REPEATS_2; 3.

PROSITE; PS50294; WD_REPEATS_REGION; 1.
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EMBL; AF071281; AAC64041.1; -.
EMBL; AF071281; AAC64041.1; -.
EMBL; AE003441; AAF46267.1; -.
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ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A SHORT FORM, ARE PRODUCED BY ALTERNATIVE SPLICING.

BYOTHOMY AND PRODUCED BY ALTERNATIVE SPLICING.

DEVELOPMENTAL STAGE: EXPRESSED MATERNALLY AND EMALE).

SIMILARITY: CONTAINS 4 WD REPEATS (TRP-ASP DOMAINS).
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                                                                                                                                    STSGSGS 47
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L -> LPVLSDKAEFDADVPKML (IN
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MISSING (IN SHORT ISOFORM).
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Query Match
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01-OCT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Bifunctional autolysin precursor [Includes: N-acetylmuramoyl-L-alanine amidase (EC 3.5.1.28), Mannosyl-glycoprotein endo-beta-N-acetylglucosamidase (EC 3.2.1.96)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POSTEY S.J.;
Submitted (APR-1995) to the EMEL/GenBank/DDBJ databases.

-i-FUNCTION: ENDOHYDROLYSIS OF THE DI-N-ACETYLCHITOBIOSYL UNIT IN
HIGH-MANNOSE GLYCOPEPTIDES AND GLYCOPROTEINS CONTAINING THE
-{(WAN)5 (GLCNAC)2}-ASN STRUCTURE. ONE N-ACETYL-D-GLUCOSAMINE
RESIDUE REMAINS ATTACHED TO THE PROTEIN; THE REST OF THE
OLIGOSACCHARIDE IS RELEASED INTACT.

-i- CATALYTIC ACTIVITY: Hydrolyzes the link between N-acetylmuramoyl
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Cell was
SIGNAL
                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long as modified and this statement is not removed. It entitles requires a license agreement (See hat or send an email to license@isb-sib.ch).
                                              SEQUENCE
                                                                                                                                                                                           InterPro; IPR002502; Amidase 2.
InterPro; IPR002901; Amidase 4.
Pfam; PF01510; Amidase 2; 1.
Pfam; PF01832; Amidase 4; 1.
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                                                                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                    between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "A Staphylococcus aureus autolysin that has an N-acetylmuramoyl-L-alanine amidase domain and an endo-beta-N-acetylglucosaminidase domain and an endo-beta-N-acetylglucosaminidase domain: cloning, sequence analysis, and characterization."; Proc. Natl. Acad. Sci. U.S.A. 92:285-289(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=95116542;
Oshida T., Sugai N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=RN450
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                                                                                          REPEAT
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SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE N-ACETYLMURAMOYL-L-ALANINE AMIDASE FAMILY 2.

SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO FAMILY 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      unit in high-mannose glycopeptides and glycoproteins contains the -[Man(GlcNAc)2]Asn-structure. One N-acetyl-D-glucosamine residue remains attached to the protein; the rest of the cligosaccharide is released intact.
SUBCELLULAR LOCATION: Secreted.
SUBCELLULAR LOCATION: Secreted.
SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                GLYCOSYL HYDROLASES.
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CATALYTIC ACTIVITY: Endohydrolysis of the di-N-acetylchitobiosyl
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                                              WW.
Score 7;
Pred. No.
                                                                                            BIFUNCTIONAL AUTOLYSIN.

-ACETYLMURAMOYL-L-ALANINE AMIDASE.
ENDO-BETA-N-ACETYLGLUCOSAMIDASE.
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This SWISS-PROT entry is copyright. It is produced through a collaborat to between the Swiss Institute of Bioinformatics and the EMBL outstatic the European Bioinformatics Institute. There are no restrictions on control to the by non-profit institutions as long as its content is in no condified and this statement is not removed. Usage by and for commerc entities requires a license agreement (See http://www.isb-sib.ch/annour or send an email to license agreement (See http://www.isb-sib.ch/annour corsent an email to license agreement (See http://www.isb-sib.ch/annour corsent an email to license@isb-sib.ch).

EMBL: L15286, AAA58429.1; ...

EMBL: L25286, AAA58429.1; ...

EMBL: D21230; BAA04762.1; ...

EMBL: D21230; BAA04762.1; ...

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Proc. Natl. Acad. Sci. U.S.A. 89:10144-10148 (1992).

-i- TISSUE SPECIFICITY: EXPRESSED PREDOWLNANTLY IN INTERNAL ORGANS
SUCH AS ADRENAL GLAND, PANCREAS AND KIDNEY.

-i- PIM: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING
UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS.

-i- SIMILARITY: BELONGS TO THE FIBRIL-ASSOCIATED COLLAGENS WITH
INTERRUPTED HELICES (FACIT) FAMILY.
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TISSUE-UNBilical cord;
MEDLINE-94148920; PubMed-8106446;
MEDLINE-94148920; PubMed-8106446;
MEDLINE-9418920; PubMed-8106446;
MEDLINE-9418920; PubMed-8106446;
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TISSUE-Flacenta;
MEDLINE-94140817; PubMed-8307960;
Muragaki Y., Abe N., Ninomiya Y., Olsen B.R., Ooshima A.;
"The human alpha 1(XV) collagen chain contains a large amino-terminal non-triple helical domain with a tandem repeat structure and homology to alpha 1(XVIII) collagen.";
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 544-1252 FROM N.A.
MEDLINE=93066196; PubMed=1279671;
Myers J.C., Kivirikko S., Gordon M.K., Dion A.S., Pihlajaniemi T.;
"Identification of a previously unknown human collagen chain, alph
1(XV), characterized by extensive interruptions in the triple-heli
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triple-helical
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Q9PJY2;
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SEQUENCE FROM N.A.
STRAIN-MOBEN / Nigg;
MEDLINE-20150255; PubMed=10684935;
MEDLINE-20150255; PubMed=10684935;
Read T.D., Brunham R.C., Shen C., Gill S.R., F.
White O., Hickey E.K., Peterson J., Utterback
Linher K., Weidman J., Khouri H., Craven B., F.
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Bacteria, Chlamydiales,
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PMPB OR TC0694
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SMART; SM00210; TSDN; 1.
Extracellular matrix; Connective tissue; Repeat; Hydroxylation;
Cell adhesion; Collagen; Glycoprotein; Signal.
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cer membrane protein pmpB precursor
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NOMHELICAL REGION 1 (NC1).

TRIPLE-HELICAL REGION 1 (NC2).

TRIPLE-HELICAL REGION 2 (NC2).

TRIPLE-HELICAL REGION 2 (NC3).

TRIPLE-HELICAL REGION 3 (NC3).

TRIPLE-HELICAL REGION 4 (NC4).

TRIPLE-HELICAL REGION 4 (NC4).

TRIPLE-HELICAL REGION 5 (NC5).

TRIPLE-HELICAL REGION 6 (NC5).

TRIPLE-HELICAL REGION 7 (NC5).

TRIPLE-HELICAL REGION 7 (NC5).

TRIPLE-HELICAL REGION 7 (NC7).

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O; Mismatches
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k T., Berry K., Bass
Bowman C., Dodson R.
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xPro; IPR000087; Collage xPro; IPR001791; Laminin xPro; IPR003129; TSPN. xPro; IPR003129; TSPN. ; PF01391; Collagen; 5.

Collagen. Laminin_G. TSPN.

alpha 1(XVIII) collagen."; Biol. Chem. 269:4042-4046(1994).

gene.

Biol. Chem.

269:4773-4779(1994).

"Primary structure of the alpha exon-intron organization in the

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RESULT 34
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Q1-NOV-1995 (Rel. 32, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Hypothetical protein ZK945.9 in chromosome II.
ZK945.9/ZK945.10.
                                                                                                                                                                                Durbin R.,
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
-I- SUBCELLGLAR LOCATION: Integral membrane protein (Pot-
-I- SIMILARITY: CONTAINS 1 GPS DOMAIN.
                                                                                                                                                                                                                                                                           STRAIN-Bristol N2; Wilkinson-Sproat J.; Submitted (FEB-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
EMBL; Z48544; CAB70192.1; -.
EMBL; Z48582; CAB70192.1; JOINED.
EMBL; Z48582; CAB70201.1; -.
                                                          This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Event the European Bioinformatics Institute. There are no restrue by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sorsend an email to license@isb-sib.ch).
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Eisen
                                                                                                                                                                                                                                                  REVISIONS.
                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                       Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pneumoniae AR39.";
Nucleic Acids Res. 28:1397-1406(2000)
                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -1- SIMILARITY: BELONGS TO THE PMP OUTER MEMBRANE PROTEIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S89_CAEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genome sequences of Chlamydia trachomatis MoPn and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1672 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      72 PROBABLE OUTER MEMBRANE PROTEIN PMPB 176295 MW; 4ABF190DA4DF8BD6 CRC64;
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o. 1.3e+02;
                                                                          (See http://www.isb-sib.ch/announce/
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RESULT 35
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Best Local S
Matches 7
          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P17615;
01-AUG-1990
01-AUG-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bifidobacterium longum.
Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
Bifidobacteriales; Bifidobacteriaceae; Bifidobacterium.
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TRANSMEM
                                                                                                                                                                                                                                                           Biochimie 72:207-212(1990).

-!- FUNCTION: THIS PROTEIN BELONGS TO THE HISTONE LIKE FAMILY OF PROKARYOTIC DNA-BINDING PROTEINS WHICH ARE CAPABLE OF WRAPPING DNA TO STRBILIZE IT, AND PREVENT ITS DENATURATION UNDER EXTREME ENVIRONMENTAL CONDITIONS.
                                                                                                                                                                                                                                                                                                                                                    STRAIN-ATCC 15703;
MEDLINE=90344917; PubMed=2116910;
Goshima N., Kano Y., Imamoto F.;
"Characterization of Holike protein from Bifidobacterium longum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRANSMEM
TRANSMEM
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InterPro; IPR001024; Lipoxygenase_LH2.
InterPro; IPR0010636; M+channel_nlg.
InterPro; IPR000203; PXD_cys_rich.
Pfam; PP00520; ion_trans; 1.
Pfam; PP00577; PLAT; 1.
                                                                         SEQUENCE
                                                                                                                                  PIR; A43768, A43768.
InterPro; IPR000119; Bac_DNAbind.
Pfam; PF00216; Bac_DNA_binding; 1
PROSITE; PS00045; HISTONE_LIKE; E
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                                                                                               DNA-binding; DNA condensation.
NON TER 27 27
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SMART; SM00308; LH2; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam;
                                                                                                                                                                                                                    -!- SIMILARITY: BELONGS TO THE BACTERIAL HISTONE-LIKE PROTEIN FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE.
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2071
                                                                         27 AA; 2863 MW;
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2836
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2976
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2390
2451
2483
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(Rel. 15, Last sequence update)
(Rel. 36, Last annotation updat
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          Score 6; I Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MW;
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                                                                       6A201A5965A1BD64 CRC64;
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Pred. No.
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                                                                                                                                    PARTIAL
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DB .
33;
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                              1;
                              Length 27;
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PRT6_ON P08145;

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Matches

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01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical 4.5 kDa protein in SOXC 3'region.
Sulfolobus acidocaldarius.
Archaea, Crenarchaeota, Thermoprotei, Sulfolobales,
                                                                                                                                                                                                                                YSXC SULAC
P39477;
01-FEB-1995
01-FEB-1995
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Aiken J.M., McKenzie D., Zhao H.-Z., States J.C., Dixon G.H.;
"Sequence homologies in the protamine gene family of rainbow trout.",
Nucleic Acids Res. 11:4907-4922(1983).
-i- FUNCTION: PROTAMINES SUBSTITUTE FOR HISTONES IN THE CHROMATIN OF
SPERM DURING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT
SPERM DUA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX.
-i- SUBCELLULAR LOCATION: Nuclear.
-i- TISSUE SPECIFICITY: TESTIS.
SEQUENCE FROM N.A.
STRAINATCC 33909 / NCIB 11770 /
MEDLINE=92192013; PubMed=1372250;
Luebben M., Kolmerer B., Saraste
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=83272939; PubMed=6308564;
MEDLINE=83272939; PubMed=6308564;
MCKenzie D., Zhao H.-Z.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleost
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
NCBI_TaxID=8022;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-AUG-1988 (Rel. 08,
01-AUG-1988 (Rel. 08,
15-DEC-1998 (Rel. 37,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chromosomal protein; Nucleosome core; Spermatogenesis; Testis; DNA condensation; Nuclear protein.
                                                                                                               NCBI_TaxID=2285;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; X01595; CAA25748.1; -. A21211; A21211.
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Last annotation update)
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       Saraste M.;
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Pred. No. 38
0; Mismatches
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                                                                                                                                                              Sulfolobaceae;
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Matches 6
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Matches 6
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                                                                                                                                                                                                      SMART; SMO0131; KU; 1.

PROSITE; PS00280; BPTI_KUNITZ_1; 1.

PROSITE; PS50279; BPTI_KUNITZ_2; 1.

Venom; Serine protease inhibitor.

DISULFID 5 55

BY SIMILARITY.

DISULFID 14 38 SYMILARITY.

DISULFID 30 51

REACTIVE BOND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "An archaebacterial terminal oxidase combines core structures mitochondrial respiratory complexes."; EMBO J. 11:805-812(1992).
                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR00222; Kunitz_BPTI.
Pfam; PF00014; Kunitz_BPTI; 1.
PRINTS; PR00759; BASICPTASE.
PRODOm; PD000222; Kunitz_BPTI; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea; Elapidae; Elapidae; Naja.
NCBI_TaxID=35670;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last seq
16-OCT-2001 (Rel. 40, Last ann
Venom chymotrypsin inhibitor.
Naja naja (Indian cobra)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X62643; CAA44512.1; --
PIR; S21044; S21044.
Hypothetical protein.
SEQUENCE 40 AA; 4502 MW;
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P19859;
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                                               266 GFVSSY 271
     16 GFVSSY 21
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                                                                                         Similarity 6; Conser
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                                                                                       Conservative
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ilarity 100.0%
Conservative
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                                                                                         Score 6; DB 1
Pred. No. 64;
D; Mismatches
                                                                                                                                                                                   REACTIVE BOND (BY 4BFB26A010C1737A
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Pred. No. 47
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a chymotrypsin Kunitz inhibitor cobra (Naja naja naja).";
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RESULT 37
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SEQUENCE

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Best Local Similarity
Matches 6; Conserv
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BC MAIZE STANDARD; PRT; 76 AA.

101-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
EC protein homolog (Zinc-metallothionein class II).
                                                                                                                                       SEQUENCE FROM N.A.

White C.N., Rivin C.J.;

White C.N., Rivin C.J.;

Submitted (JUN-1994) to the EMBL/GenBank/DDBJ databases.

-i- FUNCTION: BINDS 5 MOLECULES OF ZINC. MAY HAVE A ROLE IN ZN(2+)

HOMEOSTASIS DURING EMBRYOGENESIS (BY SIMILARITY).

-i- SIMILARITY: BELONGS TO THE METALLOTHIONEIN SUPERFAMILY; FAMILY 15.
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                                                                                                                                                                                                                                                                                     Zea mays (Maize).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; S10210; S10210.
Hypothetical protein.
SEQUENCE 60 AA; 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Nucleotide sequence of the region coding for 100K and 33K proteins of human enteric adenovirus type 41 (Tak)."; Nucleic Acids Res. 18:3069-3069(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=90272433; PubMed=2349115;
Slemenda S.B., Pieniazek N.J., Velarde J. Jr., Pieniazek D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human adenovirus type 41.
Viruses; dsDNA viruses, r
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01-NOV-1991 (Rel. 20, Last sequence update)
16-CCT-2001 (Rel. 40, Last amotation update)
Hypothetical 6.9 kDa protein in 100 kDa protein region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P23690;
01-NOV-1991 (Rel.
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100.0%; Pred. No. 67;
tive 0; Mismatches
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lo. 67;
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Best Local :
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PRINTS; PR00877; MTPLANTPEC.
Metal-binding; Metal-thiolate cluster; Zinc.
INIT_MET 0 0 BY SIMILARITY.
                                                                         SEQUENCE
                                                                                                                                          EMBL; Z34469; CAA84233.1; -. EMBL; U10696; AAA19405.1; -.
                                                                                                                        InterPro; IPR000316; Metallothio15.
21
                50 TSGSGG 55
                                  l Similarity
6; Conserva
TSGSGG
                                                                         76 AA; 7574 MW;
                                    Conservative
26
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                                                                         C9803CBF7F9B1D34 CRC64;
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Pred. No.
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Search completed: July 8, 2003, 11:19:16
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P91181 caenorhabdi

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Result
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Perfect score:
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seq length: 2000000000
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Match
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Q1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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O47809 enterococcu
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O82dj0 yersinia pe
O872t8 ralstonia s
O972x1 sulfolobus
O95780 uncultured
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O8mmw8 clostridium
O8ujk4 agrobacteri
O9dac7 polygonatum
O8ujk4 sureaplasma
O8vdb7 mus musculu
O9dac8 sureaplasma
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RA Harris N.L., Harvey D., Heiman T.J., Hernandz J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Liu X., Matuel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Liasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Matuel B., McIncosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
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RA Melson T.C., McHors R., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
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RA Sylrskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
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The genome sequence of Drosophila melanogaster.";
RI Science 287:2185-2195(2000).
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Bacteria; Firmicutes;
Bacillaceae; Bacillus.
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Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta, Magnoliophyta; eudicotyledons; core eu
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Submitted (AUG-1993) to
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InterPro; IPR001768; Tryy amyl inhbtr.
Pfam; PF00234; tryp_alpha_amyl; 1.
PRINTS; PR01217; PRICHEXTENSN.
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                              Scanlan E., Devine K.M.; Submitted (NOV-1997) to
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RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borriss R., Boursler L., Brans A., Braum M., Brignell S.C., Bron S.,
RA Borrilst R., Enuschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Chis S.V., Glaser P., Goffeau A., Goliythiy E.J., Grandi G.,
RA Ghim S.V., Glaser P., Goffeau A., Goliythiy E.J., Grandi G.,
RA Gliseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Guiseppi G., Guy B.J., Lauber J., Harwood C.R., Klein C.,
RA Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Parro V., Pohl T.M., Portetelle B., Rapport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
RA Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
RA Sekiguchi A., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenegger T.,
RA Witters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
Veshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;
RT Tothe Complete genome sequence of the gram-positive bacterium Bacillus
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=C-125 / JCM 9153;
STRAINE-20512582; PubMed=11058132;
Merami H., Nakasone K., Takaki Y., Mi
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EMBL; Z99111; CAB13777.1; -.
InterPro; IPR002482; LysM.
Pfam; PF01476; LysM; 1.
SMART; SM00257; LysM; 1.
                                                                                                                                      Bacteria; Firmicutes;
Bacillaceae; Bacillus
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MEDILINE-97313267; PubMed-9169871;

MEDILINE-97313267; PubMed-9169871;

Johnston M., Hillier L., Riles L., Albermann K., Andre B., Ansorge W.,

Benes V., Bruckner M., Delius H., Dubois E., Dusterhoft A.,

Entian K.D., Floeth M., Goffeau A., Hebling U., Heumann K.,

Heuss-Neitzel D., Hilbert H., Hilger F., Kleine K., Kotter P.,

Icouis E.J., Messenguy F., Mewes H.W., Miosga T., Mostl D.,

Muller-Auer S., Nentwich U., Obermaier B., Piravandi E., Pohl T.M.,

Muller-Auer S., Nentwich U., Obermaier B., Piravandi E., Pohl T.M.,

Portetelle D., Purnelle B., Rechmann S., Rieger M., Rinke M., Rose M.,

Scharfe M., Scherens B. Scholler P., Schwager C., Schwarz S.,

Underwood A.P., Utrestarazu L.A., Vandenbol M., Verhasselt P.,

Underwood A.P., Utrestarazu L.A., Vandenbol M., Verhasselt P.,

Underwood A.P., Utrestarazu L.A., Vandenbol M., Verhasselt P.,

Uderendeels F., Voet M., Volckaert G., Voss H., Wambutt R., Wedler E.,

Wedler H., Zimmermann F.K., Zollner A., Hani J., Hoheisel J.D.;

"The nucleotide sequence of Saccharomyces cerevisiae chromosome XII.",

Natura 1873.0.0/10)
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"Complete genomic sequence of the alkaliphilic bacterium Bacillus halodurans and genomic sequence comparison with Bacillus subtilis Nucleic Acids Res. 28:4317-4331(2000).

EMBL; APO01520; BAB07607.1; -
Hypothetical protein; Complete proteome.

SEQUENCE 227 AA; 25714 MW; EEBC5FACDDC3D6F3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saccharomyces cerevisiae (Baker's yeast).

Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.

NCBI_TaxID=4932;
                                                                                                                                                                                                                  Submitted (AUG-1997) to the EMBL/GenBank/DDBJ
EMBL; U17243; AAB67346.1; -.
SGD; S0004292; YLR301W.
SEQUENCE 244 AA; 27501 MW; 80D813586A1930E
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Submitted
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                                                   GSTVTSNG 228
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(NOV-1994)
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Pred. No.
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RESULT 7 Q9SET1

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RESULT 8
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Matches 8
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STRALN=COLUMBIA;
KANEKO T., KATO T., S.
Submitted (MAR-2000) t
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InterPro; IPR003882; Pistil_extensin.
InterPro; IPR003882; Pistil_extensin.
InterPro; IPR002965; P_rich_extensin.
InterPro; IPR001768; Try/amyl inhbtr.
Pfam; PF00234; tryp_alpha_amyl; 1.
PRIMTS; PR01211; PRICHEXTENSN.
PRIMTS; PR01211; PSTLEXTENSIN.
SMART; SM00499; AAI; 1.
SMART; SM00499; AAI; 1.
SMOO499; AAI; 31609 MM; P3E6385C
                                                                                                                                   "Structural analysis of A "Structural analysis of the Sequence features of the TAC and BAC clones."; DNA Res. 7:217-221 (2000). EMBL; AP001306; BAB03061... HSSP; P24337; 1HYP.
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Plant Mol. Biol. 41:
EMBL; AF104328; AAD1
HSSP; P24337; 1HYP.
InterPro; IPR003612;
InterPro; IPR003882;
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Q9SET1;
01-MAY-2000
01-MAY-2000
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPLIE9;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
similarity to cell wall-plasma membrane linker protein.
Arabidopsis thaliana (Mouse-ear cress)
Rukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheog Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
eurosids II, Brassicales; Brassicaceae; Arabidopsis.
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MEDLINE=20064977; PubMed=10598107;
Goo J.H., Park A.R., Park W.J., Park
Goo J.H., Park are a park
"Selection of Arabidopsis genes encod
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheop

Spermatophyta; Magnoliophyta; eudicotyLedons; core eudicots;

eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-WAY-2000 (TrEMBLrel. 21, Last annotation update)
01-UN-2002 (TrEMBLrel. 21, Last annotation update)
Cell wall-plasma membrane linker protein homolog.
                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. STRAIN=COLUMBIA;
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   InterPro; IPR003612;
InterPro; IPR003882;
InterPro; IPR002965;
InterPro; IPR001768;
                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=20363099; PubMed=10907853;
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; AAI.
; Pistil_extensin.
; P_rich_extensn.
; Try/amyl_inhbtr.
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) to the EMBL/GenBank/DDBJ databases.
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Pred. No.
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o. 12;
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RESULT 10
Q9UGQS
ID Q9UGC
OT 01-M2
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Q1-MAY-2000 (TrEMBLrel. 13, Cr
Q1-MAY-2000 (TrEMBLrel. 13, Lr
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Matches 8; Conser
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Q39353;
01-NOV-1996
01-NOV-1996
01-JUN-2002
                                                                                                                                                                               Homo sapiens (Human)
Bukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Transcripts of a gene encoding a putative cell wall-plasma membrane linker protein are specifically cold-induced in Brassica napus."; Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases. EMBL; X94976; CAA64425.1; -. HSSP; P24337; 1HYP. HSSP; P24337; 1HYP. InterPro; IPR003612; AAI. InterPro; IPR003612; Try/amyl_inhbtr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Brassica napus (Rape).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid
eurosids II; Brassicales; Brassicaceae; Brassica.
                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                                                      BK989H11.1 (Novel BK989H11.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00234; tryp_alpha_amyT; 1.
SMART; SM00499; AAI; 1.
SEQUENCE 376 AA; 38667 MW; 7E1
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PRINTS; PR01217; PRICHEXTENSN.
PRINTS; PR01218; PSTLEXTENSIN.
SMART; SM00499; AAI; 1.
       SEQUENCE
                            EMBL; Z83851;
NON_TER
                                                                 Submitted (OCT-1999) to the EMBL/GenBank/DDBJ
                                                                                             Ramsay H.;
                                                                                                                SEQUENCE FROM N.A.
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       88
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                                            CAB62962.1;
    9699 MW;
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Primates;
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Pred. No. 13;
  C2ED8FE7AB67CFA1 CRC64;
                                                                                                                                                                                  Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7E12AD838938A4F8 CRC64;
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Matches 7
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InterPro; IPR00302; KOW motif.
InterPro; IPR003256; Ribosomal_L24.
Pfam; PF00467; KOW; 1.
ProDom; PD001677; Ribosomal_L24; 1.
TIGREAMS; TIGR01079; rplx bact; 1.
PROSITE; P801108; RIBOSOMĀL_L24; UNKNOWN_1.
RIbosomal protein; Complete proteome.
SEQUENCE 101 AA; 10877 MW; B4CAF87BE72C90:
                                                                                                                                                                                                                                                                                                                              01-JUN-2002
01-JUN-2002
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                Q8S142;
Q8S142;
clone:P0042A10.";
Submitted (FEB-2001) to the
EMBL; AP003343; BAB90081.1;
                                                           SEQUENCE FROM N.A.
STRAIN=CV. NIPPONBARE;
Sasaki T., Matsumoto T.,
"Oryza sativa (japonica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The complete genome sequence of the lactic lactis ssp. lactis ILI403."; Genome Res. 11.731-753 (2001).
                                                                                                                                                                                                Oryza sativa (japonica cultivar-group).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzeae; Oryza.
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                                                                                                                                                                                                                                                                                         P0042A10.23.
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01-JUN-2002 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
01042A10.23 protein.
                                                                                                                                                                         NCBI_TaxID=39947
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Weissenbach J., Ehrlich
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irmicutes, Bacillus/Clostridium group; Lactobacillales;
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ilarity 100.0%;
Conservative
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1 S.D., Sorok
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                                                                cultivar-group)
                                                                                    Yamamoto
                      EMBL/GenBank/DDBJ databases
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Last annotation updat
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
0703B11.17 protein (P0485B12.9 protein).
0703B11.17 OR P0485B12.9. protein)
07072a sativa (japonica cultivar-group).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta, Liliopsida, Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
111 — TaxID=39947;
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Q9ZW16;
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TISSUE=LEAF SHEATH;
MEDLINE=99408265; PubMed=10480388;
MEDLINE=99408265. PubMed=10480388;
Ogawa M., Kusano T., Kolzumi N., Katsumi M., Sano H.;
"Gibberellin-responsive genes: high level of transcript
in leaf sheath meristematic tissue from Zea mays L.";
                                                                                                                                                                                                                                                                                                      Zea mays (Maize).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;

Panicoideae; Andropogoneae; Zea.

NCBI TaxID=4577;
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"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, clone:P0703B11.";
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
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0; Mismatches
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Ogawa M., Kusano T., Kolzumi N., Katsumi M., Sa:
Ogawa M., Kusano T., Kolzumi N., Katsumi M., Sa:
Gibberellin.responsive genes: high level of tr:
in leaf sheath meristematic tissue from Zea may.
In leaf sheath meristematic tissue from Zea may.
Plant Mol. Biol. 40:645-657(1999).
EMBL; AB018588; BAA74804.1; -
PLANTE PRO018588; BAA74804.1; -
HSSP; P24337; 1HYP.
INTERPRO; IPR001768; Try/amyl inhbtr.
Pfam; PF00234; tryp_alpha_amyl; 1.
SMART; SM00499; AAI I.
SMART; SM00499; AAI I.
SMART; SM00499; AAI I.
SEQUENCE 133 AA; 13465 MW; F2AF4E1584FF9631
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01-MAY-2000
01-JUN-2002
                                                                               01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 21, Last sequence update)
01-UNN-2002 (TrEMBLrel. 21, Last annotation update)
10-UNN-2002 (TrEMBLrel. 21, Last annotation update)
10-UNN-2002 (TrEMBLrel. 21, Last annotation update)
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EMBL; AB018587; BAA74803.1; -.
HSSP; P24337; HYP.
InterPro; IPR003612; AAI.
InterPro; IPR001768; Try/amyl_inhb!
Pfam; PF00334; tryp_alpha_amyl; 1.
SMART; SM00499; AAI; 1.
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mays L.";
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RESULT 18
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InterPro; IPRO01768; Try/amyl inhbtr.
Pfam; PP00234; tryp_alpha_amyl; 1.
SMART; SM00499; AAI; 1.
SEQUENCE 136 AA; 13982 MW; 9F785E
Q9FWP0
                                                                                                                                                                                                                                                                                                "Direct Submission.";
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; U80445; AAB37800.1; -.
Hypothetical protein.
SEQUENCE 141 AA; 15050 MW; 1F655AC7BAE14E99 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Du Z., Le T.T.;
"The sequence of C. (
Submitted (JAN-1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=BRISTOL N2;
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Eukaryota; Metazoa; Nematoda;
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Buell C.R., Yuan Q., M
Hsiao J., Zismann V.,
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Caenorhabditis.
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EMBL/GenBank/DDBJ databases.
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                                                     RP SEQUENCE FROM N.A.

RC STRAIN=C2A / ATCC 35395 / DSM 2834;

RX MEDLINE=2192760; PubMed=11932238;

RX MEDLINE=2192760; PubMed=11932238;

RA Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P.,

RA FitzHugh W., Calvo S., Engels R., Smirnov S., Atnoor D., Brown A.,

RA FitzHugh W., Calvo S., Engels R., Smirnov S., Atnoor D., Brown R.,

RA Linton L., WcEwan P., McKernan K., Talamas J., Tirrell A., Ye W.,

RA Zimmer A., Barber R.D., Cann I., Graham D.E., Grahame D.A., Guss A.M.,

RA Zimmer A., Barber R.D., Cann I., Graham D.E., Grahame D.A., Guss A.M.,

RA Zimmer A., Barber R.D., Cann I., Graham D.E., Grahame D.A., Guss A.M.,

RA Zimmer A., Barber R.D., Cann I., Graham D.E., Grahame D.A., J.A.,

RA Federich R., Ingram-Smith C., Kuettner H.C., Krzycki J.A.,

RA Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,

RA Springer T.A., Umayam L.A., White O., White R.H., de Macario E.C.,

RA Ferry J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I.,

RA Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,

RA Metcalf W.W., Birren B.;

RA Metcalf W.W., Birren B.;

RA Metcalf W.W., Birren B.;

RA Metcalf W.W., Birren B.;

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RA Metcalf W.W., Birren B.;

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RA Metc
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Matches 7
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01-UN-2002 (TrEMBLrel. 21, Last sequence update)
01-UN-2002 (TrEMBLrel. 21, Last annotation update)
Multiple resistance/pH regulation related protein E (Na+/H+',
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
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Archaea; Euryarchaeota; Methanococci;
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InterPro; IPR001768; Try/amyl inhbtr.
Pfam; P700234; tryp alpha_amyl; 1.
SMART; SM00499; AAI; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oryza sativa (Rice).
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   proteome.
165 AA;
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   18327 MW;
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   DCAB72532F74E05E
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   CRC64;
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Query Match Best Local S Matches 7

29

18 LGLIFGV 24 Similarity 7; Conserv

Conservative

2.2%; Scc 100.0%; P:

Score 7; DB : Pred. No. 76
0; Mismatches

DB 17; o. 76;

Length 165

0;

Indels

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RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT OF RESULT
RESULT 21
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AC Q9XWI
DT 01-1W
DT 01-1W
DT 101-0
DE Y54E
GN Y54E
OS Caeni
OC Euka:
OC Rhabb
OX NCB1[]
RN [1]
RP SEQUI
RP SEQUI
RN [2]
RN [2]
RN SEQUI
RX MEDNE
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Best Local S
Matches 7
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Q9XWI1;
01-NOV-1999
01-NOV-1999
01-DEC-2001
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Q926C3;
O1-DEC-2001 (TrEMBLrel. 19, Created)
O1-DEC-2001 (TrEMBLrel. 20, Last sequence update)
O1-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Probable peptidoglycan-associated lipoprocein precursor.
PAL OR R02738 OR SMC02942.
Rhizobium mellioti (Sinorhizobium mellioti).
Bacteria, Proteobacteria, alpha subdivision, Rhizobiaceae group,
Rhizobiaceae; Sinorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=21396507; PubMed=11481430;
Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut Gapela D., Barloy-Hubler F., Gouzy J., Bothe G., Arge F., Gloux Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux Boistard P., Becker A., Boutry M., Cadieu E., Lelaure V., Masuy D., Pohl T., Portetélle D., Puehler A., Purnelle B., Ramsperger U., Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F., "Analysis of the chromosome sequence of the legume symbiont Sinorhizobium melilloti strain 1021."; Sinorhizobium melilloti strain 1021."; Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
EMBL, AL591791; CAC47317.1; InterPro; IPR001145; Bac_OmpA.
Pfam; PP00691; OmpA; 1.
ProDom; PD000930; Bac_OmpA; 1.
                                                                                                                                                                                                                                                            Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Complete proteome. -
SEQUENCE 176 AA; 18735 MW; A6F162CB35042268 CRC64;
                                                                                                                                                             Submitted
                                                                                                                                                                                          SEQUENCE FROM N.A.
Lloyd C.R.;
                                                                              SEQUENCE FROM N.A.
MEDLINE=99069613; PubMed=9851916;
"Genome sequence of the nematode investigating biology.";
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Last sequence update)
Last annotation updat
                                                                                                                                                             EMBL/GenBank/DDBJ
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                            C.elegans:
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                            for
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X MEDLINESPATO, ARCC 700294 / SEROTYPE M1;

X MEDLINESPATO, McShan W.M., Ajdic D.J., Savic G., Lyon K.,

Perretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,

Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,

A Qian Y., Jia H.G., Najar F.Z., Ren Q., Zhu H., Song L., White J.,

Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;

Complete genome sequence of an M1 strain of Streptococcus pyogenes.";

Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).

EMBL; AD006556; AAX34332.1;

EMBL; AD006566; AAX34332.1;

InterPro; IPR004198; Cons hypoth95.

InterPro; IPR004198; Cons hypoth95.

InterPro; IPR002052; N6_Mtase.

Pfam; PF03602; Cons hypoth95; 1.

TIGRFAMS; TIGR00095; Cons hypoth95; 1.

PROSITE; PS00092; N6_MTASE; UNKNOWN 1.

R PROSITE; PS00092; N6_MTASE; UNKNOWN 1.

R SEQUENCE 179 AA; 19567 MW; BD3A72BFF5411137 CRC64;
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Best Local S
Matches 7
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Best Local S
Matches 7
                                                                          Sus scrofa (Pig).
Eukaryota; Metazoa; (
Mammalia; Eutheria; (
NCBI_TaxID=9823;
                                                                                                                                                            Q95KR4
Q95KR4;
01-DEC-2001
01-DEC-2001
01-JUN-2002
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01-JUN-2001 ('
01-JUN-2001 ('
01-JUN-2002 ('
Hypothetical
SPY1538.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Science 282:2012-2018(1998).
EMBL; AL032646; CAR21686.1; -
SEQUENCE 177 AA; 20062 MW; E3BA47B50CCFA329 CRC64;
         SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
Kuehl M., Glowacki G.,
"Molecular cloning and
ecto-mono (ADP-ribosyl)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptococcaceae; Streptococcus.
NCBI_TaxID=1314;
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Bacteria; Firmicutes; Bacillus/Clostridium
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                                                                                                                                                                                                                                            23
                                                                                                                                               protein
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                                                                                                                                                                                                                                                                                                                                     h 2.2%; So Similarity 100.0%; F 7; Conservative 0;
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(TrEMBLrel.
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(Tremblrel.
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(TrEMBLrel. 17, Last sequence update)
(TREMBLrel. 21, Last annotation update)
( protein SPy1538.
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                                                                                           Chordata; Craniata; Vertebrata; Cetartiodactyla; Suina; Suidae;
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Haag F., Koch-Nolte F.;
characterization of human
characterase from testis.
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Last sequence update)
Last annotation update)
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Pred. No. 82;
Mismatches
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                          ART5, a
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Q9V3T8; Q9VK86;
01-MAY-2000 (TrEMBLrel. 13, C
01-MAY-2000 (TrEMBLrel. 13, L
01-UN-2002 (TrEMBLrel. 21, L
SC35 protein (LD32469p).
SC35 OR CG5442.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=CO-92 / BIOVAR ORIENTALIS;

MEDLINE=21470413; PubMed=11586360;

Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,

Prentice M.B., Sebalhia M., James K.D., Churcher C., Mungall K.L.,

Prentice M.B., Sebalhia M., James K.D., Brooks K., Cerdeno-Tarraga A.M.,

Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,

Chillingworth T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,

Feattwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,

Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,

Simmonds M., Skelton J., Stevens K., Whitchead S., Barrell B.G.;

Simmonds M., Skelton J., Stevens K., Whitchead S., Barrell B.G.;
                                                               Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Genome sequence of Yersinia pestis,
Nature 413:523-527(2001).
EMBL, AJ414150; CAC90573.1; -.
InterPro, IPR003810; DUF204.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF02659; DUF204; 2.
Hypothetical protein; Complete
SEQUENCE 189 AA; 20660 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yersinia pestis.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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01-MAR-2002 (TYEMBLYE1: 20,
01-MAR-2002 (TYEMBLYE1: 20,
01-JUN-2002 (TYEMBLYE1: 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NON_TER
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SEQUENCE FROM N.A.
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100.0%; Pred. No.
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                                                                                                                                                                                                                                                                                                                        195 AA
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o. 86;
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., W., Hockins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blaze's R.G., Champe M., Pfelffer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blaze's R.G., Champe M., Pfelffer B.D.,
RA Ballew R.M., Basu A., An H.-J., Andrews-Pfennhoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendail J., Bayraktaroglu L., Beasley E.M.,
RA Beson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Cherraz C., Ferriera S., Fleischmann W.,
RA Gebart K., Dough L.B., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Harris N.L., Harvey D., Helman T.J., Gelbart W.M., Glasser K.,
RA Harris N.L., Harvey D., Helman T.J., Wein M.-H., Houck J.,
RA Harris N.L., Harvey D., Helman T.J., Wein M.-H., Degwam C.,
RA Harris N.L., Harvey D., Helman T.J., Wein M.-H., Degwam C.,
RA Harris N.L., Harvey D., Helman T.J., Wein M.-H., Degwam C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Krantison J.A., Kerchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Krantison J.A., Kerchum K.A.,
RA Harris N.L., Malshina N.V., Mobarry C., Worris J., Woshrefi A.,
RA Mershidov G., Milshina N.V., Mobarry C., Woshrefi A.,
RA Melson D.R., Nelson K.A., Pollard J., Puri V., Reese M.G.,
RA Harris M., Malson D.A., Weinstoc
                                                                                                                                                                                                                                                                                                         A Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
A Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
A Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
A Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K.
A Yu C., Lewis S.E., Rubin G.M., Celniker S.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
C :- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
R EMBL; AF232775; AAF43415.1; -.
R EMBL; AE003636; AAF53193.1; -.
R EMBL; AE003636; AAF53193.1; -.
R EMBL; AY069584; AAL39729.1; -.
R EMBL; AY069584; AAL39729.1; -.
PROSITION
Alternative splicing.
Alternative splicing.
WARSPLIC 183 M
WARSPLIC 195 AA; 21400 MW;
                                                                                                                      PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Characterization of the Drosophila ortholog of the mammalian splicing factor SC35.";
                                                                                                                                                                                  FlyBase; FBgn0040286; SC35.
InterPro; IPR000504; RNA_rec_mot.
Pfam; PF00076; rrm; 1.
SMART; SM00360; RRM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-BERKELEY;
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                                                                                                 PS50102; RRM RNP 1; UNKNOWN 1.
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                 MISSING (IN SHORT ISOFORM); 65E922F8C34C7536 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , George R.,
ungall C.J.,
ng S., Wan K.,
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Length 208; Indels

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RESULT 27

O881130 PRELIMINARY; PRT; 208 AA.

AC 081120;
DT 01-NOV-1998 (TYEMBLrel. 08, Created)
DT 01-NOV-1998 (TYEMBLrel. 09, Last sequence update)
DT 01-NAR-2002 (TYEMBLrel. 20, Last annotation update)
DT 01-MAR-2002 (TYEMBLrel. 20, Last annotation update)
DE CCAAT-box binding factor HAP3 homolog.
CC Arabidopsis thaliana (Mouse-ear cress)
CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Core eurosids II; Brassicales; Brassicaceae; Arabidopsis.
CC STRAIN=3702;
RN [1]
RP SEQUENCE FROM N.A.
RR SEQUENCE FROM N.A.
RR MEDLINE=98319234; PubMed=9657152;
MCDEI TAXID=98319234; PubMed=9657152;
RA Yamagishi K., Fischer R.L., Goldberg R.B., Harada J.J.;
RA Yamagishi K., Fischer R.L., Goldberg R.B., Harada J.J.;
RI Cell 93:1195-1205(1998).
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SEQUENCE FROM N.A.

STRAIN-EMMI1000;

X MEDILINE-21681879; PubMed=11823852;

X MEDILINE-21681879; PubMed=11823852;

X ALIAT M., Billault A., Brottier P., Canus J.C., Cattolico L.,

A Allat M., Billault A., Brottier P., Canus J.C., Cattolico L.,

A Chandler M., Choisne N., Claudel-Renard C., Cunnac S., Demange N.,

A Chandler M., Moisne A., Robert C., Saurin W., Schiex T.,

A Siguier P., Thebault P., Whalen M., Wincker P., Levy M.,

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"Genome sequence of the plant pathogen Ralstonia solanacearum.";

"Genome sequence of the plant pathogen Ralstonia solanacearum.";

Nature 415:497-502(202).

Nature 415:497-502(202).

NE EMBL; AL646068; CAD15754.1; -.

RE InterPro; IPR000086; NUDIX, 1.

Potams, PF00293; NUDIX; 1.

Potams, PF00293; NUDIX; 1.
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QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR6; QBXXR
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ProDom; PD004109; IPP isomerase; 1.

Hypothetical protein; Complete proteome.

SEQUENCE 205 AA; 22905 MW; 011998A4555B1B10 CRC64;
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SEQUENCE FROM N.A.

Cheuk R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C.

A Khan S., Kim C., Altafi H., Bei B., Chin C., Chiou J., Choi E.,

A Khan S., Kim C., Altafi H., Bei B., Chin C., Chiou J., Choi E.,

A Conn L., Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B.

Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N.,

A Lae J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N.,

A Mayorn M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,

A Thaveri A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N.,

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A Theologis A., Ecker J.;

Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.

EMBL, AC013482; AAF16537.1;

EMBL; AC013482; AAF16537.1;

R EMBL; P19267; 1A7W

R InterPro; IPR003959; CBFA_NFYB_domain.

InterPro; IPR003959; CBFA_NFYB_domain.

InterPro; IPR003959; CBFA_NFYB_DISS.

R Pfam; PF00808; CBFD_NFYB_HMF; 1.
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Best Local S
Matches 7
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Q9SFD8;
01-MAY-2000 (TrEMBLrel. 1
01-MAY-2000 (TrEMBLrel. 1
01-MAR-2002 (TrEMBLrel. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Khan S.

Kim C., Altafi H., Bei B., Chin C., Chiou J., Choi E., Conn L.,

Kim C., Altafi H., Bei B., Chin C., Chiou J., Choi E., Conn L.,

Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B., Lee J.

Lenz C., Li J., Liu A., Liu S., Mukharsky N., Nguyen M.,

Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A.,

Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N., Theologis J.

Ecker J.,

Ecker J.,

Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ecker J.R.;
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. Ecker J.R.;
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Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Khan S Shinn P., Brooks S., Buehler E., Chiou J., Choi E., Conn L., Kim C., Altafi H., Bei Q., Chin C., Chiou J., Choi E., Conn L., Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B., Lee J Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B., Lee J Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N., Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A., Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A., Ecker J.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana (Mouse-ear cress).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eddicotyledons; core eudicots; Rosidae;

Spermatophyta; Magnoliophyta; eddicotyledons; core eudicots; Rosidae;

eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR003958; CBFA_NFYB_domain.
InterPro; IPR003957; CBFA_NFYB_topis.
InterPro; IPR004822; Histone_core.
Pfam; PF00808; CBFD_NFYB_HMF; 1.
PRINTS; PR00615; CCGATSUBUNTA.
SEQUENCE 208 AA; 22693 MW; 4E2D249AE2525DDB CRC64;
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P19267; 1A7W.
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Similarity 100.0%; Pred. No. 94;
7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence for Arabidopsis thaliana BAC T26F17 from
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13,
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Last sequence update)
Last annotation update)
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Best Local Similarity
Matches 7; Conserv
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                                                                                                                                                                        Q9FYQ4;
01-MAR-2001
01-MAR-2001
01-DEC-2001
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Q9S2U3;
01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
Rabbinowitsch B., Rajandream M.A., Rutherford K., Rutter S.,
Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
           STRAIN=CV. NIPPONBARE;
Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic
clone:P0433F09.";
                                                                                              Eukaryota; Viridiplantae; Stro
Spermatophyta; Magnoliophyta;
Ehrhartoideae; Oryzeae; Oryza
                                                                                                                                                                                                                                                                                                                                                                                                    "Complete genome sequence of coelicolor A3(2).";
Nature 417:141-147(2002).
EMBL; AL096884; CAB51434.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thomson N.R., James K.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=A3(2) / M14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PRO0615; CCAATSUBUNTA. SEQUENCE 208 AA; 22679 MW;
                                                                                                                                     Oryza sativa (Rice).
                                                                                                                                                 Hypothetical P0011G08.31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=1902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Firmicutes; Actinobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptomyces coelicolor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SC02042 OR SC4G6.
                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                           Q9FYQ4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     membrane protein.
(JUN-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  208 AA;
                                                                                                                                                                                                                                                                                                                                                                                         211 AA; 21223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TrEMBLrel. 13, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
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                                                                                                                                                          (TrEMBLrel. 16, Created)
(TrEMBLrel. 16, Last sequence update)
(TREMBLrel. 19, Last annotation update)
uprotein (P0011G08.31 protein).
                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                           PRELIMINARY;
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100.0%; Pr
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                                                                                                         Streptophyta; Embryophyta; Tracheophyta;
yta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                         of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cerdeno-Tarraga A.-M., Challis G.L., farris D.E., Quail M.A., Kieser H.,
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Pred. No.
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                    DNA,
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o. 95;
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                       chromosome
                                                                                                                                                                                                                                                                                                                                      0;
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RA Adams M.D., Celniker S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Barandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Barandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borkova D., Botchan R.R., Bouck J., Brokstein P., Brottier P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Dew I., Dietz S.M.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Dew I., Dietz S.M.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Dew I., Dietz S.M.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Dew I., Dietz S.M.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Dew I., Dietz S.M.,
RA Godson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Godson K., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Scheeler F., Shen H.,
RA Kanner S. M., Woodage T., 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AP002539; BAB08181.1; -.
EMBL; AP003225; BAB64659.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pterygota; Neoptera; Endopterygota; Diptera; Ephydroidea; Drosophilidae; Drosophila.
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"Oryza sativa nipponbare(GA3)
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Gibbs R.A., Myers E.W., Rubin G.M.,
"The genome sequence of Drosophila
Science 287:2185-2195(2000).
EMBL; AE003496; AAP48376.2; -
FlyBase; FBgn0030571; CG14414.
Interpro; IPR000504; RNA_rec_mot.
Pfam; PF00076; rrm; 1.
SMART; SM00360; RRM; 1.
PROSITE; PS00030; RRW; 1.
PROSITE; PS00030; RRW; 1.
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MEDLINE=94250697; PubMed=8193167;
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                                                                                                                                     Schlunegger B., Stutz B.; "The Englena gracilis chioroplast genome: structural features of region possibly carrying the single origin of DNA replication."; Curr. Genet. 8:629-634(1984).
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processed into photosystem I and II mRNAs that accumulate
differentially depending on the conditions of cell growth.";
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Nucleic Acids Res. 21:3537-3544(1993).
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NCBI_TaxID=3039;
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Chloroplast.
                                                                        SEQUENCE FROM N.A. STRAIN=Z;
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Hong L., Hallick R.B.;
"A group II intron is formed fro
introns.";
                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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RR STRAIN=VC-16 / DSM 4304 / ATCC 49558;

RC STRAIN=98049343; PubMed=9389475;

RX MEDLINE=98049343; PubMed=9389475;

RX MICHAFINE=98049343; PubMed=9389475;

RX Klenk H.-P. Clayton R.A., Tomb J.-F., White O., Nelson K.E.,

RA Klenk H.-P. Clayton R.A., Tomb J.-F., White O., Nelson K.E.,

RA Klenk H.-P., Clayton R.A., Gomban D.E., Krypides N.C.,

RA Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,

RA Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,

RA Kirkness E.F., Dougherty B.A., McKenney T.H., Glodek A., Zhou L.,

RA Cyerbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,

RA Cyerbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,

RA Cyerbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,

RA Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,

RA Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,

RA Wenter J.C.;

"The complete genome sequence of the hyperthermophilic, sulphate-

RT Teducing archaeon Archaeoglobus fulgidus.";

RMBL, AE001074; AABS0793.1; -.

DR TIGR, AF0441; -.

DR TIGR, AF0441; -.
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Best Local S
Matches 7
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01-JAN-1998
01-JAN-1998
01-MAR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Archaeoglobus fulgidus.
Archaee; Buryarchaeota; Archaeoglobi; Archaeoglobales;
Archaeoglobaceae; Archaeoglobus.
NCBI TaxID=2234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gracilis chloroplast DNA: evidence for cundergoing differential processing."; aliochim. Biophys. Acta 1218:75-81(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hallick R.B.;
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ
EMBL; X70810; CAC69148.1; -.
Chloroplast.
SEQUENCE 216 AA; 25364 MW; BFBF1385921BC18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=Z;
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"Alternative splicing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=96079990;
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Pro; IPR001989; Radical_activat
    PF02143; Radical_activat; 1.
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7; Conservative
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100.0%; Pr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
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Pred. No. 97;
0; Mismatches
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the beta and epsilon subunits of the
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Matches 7
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Best Local S
Matches 7
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Q9H5P8;
Q1-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein R00142.
R00142 OR SMC04110.
Rhizobium meliloti (Sinorhizobium meliloti).
Bacteria; Proteobacteria; alpha subdivision;
Rhizobiaceae; Sinorhizobium.
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Q92KU4;
Isogai T., Sugano S.,
Isogai T., Sugano S.,
"NEDO human cDNA sequencing
Submitted (AUG-2000) to the
AKN26842; BAB15572.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S. Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D., Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U., Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.; "Analysis of the chromosome sequence of the legume symbiont Sinorhizoblum meliloti strain 1021."; Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
                                                                           Kawakami T., Noguchi S., Itoh T., Shigeta K., Nakajima Y., Mizuno T., Morinaga M., Tanigami Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmoo Obayashi M., Nishi T., Shibahara T., Tanaka T Isogai T., Sugano S.,
                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
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SEQUENCE 2:
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01-DEC-2001
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                                                                                                                                                                                              TISSUE=LUNG;
                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
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226 AA; 24278 MW; CF2611BE91D7B48E CRC64;
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100.0%; Pr
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Primates;
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                                   project.";
EMBL/GenBank/DDBJ
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Pred. No
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Catarrhini;
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Mismatches
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                                                                                                       , Tanigami A., Fu
o M., Ohmori Y.,
, Tanaka T., Naka
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b. le+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 16;
                                                                                                                                                                                                                                                                                      Vertebrata; Euteleostomi; i; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1e+02;
                                                                                         , Senba T., Malbumman M A., Fujiwara T., Ono T Mori Y., Ota T., Suzuki Y Nakamura Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rhizobiaceae
                                     databases
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                                                                                                                     Ja T., Matsumura K.,
Jayara T., Ono T.,
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STRAIN=AV19 / DSM 6324 / JCM 9639;
MEDLINE=21927647; PubMed=11930014;
Slesarev A.I., Mezhevaya K.V., Makarova K.S., Polushin / Sheherbinina O.V., Shakhova V.V., Belova G.I., Aravind Natale D.A., Rogozin I.B., Tatusov R.L., Wolf Y.I., Ste Malykh A.G., Koonin E.V., Kozyavkin S.A.;
Malykh A.G., Koonin E.V., Kozyavkin S.A.;
mm. complete genome of hyperthermophile Methanopyrus }
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Q8TUT2;
Q1-JUN-2002
01-JUN-2002
01-JUN-2002
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Q9KLV7;
01-OCT-2000
01-OCT-2000
01-MAR-2002
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STRAIN-EL TOR N16961 / SEROTYPE 01;

MEDLINE=20406833; PubMed=10952301;

Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers
McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C
Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical SEQUENCE 2
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                                                                                                                                                                                                                                                                                                                                                                                          Methanopyrus kandleri.
Archaea, Euryarchaeota,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "DNA sequence of both chromosomes cholerae.";
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Bacteria; Proteobacteria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 406:477-483(2000)
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241 AA; 27259 MW;
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(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 20, Last annotation update)
protein VCA0634.
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Pred. No
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WA MEDLINE-2016/483; PubMed=11016950;

WA MY V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,

Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,

Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,

AL Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,

AMA Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,

Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,

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AL Ham M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,

Behardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.;

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Proc. Natl Acad. Sci. U.S.A. 97:12176-12181(2000).

REMBL; AE003508; AAG20087.1; -.

DR InterPro; IPR003439; AAA, FTBASE.

DR InterPro; IPR003439; AAB, Transportr.

DR Probom; PD00006; ABC_transportr; 1.
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Q9HNY3;

O1-MAR-2001 (TrEMBLrel. 16, Created)

O1-MAR-2001 (TrEMBLrel. 16, Last sequence)

O1-JUN-2002 (TrEMBLrel. 21, Last annotat)

ABC transport protein.

TRP2 OR VNG1893G.

Halobacterium sp. (strain NRC-1).

Archaea; Euryarchaeota; Halobacteria; Ha
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O1-JUN-1998 (
O1-JUN-1998 (
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Hypothetical
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Proc. Natl. Acad. Sci. U.S.A. 99:4644-4649(2002)

EMBL; AE010456; AAM02884.1; -.

Complete proceome.

SEQUENCE 241 AA; 25264 MW; E1C25302FBF7F6B6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Complete
SEQUENCE
                                     Borrelia burgdorferi (Lyme disease spirochete).
Bacteria; Spirochaetales; Spirochaetaceae; Borrelia.
NCBI TaxID=139;
   SEQUENCE
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249 AA; 26679 MW;
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protein BB0412.
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RM MEDLINE=98065943; PubMed=9403685;

AA Lathigra R., DubMed=9403685, M., Sutton G.G., Clayton R.A.,

AA Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M.,

AA Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D.,

AA Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson M.,

AVA Van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J.,

AVA Utterback T., Watthey L., McDonald L., Artiach P., Bowman C.,

AA Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B.,

Smith H.O., Venter J.C.;

"Genomic sequence of a Lyme disease spirochaete, Borrelia

"Genomic sequence of a Lyme disease spirochaete, Borrelia

"TIGR; BB0412; -.

TIGR; BB0412; -.

TIGR; BB0412; -.

SO SEQUENCE 259 AA, 30809 MW; 2137010F9140D0FF CRC64;
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01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical 30.2 kDa protein.
F55A4.4.
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Q94238;
01-FEB-1997
01-FEB-1997
01-DEC-2001
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Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
NCBI — TaxID=6239,
                                                                                                  Waterston R.;
"Direct Submission.";
submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; U679.49; AAB07562.1;
HSSP, Q91836; D12.
InterPro, IPR001159; DS_RBD.
Pfam; PF00035; dsrm; 2.
SMART; SM00358; DSRM; 2.
SMART; SM00358; DSRM; 2.
PROSITE; ESS0137; DS_RBD; 2.
Hypothetical protein.
Hypothetical Protein.
SEQUENCE 269 AA; 30169 MW; 2028FE3245563191 CRC64;
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Submitted (SEP-1996)
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STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
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STRAIN=BRISTOL N2;
MEDLINE=99069613; PubMed=9851916;
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STRAIN-BRISTOL N2;
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ive 0; Mismatches
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Total number of hits satisfying chosen parameters: Searched: 2054640 seqs, 14551402878 residues 4109280

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ALIGNMENTS

Db 40970 AGTACCTCAGGTTCGGGCAGTCA	Oy 201 ATGIYYEFOVALGIYALƏTINEASDEFOVALVALAEGSEFGEFORGIYEDINEALƏTINEVALALA 220
41	541 GTTGCCCCACCAGTGACAGAAGCACCATTTGCCACGGGTAGCTCAGGGGTGATGCAATTT 6
Db 40910 ATTTTTGGTGTGATCACCACTTG	181 ValAlaProProValThrGluAlaProP
21	481 CCTGTTGTTGTGGTAAAAAACCCACACCGACTCCGCCTGTGGTTCAGCAGCCAGC
4085	Qy 161 ProValValValValLysLysProThrProThrProProValValGlnGlnProAlaPro 180
US-10-018-706-2 (1-322) x AX067452 (1-327) x AX067452 (1-327) x AX067452 (1-327) x AX067452 (1-327) x AX067452	Qy 141 AlaValGliSerSerArgProProValGlinGlinHisProAlaValGlinLysProThrPro 160 Db 421 GCGGTTCAGTCAAGCACACCAGTACAGCAGCTCCTGCCGTTCAAAAACCCAGCCA 480
Query Match: 100.00% DB:	361 AAGGTGCGTAAGCATATCAGCTCTGGTGTAAATACAGCTCACACACCTTCGCCTGTG
milarity: 1670.00	Db 301 CTAAATAGCAGTTATACGATTTATACAGGTCAATGGCTGACTTTATGGTCAGGTGATCTC 360
Alignment Scores: 8.02e-89	101 LeuAsnSerSerTyrThrIleTyrThrGlyGlnTrpLeuThrLeuTrpSerGlyAspLeu 1
14211 a	Qy 81 ValSerLysileAlaGlnArgTyrGlyLeuAsnTrpArgGluIleGlyHisIleAsnAsn 100
/oz /dk	181 CAGGTTATCACGGACAGTCAGGGCGTACCAAATCGCTATCAGGTGAAGCAGGGCGATACT 2
FEATURES INCYCE GENORICS, INC. (US FEATURES LOCATION/Qualific SOURCE 148328	Oy 61 GlnVallleThrAspSerGlnGlyValProAsnArqTyrGlnValLysGlnGlyAspThr 80
TITLE Nucleotide sequences of mo JOURNAL Patent; WO 0078968-A 27 21	41 SerThrSerGlySerGlySerHisArgThrSerGlySerGlyGlyLeuAlaIleGlySer 60
Moracella, Fluctobactella, Moracella, Fluctobactella, Moracella, Fluctobactella, REFERENCE 1 (bases 1 to 48328) AUTHORS Lagace R.E. Patterson C.	Db 61 ATTITIGGTGTATCACCACTTGCATTTTGGCAGGATGTGCCAGTAAGCCAACCTATAAT 120
Moraxella catarrhalis. M Moraxella catarrhalis	1 AIGACTGTGACGATAGCAATCAATTCACAAAATCAAAAACCCATCAAGCGATTGGGCTTG
	1 MetThrValThrIleAlaIleAsnSerGlnAsnGlnLysProIleLysArgLeuGlyLeu 2
DEFINITION Sequence 27 from Patent WG ACCESSION AX067452	US-10-018-706-2 (1-322) x AX063563 (1-969)
452 AVOCATES	h: 100.00% Indels: Gaps:
Db 961 CTTAAA 966	SCOTE: 322 Percent Similarity: 100.00% Conservative: 0 Best Local Similarity: 100.00% Vismatches: 0
321	Scores: 1.07e-90 Length:
Qy 301 AlaAlaLeupheGlupheArgil	BASE COUNT 265 a 214 C 242 g 248 t ORIGIN
	source 1969 /organism="Moraxella catarrhalis" /db_vref="t=vro.480"
281	SMITHKLINE BEECHAM BIOLOGICALS (S.A.) FEATURES Location/Qualifiers
Qy 261 IleGlnHisThrAsnGlyPheVa 1 ATTCAGCATACCAATGGATTTGT	AUTHORS Thornard, J.S. AUTHORS Thornard, J.S. TITLE Cloning of basb110 antigen from moraxella (branhamella) catarrhalis JOURNAL Patent: WO 0100838-A 1 04-JAN-2001;
Db 721 GCCAGTAATGCAGGCACAGTCAT	Hacteria; Prote Moraxella.
241 AlaSerAsnAlaGlyThrValI	Moraxella catarrhalis. SM Moraxella catarrhalis
Oy 221 GlySerThrValThrSerAsnGl:	AX063563 AX063563.1 GI:12541291
Db 601 CGCTATCCTGTTGGTGCGACCAA	AX063563 LOCUS AX063563 DEFINITION Sequence 1 from Patent WO0100838.

Qy Db 409	Qy Db 409	Qy Db 400	US-10-018-	Alignment of Pred. No.: Score: Score: Percent Sin Best Local Query Match DB:	BASE COUNT ORIGIN	sourc	FEATURES	REFERENCE AUTHORS TITLE JOURNAL	SOURCE ORGANISM	RESULT 2 AX067452 LOCUS DEFINITION ACCESSION VERSION	Дb	8		ο _γ	B 8	В	8		&		<i>₽</i>	Дb
41 SerThrSerGlySerGlySerHisArgThrSerGlySerGlyGlyLeuAlaIleGlySer 60 	21 IlePheGlyVallleThrThrCysIleLeuAlaGlyCysAlaSerLysProThrTyrAsn 40 	1 MetThrValThrIleAlaIleAsnSerGlnAsnGlnLysBroIleLysArgLeuGlyLeu 20 	706-2 (1-322) x AX067452 (1-48328)	Inent Scores: 8.02e-89 Length: 48328 .No.: 1670.00 Matches: 322 ent Similarity: 100.00% Conservative: 0 Local Similarity: 100.00% Mismatches: 0 Match: 100.00% Indels: 0 Gaps: 0 0	14211 a		Incyte Genomics, Inc. (US) Location/Onalifiers	noraxella. 1 (bases 1 to 48328) Legace, R.E., Patterson, C. and Berg, K.L. Nucleotide sequences of moraxella catarrhalis genome Patent: WO 0078988-A 27 28-DEC-2000;		AX067452 48328 bp DNA linear PAT 24-JAN-2001 Sequence 27 from Patent WO0078968. AX067452 AX067452.1 GI:12545072	961 CTTAAA 966	321 LeuLys 322	01 GCGCACTATTIGAATTTAGAATTTCTAGAAATGGCGTGTATGTTGATCCATTGACAGTA	301 AlaAlaLeuPheGluPheArqIleSerArqAsnGlyValTyrValAspProLeuThrVal 320	281 ThrolyAspThrVallArgThrGlyGlnArgTleAlaSerWetLysAsnGlnProSerGly 300	781 ATTCAGCATACCAATGGATTTGTTTCAAGCTATATCCATATTAAGGACGCTCAAGTTAAA 840	261 IleGlnHisThrAsnGlyPheValSerSerTyrIleHisIleLysAspAlaGlnValLys 280	721 GCCAGTAATGCAGGCACAGTCATTCAAGCTGATCACAATATGGACGGGGCGAGTATTGTG 780	laGlyThrValIleG	661 GGCTCAACTGTTACCAGTAATGGCATGTGGTTTTCTGGACGAGATGGCGATTTAATTAA	lThrSerAsnGlyMet	601 CGCTATCCTGTTGGTGCGACCAATCCAGTGGTTCGACGCTTTGGTACGGCGACAGTGGCC 660

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AX063565 AX063565 N AX063565 AX063565.1 GI:12541292 Moraxella catarrhalis. Moraxella catarrhalis Bacteria; Proteobacteria; gamma subdivision; Moraxellaceae; Moraxella. 1 to 966) E 1 (bases 1 to 966) S Thonnard, J. S. Cloning of basb110 antigen from moraxella (branhamella) catarrhalis Patent: WO 0100838-A 3 04-JAN-2001; SMITHKLINE BEECHAM BIOLOGICALS (S.A.)	301 AlaAlaLeuPheGluPheArgIleSerArgAsnGlyValTyrValAspProLeuThrVal 320		241 AlaSerAsnAlaGlyThrVall1eGlnAlaAspHisAsnMetAspGlyAlaSerIleVal 260	221 GlySerThrValThrSerAsnGlyMetTrpPheSerGlyArgAspGlyAspLeuIleAsn 240 	201 ArgTyrProValGlyAlaThrAsnProValValArgArgPheGlyThrAlaThrValAla 220	181 ValAlaProProValThrGluAlaProPheAlaThrGlySerSerGlyValMetGlnPhe 200 	161 ProvalvalvalvaliysiysProThrProThrProProValvalGlnGlnProAlaPro 180 41330 CCTGTTGTTGTGTAAAAAAACCCACACCGACTCCGCCTGTGGTTCAGCAGCCAGC	141 AlaValGinSerSerArgProProValGinGinHisProAlaValGinLysProThrPro 160 	61 GlnValileThrAspSerGlnGlyValProAsnArgTyrGlnValLysGlnGlyAspThr 80
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Qy 201 ArgTyrProValGlyAlaThrAsnProValValArgArgPheGlyThrAlaThrValAla 220	Qy 161 ProValValValValLysLysProThrProThrProProValValGlnGlnProAlaPro 180	361 AAGGTGCGTGAGCGTAGTATCAGCTCTGGTGTGAATACAGCTCACACACCTTCGCCTGTG 141 AlaValGlnSerSerArgProProValGlnGlnHisProAlaValGlnLysProThrPro	Qy . 101 LeuAsnSerSerTyrThrIleTyrThrGlyGlnTrpLeuThrLeuTrpSerGlyAspLeu 120	Qy 81 ValSerLysIleAlaGlnArgTyrGlyLeuAsnTrpArgGluIleGlyHisIleAsnAsn 100	Qy 61 GlnValileThrAspSerGlnGlyValProAsnArgTyrGlnValLysGlnGlyAspThr 80	Qy 41 SerThrSerGlySerGlySerGlySerGlySerGlySerGlyGlyLeuAlaTleGlySer 60	Qy 21 IlePheGlyValIleThrThrCysIleLeuAlaGlyCysAlaSerLysProThrTyrAsn 40	Qy 1 MetThrValThrIleAlaIleAsnSerGlnAsnGlnLysDroIleLysArgLeuGlyLeu 20	FEATURES BOUICE 1966 /organism="Moraxella catarrhalis" /ob_xref="taxon:480" BASE COUNT 263 a 214 c 242 g 247 t ORIGIN Alignment Scores: Pred. No.: 1.85e-90

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Direct Submission

Submitted (11-DEC-1993) Hideo Takahashi, The University of Tokyo,
Submitted (11-DEC-1993) Hideo Takahashi, The University of Tokyo,
Inst. of Mol. & Cell. Biosci., Yayoi 1-1-1, Bunkyo-ku, Tokyo 113,
Japan (Tel:03-3812-2111(ex.7825), Fax:03-3813-0539)

Location/Qualifiers
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Pseudomonas aeruginosa
Bacteria, Proteobacteria; gamma subdivision;
Pseudomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 (bases 1 to 2910)
Tanaka, K. and Takahashi, H.
Tanaka, K. and Takahashi, H.
Cloning, analysis and expression of an rpoS homologue
Pseudomonas aeruginosa PAO1
Gene 150 (1), 81-85 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95157251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rpoS, RNA polymerase principal sigma factor; protein L-aspartyl carboxy methyltransferase.
Pseudomonas aeruginosa (strain:PAO1) DNA, clone:pDB18k, pDB19k,
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D26134
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Pseudomonas aeruginosa RNA polymerase principal sigma factor (rpoS)
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Pred. No.:
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                                   HisProAlaValGlnLysProThrProProValVal-----ValValLysLysProThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TACATCGTGCGCCGCGGCGACACCCCTGTATTCCATTGCCTTCCGCTTCGGCTGGGACTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---PheArgTyrProValGlyAlaThrAsnProValValArgArgPheGlyThrAlaThr
                                                                     ValThrGluAlaProPheAlaThrGlySerSerGlyValMetGln------
                                                                                                                                      ProThrProProValValGln------GlnProAlaProValAlaProPro
                                                                                                                                                                                 --- CCGTCCGTCGCGAAAAACACGCCGGTCGTCGCTGCGCCCCGTGGCGACCAAGCCTACC
                                                                                                                                                                                                                                                                                        ThrAlaHisThrProSerProValAlaValGln---SerSerArgProProValGlnGln 151
                                                                                                                                                                                                                                                                                                                                                                LeuThrLeuTrpSerGlyAspLeuLysValArgGluArgSerIleSerSerGlyValAsn 132
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EVVIRRFGLRGHESSTLEEVGQEIGLTRERVRQIQVEALKRLREILEKNGLSSDALFQ
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Stover,C.K., Pham,X.-Q.T., Erwin,A.L., Mizoguchi,S.D., Warrener,P.,
Hickey,M.J., Brinkman,F.S.L., Hufnagle,W.O., Kowalik,D.J.,
Hagrou,M., Garber,R.L., Goltry,L., Tolentino,E.,
Westbrook-Waddman,S., Yuan,Y., Brody,L.L., Coulter,S.N.,
Polger,K.R., Kas,A., Larbig,K., Lim,R.M., Smith,K.A., Spencer,D.H.,
Wong,G.K.-S., Wu,Z., Paulsen,I.T., Reizer,J., Saier,M.H.,
Hancock,R.E.W., Lory,S. and Olson,M.V.
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Nature 406 (6799), 959-964 (2000)
                                                                                                                                                                                                                                                           Submitted (16-MAY-2000) Department of Medicine University of Washington Genome Center, University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pseudomonas aeruginosa.
Pseudomonas aeruginosa
                                                                                                                                                                                                                                    University of Washington Genome
Box 352145, Seattle, WA 98195, U
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                                                                                                                                                                                                                                                                                                        Direct Submission
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AE004782.1 GI:9949772
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|strain="PAO1"
                                                                                                                                                                                                                ocation/Qualifiers
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Pred. No.:
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---GCCTCAAACGGAAGTTTGAATAAAGGGATTGATATAGCCGGTCAATTGGGCCAGCCT
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                                                                                                                                                      TCGACCACGACCCCACCCAGCAGCAGCGCGACTCCCGTCGTCGCGGGGCCTGCGGTGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                  ArgGluIleGlyHisIleAsnAsnLeuAsnSerSerTyrThrIleTyrThrGlyGlnTrp 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGGTGGGCATGGCCTGCGAGCGGTACT-----CTGATCGGCCGTTTT------
                                                                                                                     ---PheArgTyrProValGlyAlaThrAsnProValValArgArgPheGlyThrAlaThr 218
                                                                                                                                                                                ValThrGluAlaProPheAlaThrGlySerSerGlyValMetGln------
                                                                                                                                                                                                                                                                                                              ThrAlaHisThrProSerProValAlaValGln---SerSerArgProProValGlnGln
                                                                                                                                                                                                                                                                                                                                                                                       LeuThrLeuTrpSerGlyAspLeuLysValArgGluArgSerIleSerSerGlyValAsn 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACCAGCGGG------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ------ThrTyrAsnSerThrSerGlySerGlySerHisArgThrSerGly 52
                                                                                                                                                                                                       CCGGTTCCACCCGCAGTTAGTACGTCGGTACCTGCCAAGCCCGCACCG---GCTCCGGCC
                                                                                                                                                                                                                                  ProThrProProValValGln------GlnProAlaProValAlaProPro
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43.38%
28.00%
17.84%
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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CDS

gene

	rax:01-46-//-259/ 10-cation/Qualifiers 158996 /organism="Rubrivivax gelatinosus" /strain="T1144" /db_xref="taxon:28068"	FEATURES source
	Direct Submission Direct Submission Submitted (05-NOV-1999) Kenji VP Nagashima, Tokyo Metropolitan Submitted (05-NOV-1999) Minamiosawa 1-1, Hachiohji, Tokyo 192-0397, University, Biology, Minamiosawa 1-1, Hachiohji, Tokyo 192-0397, Japan (B-mail:nagashima-kenji@c.metro-u.ac.jp, Tel:81-426-77-2583,	TITLE JOURNAL
_	Unpublished 6 (bases 1 to 58996) Nagashima,K.V.; Igarashi,N., Harada,J., Nagashima,S., Matsuura,K.	JOURNAL REFERENCE AUTHORS
		TITLE
	5 (sites) Nagashima,K.V., Igarashi,N., Harada,J., Nagashima,S., Matsuura,K. and Shimada K	REFERENCE AUTHORS
	idpoint potential cytochrome c8 in the ubrivivax gelatinosus iochemistry (1999) In press	JOURNAL
	s induce the synthesis of	TITLE
	shida,M., Jaquinod,M., Nagashima,K.V., N	REFERENCE AUTHORS
	PHOTOSYNTHETIC GENE CLUSTER IN PURPLE BACTERIUM, RUBRIVIVAX GELATINOSUS Photosynthesis Mechanisms and Effects 4 2889-2892 (1998)	JOURNAL.
	imada,K., Matsuura,K. and Nagashin	
	J. Biol. Chem. 269 (4), 2477-2484 (1994) 94132007 8300574	JOURNAL MEDLINE PUBMED
	Primary Structure and transcription of genes encoding B870 and photosynthetic reaction center apoproteins from Rubrivivax gelatinosus	
	Photosyn. Res. 36, 185-191 (1993) 2 (Sites) Nacashims V V Materius V Obroma C and Chimada V	JOURNAL REFERENCE
,	tic ar	AUTHORS TITLE
	inosus bacteria; beta subdivision; Comamonadaceae;	-
,	AB034704 AB034704.1 GI:7416771 Rubrivivax gelatinosus (strain:IL144) DNA. clone:pgc#12. pgc#6.	ACCESSION VERSION KEYWORDS SOURCE
	AB034704 58996 bp DNA linear BCT 12-APR-2000 Rubrivivax gelatinosus photosynthetic gene cluster, complete cds, stain:III44.	RESULT 6 AB034704 LOCUS DEFINITION
	11 CCACTGCAATATTTG 9097	Db 9111
	317 ProLeuThrValLeu 321	Qy 3
	71 ACAGGAACCGATCGGGTGAAGCTGCACTTCGAGATTCGCCGCCAGGGTAAGCCTGTCGAT 9112	Db 9171
<u>_</u>	297 GlnProSerGlyAlaAlaLeuPheGluPheArgIleSerArgAsnGlyValTyrValAsp 316	Qy 2
	277 AIGINVALLYSThrGJYASpThrValArgThrGJYGINARGIIGALASerWetLysAsn 296 278 AIGINVALLYSTHRGJYASpThrValArgThrGJYGINARGIIGALASERWetLysAsn 296 279 AIGINVALLYSTHRGAYASSTRASSTRASSTRASSTRASSTRASSTRASSTRASS	Qy 277 Db 9231
	GAGTTGGTCATCATCAAACAACGAGACCTACGTGAGTGCCTACGGTCACAACCGCAGG	
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Methylobacterium extorquens AM1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               citation=[3]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="similar to orf1 protein (AAC05676.1) of Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene="ORF164"
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SG

gene

Sg

gene

Sg

complement (4158. .4991)

gene

Sg

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(coproporphyrinogen III)"

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ATCGCCGAGATGGGCGCCAGCGACGCCGACAGGGTGCAGCTGCACTTCGAGATCCGGCGT: 54257
                                        IleAlaSerMetLysAsnGlnProSerGlyAlaAlaLeuPheGluPheArgIleSerArg
                                                                                                                        TyrIleHisIleLysAspAlaGlnValLysThrGlyAspThrValArgThrGlyGlnArg
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2. (bases 1 to 3122)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (26-JUL-1997) Hitoshi Murata, Forestry and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (E-mail:murmur@ffpri.affrc.go.jp, Fax:0298-73-3795)
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Pseudomonas tolaasii
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                                                                                                                                                                                                                                                                                                           970 GAGATTCGCCGTCAAGGGAAGCCTGTAGATCCGCTGCAATTCCTG
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AP421351

Azotobacter vinelandii L-isoaspartate o-methyltransferase (pcm) gene, partial cds; murein endopeptidase (mep), stationary phase sigma factor (rpoS), aerotaxis sensor (aerP), aerotaxis transducer (aerH), and ferredoxin A (fdxA) genes, complete cds; and DNA mismatch repair protein (mutS) gene, partial cds.
                                                  Azotobacter vinelandii. Azotobacter vinelandii
                  Azotobacter
                                   Bacteria; Proteobacteria;
                                                                                                        AF421351.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GlnAlaAspHisAsnMetAspGlyAlaSer----IleValIleGlnHisThrAsnGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GlnProAlaProVal----AlaProProValThrGluAlaProPheAlaThrGly-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TACGCCGGGAGTGGTTTGCGGGGGCTACGGCGAGCTGGTCATCATCAACACAGCGATACC
                                                                                                                                                                                                                                                                                                                                           ArgileSerArgAsnGlyValTyrValAspProLeuThrValLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  TACGTCAGTGCTTACGGCCACAACCGTAGGCTGTTGGTTCGGGAGGGCAGCAGGTCAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTGATATCGCCGGAGATTTGGGACAGCCTGTTTTAGCTGCGTCTGATGGGACAGTGGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PheGlyThrAlaThrValAlaGlySerThrValThrSerAsnGlyMetTrpPheSerGly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SerGln---ValIleThrAspSerGlnGlyValProAsnArgTyrGlnValLysGlnGly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PheValSerSerTyrIleHisIleLysAspAlaGlnValLysThrGlyAspThrValArg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AspThrValSerLysIleAlaGlnArqTyrGlyLeuAsnTrpArgGluIleGlyHisIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTC-----TCTTCAAACGGTAGTTTGAATAAAGGC
(bases 1 to 5876)
                                                                                                          GI:20455801
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                                 gamma subdivision; Pseudomonadaceae;
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306 909 286 849 266 789 248 729 233 699 615

555 158 519 138 480

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Aerotaxis in Azotobacter vinelandii
Unpublished
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Location/Qualifiers
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Submitted (19-SEP-2001) Biological Sciences, University of Alberta, CW405 Biological Sciences Bldg., Edmonton, Alta T6G 2E9, Canada 4 (bases 1 to 5876)
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Tindale, A.E., Meakin
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The stationary phase
Unpublished
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Direct Submission
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Best Local Similarity:
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US-10-018-706-2 (1-322) x AF421351 (1-5876)
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                                                                                                                                                                               |||:::|||
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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Simpson, A.J., Reinach, F.C., Arruda, P., Abreu, F.A., Acencio, M., Alvaranga, R., Alves, L.M., Araya, J.E., Baia, G.S., Baptista, C.S., Barros, M.H., Bonaccorei, E.D., Bordin, S., Bove, J.M., Briomes, M.R., Bueno, M.R., Camargo, A.A., Camargo, L.E., Carraro, D.M., Carrer, H., Colauto, N.B., Colombo, C., Costa, F.F., Costa, M.C., Costa-Neto, C.M., Coutinho, L.L., Cristofani, M., Dias-Neto, E., Docena, C., El-Dorry, H., Facincani, A.P., Ferreira, A.J., Ferreira, V.C., Ferro, J.A.,
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                                                                                                                                                               Bacteria;
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RS Simpson, A.J.G., Reinach, F.C., Arruda, P., Abreu, F.A., Acencio, M., Alvarenga, R., Alves, L.M. C., Araya, J.E., Baia, G.S., Baptista, C.S., Barros, M.H., Bonaccorsi, E.D., Bordin, S., Bove, J.M., Briones, M.R.S., Bueno, M.R.P., Camargo, A.A., Camargo, L.E.A., Carraro, D.M., Costa, M.R.P., Camargo, A.A., Camargo, L.E.A., Carraro, D.M., Carrer, H., Colauto, N.B., Colombo, C., Costa, F.F., Costa, M.C.R., Costa-Neto, E., Locar, C., El-Dorry, H., Factincani, A.P., Ferreira, A.J.S., Perreira, V.C.A., Ferro, J.A., Fraga, J.S., Franca, S.C., Franco, M.C., Frohme, M., Furlan, L.R., Garnier, M., Goldman, G.H., Goldman, M.L.S., Gomes, S.L., Gruber, A., Ho, P.L., Hoheisel, J.D., Junqueira, M.L., Lopes, S.L., Gruber, A., Ho, P.L., Hoheisel, J.D., Junqueira, M.L., Lopes, S.L., Gruber, A., Ho, P.L., Hoheisel, J.D., Junqueira, M.L., Machado, J.A., Machado, M.A., Madeira, A.M.B.N., Madeira, H.M.F., Matsukuma, A.Y., Menck, C.F.M., Miracca, E.C., Miyaki, C.Y., Monteiro-Vitcorello, C.B., Moon, D.H., Nagai, M.A., Nascimento, A.L.T.O., Netto, L.E.S., Nhani Jr., A., Nobrega, F.G., Nunes, L.R., Oliveira, M.A., de Oliveira, M.C., de Oliveira, R.C., Palmieri, D.A., Paris, A., Peixoto, B.R., Pereira, G.A.G., Pereira, Jr., H.A., Pesquero, J.B., Quaggio, R.B., Roberto, P.G., Santelli, R.V., Sawasaki, H.B., da Silva, A.C.R., da Silva, F.R., Ga Silva, A.M., Verjovski, Almeida, S., Vettore, A.L., Zago, M.A., Zatz, M., Meidanis, J. and Setubal, J.C., Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (02-JUN-2000) Organization for N Analysis, Bioinformatics Lab - IC/Unicamp,
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1363. .2460
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/gene="xF0852" /gene="similar to Sp|p06655 (percent identity: 45 %/que /note="similar to Sp|p06655 (percent identity: 45 %/que

%/query

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complement (5001...5077)
/gene="tRNA-Pro-2"
/product="tRNA-Pro"
/note="found by tRNAscan"
complement (5599...6327)
/gene="XF0855"
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ADGYPYFAVGTFFLLVDGRVCPLIGRVSNDMLTVDLTDHPQADVGSQVQLWGVQDGVVA
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IGLYEPVVDSKGGRLLLRASEMPCLVLGDATRLRQIEBLLSNALKFTPTDGCIDVET
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similarity; putative; ORF located using Glimmer/RBSfinder"
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                                                                                                                       AspLeuLysValArgGluArgSerIleSerSerGlyValAsnThrAlaHisThrProSer 138
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complement (6964...7641)
/gene="XF0857"
complement (6964...7641)
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complement (6327. .6944)
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                                                                                                                                                                                                       Submitted (24-OCT-2000) Department of Veterinary Pathobiology, University of Minnesota, 1971 Commonwealth Ave., St. Paul, MN
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Pasteurella multocida PM70 section
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Zhang, Q. and Kapur, V.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GlnPheArgTyrProValGlyAlaThrAsnProValValArgArgPheGlyThrAlaThr 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACACCCTCAAAACCCATCCCCAACGACAACCATCACCGCTCCGGCAAATAGCGGTTTCAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCATTGCTTTATCTC 5611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----IleValIleGlnHisThrAsnGlyPheValSerSerTyrIleHisIleLysAsp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ValAlaGlySerThrValThrSerAsnGlyMetTrpPheSerGlyArgAspGlyAspLeu 238
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US-10-018-706-2 (1-322) x AE006198 (1-12956)

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93 ArgGluIleGlyHisIleAsnAsnLeuAsnSerSerTyrThrIleTyrThrGlyGlnTrp
:::|||:::
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gene CDS

ValValLysLysProThrProThrProProValValGlnGlnProAlaProValAla 182

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CAAGCGGTGAATGCCGCCGCCGCCAGGCAGAGTGGTTATGCGGGTAATGCATTACGTGGT 10749 AspLeuIleAsnAlaSerAsnAlaGlyThrValIleGlnAlaAspHisAsnMetAspGly 256

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REFERENCE
AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cloning and characterisation of the rpoS gene fro
growth-promoting Pseudomonas putida WCS358: RpoS
siderophore and homoserine lactone production
Biochim. Biophys. Acta 1489 (2-3), 413-420 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            fdxA gene; ferrodoxin; lipoprotein; mismatch binding protein; muts gene; nlpD gene; RNA polymerase sigma factor; rpoS gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAAAGTATTTTAGTCAAAGATCAGCAAGAAGTTCGTGCGGGTCAACAGATTGCCAAAATG
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ProValAlaValGlnSerSerArgProProValGlnGlnHisProAlaValGlnLysPro
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                                                                                                                                                                                                 Direct Submission
Submitted (16-Misconsin, 445 Henry Mall, Madison, WI 53706, USA.
University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA.
Email: ecol@genetics.wisc.edu Phone: 608-262-2534 Fax:
               Submitted (02-SEP-1997) Guy Plunkett III, Laboratory of Genetics; University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA. Email: ecoli@genetics.wisc.edu Phone: 608-262-2534 Fax:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Blattner, F.R., Plinkett, G. III, Bloch, C.A., Perna, N.T., Riley, M., Collado-Vides, J., Glasner, J.D., Rode, C.K., May Gregor, J., Davis, N.W., Kirkpatrick, H.A., Goeden, M.A., R. Mau, B. and Shao, Y.
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Escherichia coli K12
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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Escherichia coli K12 MG1655 (
                                                                                                  Direct Submission
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Blattner, F.R.
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AL Submitted (13-OCT-1998) Laboratory of Genetics, University of Submitted (13-OCT-1998) Laboratory of Genetics, University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA

On Sep 9, 1997 this sequence version replaced gi:1789214.

This sequence was determined by the E. coli Genome Project at the University of Wisconsin-Madison (Frederick R. Blattner, director).

Supported by NIH grants HG00301 and HG01428 (from the Human Genome Project and NGHGR). The entire sequence was independently determined from E. coli K12 strain MG1655. Predicted open reading frames were determined using GeneMark software, kindly supplied by Mark Borodovsky, Georgia Institute of Technology, Atlanta, GA, 30332 (e-mail: markgamber.gatech.edu). Open reading frames that have been correlated with genetic loci are being annotated with CG site Nos., unique ID nos. for the genes in the E. coli Genetic Stock Center (CGSC) database at Yale University, kindly supplied by Mary Berlyn. A public version of the database is accessible Mary Berlyn. A public version of the database is accessible (http://ogsc.biology.yale.edu). Annotation of the genome is an ongoing task whose goal is to make the genome sequence more useful by correlating it with other data. Comments to the authors are appreciated. Updated information will be available at the E. coli Genome Project's World Wide Web site

(http://www.genetics.wisc.edu). *** The E. coli K12 sequence and its annotations are periodically updated; this is version M54. No sequence changes. Annotation updates: updated gene identifications and products; added promoters, protein binding sites, and repeated

Riley; added promoters, protein binding sites, and repeated or mames. This should allow them to be searched for in Entrez as gene names.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note="central position to predicted promoter:
'bound_moiety="Fur predicted site"
/product="orf, hypothetical protein"
/protein_id="AAC75893.1"
                                   'codon_start=1
'transl_table=
                                                                                                                                                                                                                     'note="factor Sigma70;
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gene="ygeH"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="factor Sigma70; predicted +1 start at 2991625"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="factor Sigma70; predicted +1 start at 2991612"
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                                                                         P43018"
                                                                                      aa ORF is 39 pct identical (7 approx. 168 aa protein IAGB_S;
                                                                                                                                                                                                                   predicted +1
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Best Local Similarity:
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 ValArgArgPheGlyThrAlaThrValAlaGlySerThrValThrSerAsnGlyMetTrp 230
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US-10-018-706-2 (1-322) x AE000369 (1-9720)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56 LeuAlaIleGlySerGlnValIleThrAspSerGlnGlyValProAsnArgTyrGlnVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36 LysProThrTyrAsnSerThrSerGlySerGlySerHisArgThrSerGlySerGlyGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LysGlnGlyAspThrValSerLysIleAlaGlnArgTyrGlyLeuAsnTrpArgGluIle 95
                                             AlaThrGlySerSerGlyValMetGlnPheArgTyrProValGlyAlaThrAsnProVal 210
                                                                                                                                                                                                                                                      GlnHisProAlaValGlnLysProThrProProValValValValLysLysProThrPro 170
                                                                                                                                                                                                                                                                                                            AAAACCGCATCGGTTACACCGTCATCAGCGGTACCGAAATCATCCTGGCCGCCAGTAGGG 908
                                                                                                                                                                                                                                                                                                                                              AsnThrAlaHis---ThrProSerProValAlaValGlnSerSerArgProProValGln 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                            TrpSerGlyAspLeuLys----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCGCGACTGAACGGCATTTCCCCCCCCTTACACCATTGAAGTTGGTCAGAAACTAAAACTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GlyHisIleAsnAsnLeuAsnSerSerTyrThrIleTyrThrGlyGlnTrpLeuThrLeu 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAACGGGGGATACGCTATATCGTATTTCGCGCACCACGGGAACCAGCGTAAAAGAACTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAATCTCTGGGTATCGTGATGTTGTTATCGGTTGGACTGCTTTTGGCCGGGCTGT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LysArgLeuGlyLeuIlePheGlyValIleThrThrCysIleLeuAlaGlyCysAlaSer
                                                                                                                                                   ThrProProValValGlnGlnProAlaProValAlaProProValThrGluAlaProPhe 190
                                                                                                                                                                                                      CAACGTTGTTGGTTATGGCCAACGACAGGGAAAGTTATCATG----
                                                                                                                                                                                                                                                                                                                                                                                                            -----GGTGGGGCGAAAAGTAGCAGTATTACACGTAAATCAACCGCCAAATCAACGACC 9148
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NNNIKSLDYWLMQINQMHIPLLKKRGIIKDERDLLDNPCLNIKIGTEILYNHFSRCGV
TWQCLGTYNAGFAMDNQKKRQQYAPKYILYIPGLMN"
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NKEIANFLQLSRKTVETHRLNIMKKLDVHSGIELIKTALRMGVCTI"
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'protein_id="AAC75894.1"
'db_xref="GI:1789219"
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24.92%
14.25%
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Matches:
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AUTHORS
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ECU28375/c
LOCUS
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (01-JUN-1995) Guy Plunkett, Laboratory of Genetics, University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA This sequence was determined as part of the E. coli Genome Project (Frederick R. Blattner, director) at the University of Wisconsin-Madison. Supported by award H600301 from the NIH Human Genome Project. The entire sequence was independently determined from E. coli MG1655; overlaps with other sequence determinations are annotated. This entry should be considered somewhat provisional; it will be updated and merged with others at a later date.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ECU28375
Escherichia coli K-12 genome;
U28375
U28375.1 GI:887800
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SerSerTyrIleHisIleLysAspAlaGlnValLysThrGlyAspThrValArgThrGly 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGCAACCAGCTGGCTACGGTAATCTCATCATTAAACACAGTGAAGATTACATT 8887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AspHisAsnMetAspGlyAlaSer-----IleValIleGlnHisThrAsnGlyPheVal 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATCTCAGCTCCACGGGTACACCTATTTACGCCGCGGGTGCAGGAAAGGTGGTGTATGTG 8947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PheSerGlyArgAspGlyAspLeuIleAsnAlaSerAsnAlaGlyThrValIleGlnAla 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGTTACCGTGCAACGGCAATTGATCCGCTACGTTACTTG 8728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SerArgAsnGlyValTyrValAspProLeuThrValLeu 321
                                                                                                                                                                                                                                                                           /map="approximately 64 to 65 minutes"
/note="this sequence comprises the following lambda
/notes: DD644(EC30K464-1), DD645(EC27-1154),
DD649(EC22-159), and DD653(EC18-341); M13Janus vector was
used for subcloning"
                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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                                                                                                    /1 abel=ÖRF 0148
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                                                                                                                                                                                                                  complement (5131. .5562)
note="ORF_f143"
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/tabel=ORF f136
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672; alternate gene names suA3
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Svpnilnstgaatdksylslnpdkypnyrllihagkloneikshytkdeiqglitlte
Ntrlitekpmgtfilastfeddktaalthydavmlrdslmgkvalvsdgansvaak
KVLLTLMDYMSTPDQIKRMQDVISNPKRLDGIPVQMAAVHIRPDSNSPVMADVQEEGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AVTTGGFNSETVQDVMLGAVERRFGNDLPSSPVEWLTDNGSCYRANETRQFARMLGLE
PKNTAVRSPESNGIAESFVKTIKRDYISIMPKPDGLTAAKNLAEAFEHYNEWHPHSAL
GYRSPREYLRQRACNGLSDNRCLEI"
                                                                                                                                                     /note="corresponds to X52798 differences outside tRNA"
                                                                                                                                                                                                              DS"
                                                                                                                                                                                                                                                                                                                                                                                                                     complement(7851. .8687)
/note="was £268 and £157p before splice"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MTVSLVARQHGVAASQLFLWRKQYQEGSLTAVAAGEQVVPASELAAAMKQIKELQRLL
GKKTMENELLKEAVEYGRAKKWIAHAPLLPGDGE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="corresponds to V00610 (ISIS2X) 1. .1327"
complement(6189. .7094)
/note="ORF_f301"
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Lrdylsaipleinekarykpgianyhniitcgfstllpyirqqplamqqrfnllfpdf
VDHIQSPLPLASTLLERITFYAKKNRDELDKISCKWCCD"
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complement (5779. .6204)
/note="ORF_f141"
                                                                                             complement (8801.
                                                                                                                                 complement (8801. .8874)
                                                                                                                                                                                        complement (8664. .8962)
                                                                                                                                                                                                                                PQLWNHKQNDALGLYLDLLIQAINTGTINAEDWQKGDRLKSVALLIAYLDKANFYVME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement (7506. .7805)
/note="ORF_f99"
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LERKPAVPPSKRAHTGRVAVKESNQRWCSDGFEFCCDNGERLRVTFALDCCDREALHW
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                                                       product="tRNA-Gly"
                                                                           gene="glyU"
                                                                                                               gene="glyU"
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                                                                                                                                                                                                                                                                                                                                              protein_id="AAA83045.1"
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transl_table=
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                                                                                               .8874)
                 GGG; aa: Glycine; CG Site No.
suA36, sufD, sumA, sumB, sup
                                                                                                                                                                     (ECTRNAG); 4 sequence
                   sumB, supT"
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                   ACGGCTTACGCCCATAATGACACGATGCTGGTAAATAATGGGCAAAGCGTGAAGGCTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCGCGACTGAACGGCATTTCCCCCCCCTTACACCATTGAAGTTGGTCAGAAACTAAAACTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GlyHisIleAsnAsnLeuAsnSerSerTyrThrIleTyrThrGlyGlnTrpLeuThrLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LysGlnGlyAspThrValSerLysIleAlaGlnArgTyrGlyLeuAsnTrpArgGluIle
                                                   SerSerTyrIleHisIleLysAspAlaGlnValLysThrGlyAspThrValArgThrGly
                                                                                             GGCAACCAGCTGCGTGGCTACGGTAATCTCATCATGATTAAACACAGTGAAGATTACATT
                                                                                                                                 AspHisAsnMetAspGlyAlaSer-----IleValIleGlnHisThrAsnGlyPheVal
                                                                                                                                                                       ATCTCAGCTCCACGGGTACACCTATTTACGCCGCGGGTGCAGGAAAGGTGGTGTATGTG
                                                                                                                                                                                                          PheSerGlyArgAspGlyAspLeuIleAsnAlaSerAsnAlaGlyThrValIleGlnAla
                                                                                                                                                                                                                                                                                  ValArgArgPheGlyThrAlaThrValAlaGlySerThrValThrSerAsnGlyMetTrp
                                                                                                                                                                                                                                                                                                                              TCGACAGCAGATGGCGGC--
                                                                                                                                                                                                                                                                                                                                                                AlaThrGlySerSerGlyValMetGlnPheArgTyrProValGlyAlaThrAsnProVal
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/protein_id="AAA83046.1"
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Complete nucleotide sequence of the prophage VT1-Sakai carrying the Shiga toxin 1 genes of the enterohemorrhagic Escherichia coli O157:H7 strain derived from the Sakai outbreak Gene 258 (1-2), 127-139 (2000) 20564182 4 (sites)
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Becherichia coli O157:H7 DNA,
APO02563 BA000007
APO02563.1 GI:13363121
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20198780
2 (sites
                                                                                                                                                    Direct Submission
Submitted (26-JUN-2000) Ken Kurokawa, Osaka University, Genome
Information Research Center; 3-1, Yamadaoka, Suita, Osaka 565-0871,
Japan (E-mail:ken@gen-info.osaka-u.ac.jp,
URL:http://www.gen-info.osaka-u.ac.jp/, Tel:81-6-6879-8365,
Fax:81-6-6879-2047)
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Comparative analysis of the whole set of rRNA operons between an enterohemorrhagic Escherichia coli O157:H7 Sakai strain and an Escherichia coli K-12 strain MG1655

Syst. Appl. Microbiol. 23 (3), 315-324 (2000)

20557356

3 (sites)
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Complete nucleotide sequence of the prophage VT2-Sakai carrying the verotoxin 2 genes of the enterohemorrhagic Escherichia coli O157:H7 derived from the Sakai outbreak
Genes Genet. Syst. 74 (5), 227-239 (1999)
                                                                                                                                                                                                                                                                                                                 5 (bases 1 to 266658)
Ohnishi,M., Kurokawa,K., Makino,K., Yasunaga,T.,
Hayashi,T.
                                                                                                                                                                                                                                                                                                                                                                                  Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and genomic comparison with a laboratory strain K-12 DNA Res. 8 (1), 11-22 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hayashi,T., Makino,K., Ohnishi,M., Kurokawa,K., Ishii,K., Yokoyama,K., Han,C.-G., Ohtsubo,E., Nakayama,K., Murata,T., Tanaka,M., Tobe,T., Iida,T., Takami,H., Honda,T., Sasakawa,C., Ogasawara,N., Yasunaga,T., Kuhara,S., Shiba,T., Hattori,M. and Shinagawa,H.
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Kurokawa,K., Yasunaga,T., Yokoyama,K., Makino,K., Shinagawa,H. and
Tanzahi T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Escherichia coli O157:H7
Bacteria, Proteobacteria,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Escherichia coli O157:H7 (strain:O157:H7, sub_strain:RIMD 0509952)
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|||:::||||||:::|||
CAAAAARCGCCACTATGGGGAGCACGGATGCGGCATCTGTTCGCCTGCATTTCCAGATT 9022
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                             /organism="Escherichia
/strain="O157:H7"
                                                                               1. .266658
                                                                                                       ocation/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                               /note="inhibitor of CsrA"
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complement (2444. .2989)
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|PROTECTION | PROTECTION | PROTECTION |
| CHARLIAHLHIP | IGDSKHGDLRQNRSGAEHFGLQRLMLHASQLSLTHPFTGEPLT
|| IHAGLDDTWMQALSQFKWRGLLFENERVEFSAPSGQDGERSS"
| COMPLEMENT | 1493. . . 1822)
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complement (711. 1493)
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100 in 149 aa (Conserved in E.coli K-12)"
codon_start=1
                                                                                                                                                                                                                                                                                                                                     note="similar to SYD_ECOLI gi|1789157 percent identity in 181 aa (Conserved in E.coli K-12)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    codon_start=1
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                                                                                                                                                                                                                                                                                                                 codon start=1
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in 260 aa (Conserved in E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .2233)
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.1"
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.coli K-12)"
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Best Local S:
Query Match:
DB:
                                                                                     Percent Similarity:
Best Local Similarity:
                                                                                                                                                     Score:
                                                                                                                                                                                                      Alignment Scores:
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                                                                                                                                                                                                                                                               /note="similar to SDAA_ECOLI gi|1788116 percent identity
77 in 455 aa, similar to SDAB_ECOLI gi|1789161 percent
identity 99 in 455 aa (Conserved in E.coli K-12)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene≃"EC83656"
5938. .7227
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/protein_id="BAB37077.1"
/db_xref="G1:13363126"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AIQKVPAMRKYSGHISNVFVVVMGLIAISAIFYSLFS"
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7285. .8652
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100 in 429 aa (Conserved in E.coli K-12)
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/note="similar to YGDH_ECOLI g1|1789159 percent identity
99 in 454 aa (Conserved in E.coli K-12)"
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of 460 of the complete genome. AE012272 AE008922 AE012272.1 GI:21112795
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Xanthomonas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LysArgLeuGlyLeuIlePheGlyValIleThrThrCysIleLeuAlaGlyCysAlaSer 35
CGTTACCGTGCAACGGCAATTGATCCGCTACGTTACTTG
                                                                       SerArgAsnGlyValTyrValAspProLeuThrValLeu 321
                                                                                                                                                                                                                                                                                                                       ACGGCTTACGCCCATAATGACACGATGCTGGTAAATAATGGGCAAAGCGTGAAGGCTGGG
                                                                                                                                                                                                                                                                                                                                                                                                   SerSerTyrIleHisIleLysAspAlaGlnValLysThrGlyAspThrValArgThrGly
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JOURNAL MEDLINE PUBMED REFERENCE AUTHORS
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Mature 417 (6887), 459-463 (2002)

Machado, R.B., Monteiro-Vitorello, C.B., Van Sluys, M.A., Almeida Comparison of the genomes of two Xanthomonas pathogens with Comparison of the Gruphia, J.R., Bertolini, M.C., Camaryan, F., Cardozo, J., Camaryan, F., Cardozo, J., Camaryan, F., Cardozo, J., Camaryan, F., Cardozo, J., Camaryan, F., Cardozo, J., Camaryan, F., Cardozo, J., Camaryan, F., Cardozo, J., Camaryan, F., Cardozo, J., Camaryan, F., Cardozo, J., Camaryan, F., Cardozo, J., Camaryan, F., Cardozo, J., Camaryan, F., Cardozo, J., Camaryan, F., Cardozo, J., Camaryan, F., Cardozo, J., Camaryan, F., Cardozo, J., Camaryan, F., Cardozo, J., Camaryan, F., Cardozo, J., Camaryan, F., Cardozo, J., Camaryan, F., Cardo
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Xanthomonas campestris pv. campestris str. ATCC 33913
Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
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Submitted (28-NOV-2001) Departmento
Sao Paulo, Av. Prof. Lineu Prestes
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Kitajima, J.P.
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ocated using Blastx/Glimmer/Genemark"
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Query Match:
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Best Local Similarity:
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    82
                                                                                   62
                                                                                                                                                               45 SerGlySerHisArgThrSerGlySerGlyGlyLeuAlalle------GlySerGln
                                                                                                                         GGTGGCGCTTCGCGGCCCAGTGCCGCGCGCGCGTCCGTCGGTGCCGCGTCCCGGTGCAACC
SerLysIleAlaGlnArgTyrGlyLeuAsnTrpArgGluIleGlyHisIleAsnAsnLeu 101
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located using Blastx/Glimmer/Genemark"
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ocated using Blastx/Glimmer/Genemark"
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                                                       1 (bases 1 to 10822)
Stover,C.K., Pham,X.Q., Erwin,A.L., Mizoguchi,S.D., Warrener,P.,
Hickey,M.J., Brinkman,F.S., Hufnagle,W.O., Kowalik,D.J., Lagrou,M.,
Garber,R.L., Goltry,L., Tolentino,E., Westbrock-Wadman,S., Yuan,Y.,
Brody,L.L., Coulter,S.N., Folger,K.R., Kas,A., Larbig,K., Lim,R.,
Smith,K., Spencer,D., Wong,G.K., Wu,Z. and Paulsen,I.T.
Complete genome sequence of Pseudomonas aeruginosa PA01, an
opportunistic pathogen
Nature 406 (6799), 959-
20437337
                                                                                                                                                                                                                                                                                                                                                                     Pseudomonas aeruginosa
                                                                                                                                                                                                        Pseudomonas.
                                                                                                                                                                                                                         Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
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Stover, C.K., Pham, X. Q.T., Erwin, A.L., Mizoguchi, S.D., Warrener, P., Hickey, M.J., Brinkman, F.S.L., Hufnagle, W.O., Kowalik, D.J., Lagrou, M., Garber, R.L., Goltry, L., Tolentino, E., Westbrook-Wadmann, S., Yuan, Y., Brody, L.L., Coulter, S.N., Folger, K.R., Kas, A., Larbig, K., Lim, R.M., Smith, K.A., Spencer, D.H., Wong, G.K.-S., Wu, Z., Paulsen, I.T., Reizer, J., Saier, M.H., Hancock, R.E. W., Lory, S. and Olson, M.V.

Direct Submission
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/gene="PA4925"
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/gene="PA4925"
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/gene="PA4924"
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/gene="PA4926"
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'protein_id="AAG08308.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ThrProThrProProValValGlnGlnProAlaProValAlaProProValThrGluAla 188
                                                                                                                                                                                                                                                                                                    ValGlnGlnHisProAlaValGlnLysProThrProProValValValValLysLysPro 168
                                                                                                                                                                                                                                                                                                                                                                                        SerGlyValAsnThrAlaHisThrProSerProValAlaValGlnSerSerArgProPro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ValProAsnArgTyrGlnValLysGlnGlyAspThrValSerLysIleAlaGlnArgTyr 88
                                    ProValValArgArgPheGlyThrAlaThrValAlaGlySerThrValThrSerAsnGly 228
                                                                                                                         ProPheAlaThrGlySerSerGlyValMetGlnPheArgTyrProValGlyAlaThrAsn 208
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GDGETPLVVLLTPGRFWETYFEHLYLARQLGF PLAGHDITVRADATLYLKTLGGLKRV
HAVLKRLDDDPCDFLEKTDSALGI FGLLEAVEQGRVLVANALGSGVLESPGLLGFD
QACRRLLGEBLALFSLDTRWCGBPQALEAI LAALFDLVI KPAFPGQRCEPLFGHALDS
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ALDPARTDIGEALDFINRILWSIAAALSGFALDDMTRDDGWRFINIGRRI ERVRFFAES
IAAFIGSAWDAGALBWILEIGNSGITYRSRYIASPQLVPVLDILLLHENGDHSIJRFOL
QALERSIERIHEEFGAPREREIRTIGERLRSPDIAALESPLFGAAGIDEVIVGIARIL
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YWVMPGGLTRVASAADAEVVSMQRGGASKDTWVLAERAVGGEPLRPRRLGVRDLVRED
PYLPSRVVENLFWYGRYAERCDDHARLLRVVLSRYVDADGDEEALRSALALAGGIGLL
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(db_xref="GI:9951205"
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LNALLADLYGDQRLLAEGLLPSELVFGHPNFLWPALGIRPFGGIFLHSYAVDLARDAD
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/gene="PA4927"
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LLVAAAALMEKIFREFALFDAQATQVATPLDEVLLERRRGVCQDFAHLMLACLRARGLAA
RYVSGYLLTREPPGQARLIGADASHARVSLYCPERIGWUPFDPTNDLLFDLEHITLAWG
RDFSDVSPLRGVILGGGSHDPEVRVTVLPLQETAG"
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Latreille,P., Courtney,L., Porwollik,S., Ali,J., Dante,M., Du,F.,
Hou,S., Layman,D., Leonard,S., Nguyen,C., Scott,K., Holmes,A.,
Grewal,N., Mulvaney,E., Ryan,E., Sun,H., Florea,L., Miller,W.,
Stoneking,T., Nhan,M., Waterston,R. and Wilson,R.K.
Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                          EC numbers were kindly provided by Junko Yabuzaki and the Kyoto Encyclopedia of Genes and Genomes; http://www.genome.ad.jp/kegg/, and Pedro Romero and Peter Karp at EcoCyc; http://ecocyc.PangeaSystems.com/ecocyc/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (29-MAR-2001) Genome Sequencing Center, Department Genetics, Washington University School of Medicine, 4444 Fore Park Boulevard, St. Louis, MO 63108, USA COMMENT Supported by NIH grant 5U 01 AI43283
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AE008839 AE006468
                                                                    This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistries or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Coding sequences below are predicted from manually evaluated computer analysis, using similarity information and the progiging from the progiging in the programmer; http://www.tigr.org/softlab/glimmer/glimmer.html and GeneMark; http://opal.biology.gatech.edu/GeneMark/
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The Salmonella typhimurium Genome Sequencing Project.
Direct Submission
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Salmonella typhimurium LT2
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                                                                                                                                                                                                http://kinich.cifn.unam.mx:8850/db/regulondb_intro.frameset
                                                                                                                                                                                                                                ReguonDB;
                                                                                                                                                                                                                                                   The analyses of ribosome binding sites and were kindly provided by Heladia Salgado, Ju
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 413 (6858), 852-856 (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MetTrpPheSerGlyArgAspGlyAspLeuIleAsnAlaSerAsnAlaGlyThrValIle 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ArgIleSerArgAsnGlyValTyrValAspProLeuThrValLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TACACCAGCACCTACGCGCACAACAGCCGCTTGCTGGTGAAGGAGGGGCAGATGGTCGGC 5368
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                       compressions and repeats; all regions were covered by sequence om more than one ml3 subclone.
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Location/Qualifiers
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Complement (1542. .2405)

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identity in aa 1 - 408"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="similar to E. coli orf, hypothetical (AAC75167.1); Blastp hit to AAC75167.1 (274 dentity in aa 1 - 274"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     transl_table=11
product="putati
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protein_id="AAL21898.1"
db_xref="GI:16421573"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="putative RBS for yohL; RegulonDB:STMS1H003070"
                                                                                                                                                                                                                                                                                                                                            codon_start=1
transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene="yohM"
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                                                                                                                                                                                                                                                                                                                                                                                                      note="transcriptional regulator SprB (gi|5007028)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="putative RBS for yohm; RegulonDB:STMS1H003071"
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RBS for STM3025; RegulonDB:STMS1H003072"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTGAATGGCATTTCTCCGCCTTATACTATTGAGGTGGGGCAGCGAATTAAAGTG---CGC
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                                                                                                                                                                  CAGCTGCGCGGTTACGGCAATCTCATCATGATTAAGCACAATGAAGATTACATTACGGCT
                                                                                                                                                                                                          AsnMetAspGlyAlaSer-----IleValIleGlnHisThrAsnGlyPheValSerSer
                                                                                                                                                                                                                                                                                                                                                                               ArgPheGlyThrAlaThrValAlaGlySerThrValThrSerAsnGlyMetTrpPheSer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGCAGCGCAAAGAGTAGCACTTCAACACGCAAAACCAGCAATAAAACAGCAACAAAAACT 18602
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGCGATACGTTGTATCGTATATCGCGCGCTACGGGAACCAGCGTGAAAGAACTGGCCCGA 18719
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ATCGCTACGATGGGCACGGATGCCGCATCCGTAAGACTACACTTCCAGATTCGCTAC 18221
                               TACGCTCATAATGACACCATGCTGGTTAATAATGGACAAAGCGTTAAAGCGGGGCAAAAA 18281
                                                                                                                      TyrIleHisIleLysAspAlaGlnValLysThrGlyAspThrValArgThrGlyGlnArg
                                                                                                                                                                                                                                                       GGCGCGCGGAACGCCTGTTTATGCGGCGGGAGCGGGTAAAGTTGTCTATGTCGGGAAC
                                                                                                                                                                                                                                                                                             GlyArgAspGlyAspLeuIleAsnAlaSerAsnAlaGlyThrValIleGlnAlaAspHis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGTTGGGTATGGCCTGCTAACGGTAAAGTGATTTTA--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GlyAspLeuLys-----ValArgGluArgSerIleSerSerGlyValAsnThr 133
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AUTHORS
TITLE
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AL627277/c
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MEDLINE
PUBMED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Parkhill, J., Dougan, G., James, K.D., Thomson, N.R., Pickard, D., Wain, J., Churcher, C., Mungall, K.L., Bentley, S.D., Holden, M.T.G., Sebaihia, M., Baker, S., Basham, D., Brooks, K., Chillingworth, T., Connerton, P., Cronin, A., Davis, P., Davies, R.M., Dowd, L., White, N., Farrar, J., Feltwell, T., Hamlin, N., Haque, A., Hien, T.T., Holroyd, S., Jagels, K., Krogh, A., Larsen, T.S., Leather, S., Moule, S., O'Gaora, P., Parry, C., Quail, M., Rutherford, K., Simmonds, M., Skelton, J., Stevens, K., Whitehead, S. and Barrell, B.G. Stevens, K., Whitehead, S. and Barrell, B.G. Complete genome sequence of a multiple drug resistant Salmonella enterica servorar Typhi CT18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AL627277 AL513382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (25-OCT-2001) Submitted on behalf of the sequencing team, Sanger Centre, Wellcome Trust Geno Hinxton, Cambridge CB10 1SA, UK E-mail: parkhill@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Salmonella enterica subsp. enterica serovar Typhi.
Salmonella enterica subsp. enterica serovar Typhi
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Details of S. typhi sequencing at the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Notes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Parkhill,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 413 (6858), 848-852 (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (bases 1 to 230050)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           http://www.sanger.ac.uk/Projects/S_typhi/).
                                                   /transT_table=11
/product="putative serine transporter"
/protein_id="Cab2796.1"
/protein_id="Cab2796.1"
/db_xref="GI:16504050"
/db_xref="GI:16504050"
/db_xref="SPTREMBL:Q8Z435"
/translation="MKTTQ755TIASIDSRSAWRKTDTWWMLGLYGTAIGAGVLFLPIN
ACVGGMIPLIIMAILAFWTTPTASIDSRSAWRKTDTWWMLGLYGTAIGAGVLFLPIN
ACVGGMIPLIIMAILAFAHRGLTRFVLSGKNPGEDITEVVBEHFGIGAGKLIT
LLYFPAIYPILLVYSVAITMTVESFLTHQLAINPPPRAILSILLIVGMWTIVRFGEQM
IVKAMSILVFPFVAALMLLALYLIPQWNGAALETLSFDSAASTGNGLWMTLWLAIPVM
VFSFNHSPIISSFAVAKREEYGEGAEKKCSKILAFAHIMWULTVMFFVFSCULSLTPA
                                                                                                                                                                                                                                                                                        Orthologue of E. coli sdaC (SDAC_ECOLI);
SDAC_ECOLI (429 aa), 95% identity in 429
               DLAAAKEQNISILSYLANHENAPIIAWMAPIIAMIAITKSELGHYLGAREGENGWVIK
SLRGKGKSIEINKLNKITALEMLVTTWIVATLNPSILGMIETLGGPIIAMILFLMEMY
                                                                                                                                                                                                                                                                                                                                         overtap
                                                                                                                                                                                                                                                                                                                                                                               aa overlap
                                                                                                                                                                                                                                                                                                                                                         Fasta hit to TDCC_ECOLI (443 aa), 50% identity in 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="STY3109"
/note="sdaC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Salmonella enterica subsp. enterica serovar
Typhi"
                                                                                                                                                                                                                                                                                                                                                                                                   /note="Fasta hit to Q46940 (409 aa), 40% identity in 416
                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="STY3109"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                         codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         strain="CT18"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   _xref="taxon:90370"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genome Campus,
                                                                                                                                                                                                                                                                                             Fasta hit to
aa overlap"
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available

gene CDS

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misc_feature
                         /protein_id="CAD02799.1"
/db_xref="G1:16504053"
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CVANAILLAPHVMRFNAGSTNEKFRDIARAMGVKVEGLSLEEARNAAVEAVFTLNRDVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="Sptrembl:002434"
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AEUGCGGEUGYACSMANAGLAELIGGSPAQVCITAREIAMFTGKDMNAKYRETSRGGLAMK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Pfam match to entry PF01367 5_3_exonuclease, 5'-3' exonuclease, score 120.40, E-value 3.3e-32" complement (4042. .5190)
/gene="STY3.12"
                                                                                                                                                                                                                                                                                                                                                                        Orthologue of E. coli fu
FUCO_ECOLI (383 aa), 91%
/codon_start=1
/transI_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3201. .3947
/gene="STY3111"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="mlasprecyptrefvrentvaahllivdalnlirrihavqgsp
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nlegiyahldevpekwrkklethkemaflcrdiarlqtdlhidgnlqdlrlvr"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fasta hit to SDHL_ECOLI (454 aa), 77% identity in 455
                                                                                                                                                                                                                                                                                                         /product="1,2-propanediol oxidoreductase (lactaldehyde
reductase)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fasta hit to ADH2_ECOLI (383 aa), 44% identity in 371 aa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement (4042. .5190)
/gene="STY3112"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gene="STY3110"
/note="Fasta hit to TDCG_ECOLI (454 aa), 73% identity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .657. .3024
/gene="STY3110"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="5'-3' exonuclease"
/protein_id="CAD02798.1"
/db_xref="GI:16504052"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Orthologue of E. coli exo (EX9 ECOLI); Fasta hit
3X9 ECOLI (281 aa), 88% identity in 264 aa overlap"
/codon start=1
/rrans1 table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       135. .3950
gene="STY3111"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="Fasta hit to EUTG_ECOLI (395 aa), 40% identity in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               135. .3950
gene="STY3111"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :e="sdaB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            xref="SPTREMBL:Q8Z433"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  _table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                          coli fucO (FUCO_ECOLI); Fasta hit to
a), 91% identity in 382 aa overlap"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     dehydratase
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                                                       US-10-018-706-2 (1-322) x AL627277
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18 LeuGlyLeuIlePheGlyValIleThrThrCysIleLeuAlaGlyCysAlaSerLysPro
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Sato gene

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37

gene CDS

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Percent Similarity:
Best Local Similarity:
Query Match:
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EENLDKALMIAHEVEYLAQIYLSTLAIVDPVPYLDDEAIAIVLEKFKTYGLRIEE"
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/note="Pfam match to entry PF00465 Fe-ADH, Iron-containing alcohol dehydrogenases, score 655.70, E-value 2.4e-193"
complement(4354. .4416)
                                                                                                                                                                                                                                                                                                                                       AMLLCLISAFSGGHIGLLALTLCSAFMSIQYPTIFSLGIKNLGODTKYGSSFIVMTII
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                                                                                                                                                                                                                                                                                                                                                                                    /t-anslation="MGNTTIOTOSFRAVDAROSKSKRYIIPRALICSLFFLMAVANNI
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CWSYLIRYAIEEIPGMTPGFAANYLTGTMVCFFIGRTTGTWLISRFAPHKVLAAYALL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               // note="orthologue of E. coli fucp (FUCP_ECCLI); Fasta hit
to FUCP_ECCLI (438 aa), 92% identity in 438 aa overlap"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6410. .7726
/gene="STY3115"
/note="fucP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Pfam match to entry PF00596 Aldolase_II, Class II Aldolase and Adducin N-terminal domain., score 337.10, E-value 2e-97"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Orthologue of E. coli fucA (FUCA_ECOLI); Fasta hit to FUCA_ECOLI (215 aa), 92% identity in 215 aa overlap"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement (4069.
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/note="Fasta hit to YGBL_ECOLI (212 aa),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement (5207.
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/gene="STY3112"
                                                                                                                                                                                                                                         /gene="STY3116"
/note="fucI"
7758. .9488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="PS00913 Iron-containing alcohol dehydrogenases"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="PS00060 Iron-containing alcohol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             product="L-fucose permease"
protein_id="CAD02801.1"
db_xref="GI:16504055"
db_xref="SPTREMBL:Q8Z430"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      transl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            product="fuculose-1-phosphate aldolase"
protein_id="CAD02800.1"
db_xref="0]:15504054"
                                                                    0.00535
232.50
40.19%
24.44%
13.92%
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Matches:
Conservative:
Mismatches:
Indels:
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AF260132
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                                                                                       AF260132 DNA linear Pseudomonas putida putative protein-L-isoaspartate O-methyltransferase (pcm) gene, partial cds; and NI
Pseudomonas putida.
                                                          AF260132
                                        AF260132.1
                                                                                                                                                                                                                                                                                                                                                                                                                                   CAGCTGCGCGGTTACGGCAATCTCATCATGATTAAGCACAATGAAGATTACATTACGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GlyArgAspGlyAspLeuIleAsnAlaSerAsnAlaGlyThrValIleGlnAlaAspHis
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                                                                                                                                                                                                           CGGGCGACGCCATCGATCCGCTGCGTTATCTG
                                                                                                                                                                                                                                            AsnGlyValTyrValAspProLeuThrValLeu
                                                                                                                                                                                                                                                                                                                  IleAlaSerMetLysAsnGlnProSerGlyAlaAlaLeuPheGluPheArgIleSerArg
                                                                                                                                                                                                                                                                                                                                                                                            TyrIleHisIleLysAspAlaGlnValLysThrGlyAspThrValArgThrGlyGlnArg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCTGCGGTCAGACCGTCATCTTCGGTGCCAAAATCCTCCTGGCCGCCGGTGGGGCAGCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AlaHisThr---ProSerProValAlaValGlnSerSerArgProProValGlnGlnHis 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGCAGCGCAAAGAGTAGCAGTTCAACACGCAAAAACCAGCAATAAAACAGCAACAAAAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GlyAspLeuLys----
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                                      GI:7839529
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   73
                                                                         60 SerGlnVallleThrAspSerGlnGlyValProAsnArg------
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Ojangu, E.-L., Tover,
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                                                                                                                                                                                                                     LeullePheGlyVallleThrThrCysIleLeuAlaGlyCysAlaSerLysProThrTyr
 TyrGlnValLysGlnGlyAspThrValSerLysIleAlaGlnArgTyrGlyLeuAsnTrp
                                      GCGCGGGTGGTCGACCGCAACAACACCGTGCCCCAAGCGCCCGGCGGTGACTTCTGGGCAA
                                                                                                                                               AsnSerThrSerGlySerGlySerHisArgThrSerGlySerGlyGlyLeuAlaIleGly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /trānslation="MGSLLVGCSSTSSNSARVVDRNNTVPKRRAVTSGQYIVRGDTLFSIAFRYGMYKELAARNGIQAFYIIRFQQAIRFSGSSSRTTVVSSPSSSSRTTVTTRRPUGSTATRAKSTSKRATSABSAFAVVATVPAAAERAVGGSWTWPRANGVLIGKFASNGSLAKGIDIAGDLGQPVFAASDGAVVYAGSGLRGYGELIIIKHSDTYVSAYGHNRRLLVR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="NlpD"
/protein_id="AAF70311.1"
/db_xref="GI:7839531"
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                                                                                                                                                                                                                                                                                                                                                                                             Coxiella burnetii SurE, lii
response sigma factor RpoS
AF244357
2 (bases 1551 to 2609)
Seshadri,R. and Samuel,J.E.
Direct Submission
Submitted (10-MAR-2000) Medical Microbiology and Immunology, Texas
A and M Health Science Center, 407 Reynolds Medical Bldg., College
Station, TX 77843-1114, USA
                                                                                                                                                                                               Bacteria; proteobacteria; gamma subdivision; Legionellaceae group; Coxiella Group; Coxiella.

1 (bases 1 to 2609)
Seshadri, R. and Samuel, J.E.
Characterization of a stress-induced alternate sigma factor, RpoS, of Coxiella burnetii and its expression during the development
                                                                                                                                                                                                                                                                                                                     Coxiella burnetii.
Coxiella burnetii
                                                                                                                                          Infect. Immun. 69
21340372
                                                                                                                                                                                                                                                                                                                                                                                 AF244357.2 GI:8141681
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lipoprotein precursor NlpD,
poS genes, complete cds.
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Direct Submission
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 Perna, N.T., Plunkett, G. III, Burland, V., Mau, B., Glasner, J.D., Rose, D.J., Mayhew, G.F., Evans, P.S., Gregor, J., Kirkpatrick, H.A., Posfai, G., Hackett, J., Klink, S., Boutin, A., Shao, Y., Miller, L., Grotbeck, E.J., Davis, N.W., Lim, A., Dimalanta, E., Potamousis, K., Apodaca, J., Anantharaman, T.S., Lin, J., Yen, G., Schwartz, D.C., Welch, R.A. and Blattner, F.R.
                                                                                                                                                               Escherichia coli O157:H7 EDL933
Escherichia coli O157:H7 EDL933
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SVFNILNSTGAATDKSYLSLNPDKYPNYRLLIHSAKLQNEIKSHYTKDEIQGLLTLTE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /function="orf; Unknown function"
/note="Residues 87 to 185 of 342 are 97.97
to residues 1 to 99 of 99 from Escherichia
Strain MG1655: B2862"
                                   KVLLTLWDYMSTPDQIKRMQDIISNPKRLDGIPGQMNAVHI"
                                                                                                                                                                                                                                                                  complement (1492. .2097)
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/gene="Z4201"
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                                                                                                                                                         /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       transl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Escherichia
/strain="EDL933"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="Z4200"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="Z4200"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /protein_id="AAG57991.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                transl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="Z4199"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="enterohemorrhagic"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        translation="MINKLLLAYLIGLVVTSTLIFIFSEEKVTYRLFAAIITGLTWPL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="No significant matches"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  _xref="taxon:155864"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           start=1
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#116; Region of the
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1 of 201 are 99.00
8 from Escherichia
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I 53706, USA
 EDL933
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coli K-12 Strain
 chromosome
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RGYGNLLMIKHSEDYITAYAHNDTMLVNNGQSXEGMAKNRHHGEHGCGICSPAPPDSL
PCNGN"
3652. .5910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ffunction="RNA; tRNA"

complement (2487. .3158)

/gene="Z4203"

complement (2487. .3158)

/gene="Z4203"

/function="putative structure; Not classified"

/functe="Residues 1 to 192 of 223 are 98.95 pct identical to residues 22 to 213 of 259 from Escherichia coli K-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                homologous to E. coli K-12 complement (2289. .2362)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codon_start=1
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/product="tRNA-Gly"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nt (2289. .2362)
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Query Match:
DB:
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Best Local Similarity:
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                      132 AsnThrAlaHis---ThrProSerProValAlaValGlnSerSerArgProProValGln 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         LysGlnGlyAspThrValSerLysIleAlaGlnArgTyrGlyLeuAsnTrpArgGluIle 95
                                                                                                                                                              .TrpSerGlyAspLeuLys-------ValArgGluArgSerIleSerSerGlyVal
                                                                                                                                                                                                                                                                                                            GlyHisIleAsnAsnLeuAsnSerSerTyrThrIleTyrThrGlyGlnTrpLeuThrLeu 115
                                                                                                                                                                                                                                                                                                                                                                                                    AAACGGGGGGATACGCTATATCGTATTTCGCGCACCACGGGAACCAGCGTAAAAGAGCTG.3006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LeuAlaIleGlySerGlnValIleThrAspSerGlnGlyValProAsnArgTyrGlnVal
                                                                                            -----ĠĠŤGGGGCGAAAAGTAGCAGTAGTACAĊĠŤAAATCAACCGCCAAAŤĊAACGACC 2892
                                                                                                                                                                                                                                              GCGCGACTGAACGGCATTTCCCCCCCTTACACCATTGAAGTTGGTCAGAAACTAAAACTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /COGOT_Start=1
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RVMRQLKRLISRIAPSPSSVMVVGESGTGKEVVARAIHKLSGRRNKPFIAINCAAIPE
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residues 1 to 592 of 592 from Escherichia coli
MG1655: B2869"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MNHSETITIECTINGMPFQLHAVPGTPLSELLREQGLLSVKQGC
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MG1655: B2868"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="Z4207"
6796. .7275
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/db_xref="GI:12517386"
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Conservative:
Mismatches:
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TITLE
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                                                                                                                                                                                                                    JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        231 PheSerGlyArgAspGlyAspLeuIleAsnAlaSerAsnAlaGlyThrValIleGlnAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    191 AlaThrGlySerSerGlyValMetGlnPheArgTyrProValGlyAlaThrAsnProVal 210
Submitted (05-DEC-2001) Genoscope and CNRS UMR-8030, 2 rue Gaston Cremieux, CP5706, 91057 Evry Cedex, France, Laboratoire de Biologie Moleculaire des Interactions Plantes-Microorganismes INRA-CNRS, BP27, 31326 Castanet-Tolosan Cedex, France, Fondation Jean Dausset-CEPH, 27 rue Juliette Dodu, 75010 Paris, France, IMGM CNRS 118 Route de Narbonne, F 31062 Toulouse Cedex 4, Genoscope and INRA URGV, 2 rue Gaston Cremieux, CP5706, 91057 Evry Cedex, France, Laboratoire de Biometrie et Intelligence Artificielle INRA, BP27, F31326 Castanet-Tolosan Cedex. Laboratoire de Genetique Cellulaire INRA, BP27, F31326 Castanet-Tolosan Cedex
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Ralstonia solanacearum GMI1000 c
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AL646063 AL646052
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ralstonia
                                                                                                                                                                                                                                        Direct Submission
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http://sequence.toulouse.inra.fr/R.solanacearum.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          predicted by predicted by predicted by
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  /protein_id="CAD14852.1"
/protein_id="CAD14852.1"
/db xref="GI:171428164"
/translation="MARPGAAFRAWRGIADALAMLAATAAPAAPKGHATAAPAAPACF
TFAVVGNVPQRPEDVAPARALLDAIDTEHPAFVVHLGNLKGRDESCTDNLLEERHDLL
                                                                                                                                                                                                                    predicted
                                                                                                                                                                                                                                      /function="miscellaneous; unknown"
/note="Product confidence : probable
Gene name confidence : hypothetical
                                                                                                                                                                                                                                                                                                           complement (2152. .3216)
/gene="RSc1150"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                predicted by Homolog
predicted by FrameD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gene name
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="MNELPLYAAARGVQPGLAAGRPAQLLGGLSPRODMRTHWQKKPL
LIRQALSPEDMRALHPPLSPDALIKLAREDVESRLIAQTRGRWTENHGPFNERPLPS
RKARNWTLLVGGVNLVEPAVDALMQRFRFIPDARLDDVMISPATDGGGVGPHPDSSDV
FLLQAHGRRRWRISSQNDLTLVPDLPLKILANFTPEEEFILEPGDMLYLPPHYAHDGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(332.
/gene="RSc1148"
                                                                                                                                                                                            predicted by Codon_usage
predicted by FrameD"
                                                                                                                                                                                                                                                                                                                                                                                                         complement (2152. .3216):
                                                                                                                                                                                                                                                                                                                                                                                                                                       VADEDDEEPPRTLH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ebaldgheqgfetklqlepddafgeydqelikibprdrfpeplevgmqfegvpedgdd
edaiiytvtdvaedkvvldgnhplagmalrfdlrvtdvreataeeiehghvhgengle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       predicted
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AMVRALAQKLNALRWTPELVGEFFGAYLTEPKDHVEFVTQPRLSLARFTARARKEGIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement (332. .1561)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   function="cell processes; chaperoning"
/note="Product confidence ; probable
Jene name confidence ; probable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LDARTQALYDAQRFWINGDTFEPSDTLLAWLSALSDQRGASAEAVDAAADLPDLMDTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /function="miscellaneous; hypothetical/global homology"
/note="Product confidence : hypothetical
                                                                                                product="PROBABLE TRANSMEMBRANE
                                                                                                                    /evidence=not_experimental
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                               note="RS04601"
                                                                                                                                                                                                                                                                                                                                                                                     gene="RSc1150"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein_id="CAD14851.1"
/db_xref="GI:17428163"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /evidence=not_experimental
/transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="RSc1149; RS04602"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /protein_id="CAD14850.
/db_xref="GI:17428162"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            product="CONSERVED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'gene="RSc1148"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="RS04604"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organism="Ralstonia solanacearum"
strain="GMI1000"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         translation="MKIAKNTVVSVAYKLSDAQGNVIEESDEPMVYLHGGYDGTFPKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOMERASE (ROTAMASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EC_number="5.2.1.8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           evidence=not_experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      codon_start=1
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                                                                                                                                                                     codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          product="PROBABLE FKBP-TYPE PEPTIDYL-PROLYL CIS-TRANS
SOMERASE (ROTAMASE) PROTEIN"
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Homology
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                                                                                                  PROTEIN"
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DB:
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                              GlnSerSerArgProProValGlnGlnHisProAlaValGlnLysProThrProProVal 162
                                                                                                                                                                                                                                                                                                                                                          CCGCCGAATGCGGACGCCAGCGACGACGACGCGACGCCG---
                                                                                                                                                                                                                                                                                                                                                                                                                ArgGluArgSerIleSerSerGlyValAsnThrAlaHisThrProSerProValAlaVal 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AACCCGAACCAGATCGAAGTCGACCAACTGATCCGCGTG------GTG 70961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SerSerTyrThrIleTyrThrGlyGlnTrpLeuThrLeuTrpSerGlyAspLeuLysVal 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LysileAlaGlnArqTyrGlyLeuAsnTrpArqGluIleGlyHisIleAsnAsnLeuAsn 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCGCCGCTGGAACCGCCTCCGCCCCGCTACTATCGGGTCAAGCGTGGCGATACGCTCTAC 70859
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                                  ValValValLysLysProThrProThrProProValValGlnGlnProAlaProValAla 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TCGCGTGCGGGCAGT-----GCGCCCGCC 70799
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                                                                                 ProProValThrGluAlaProPheAlaThrGlySerSerGlyValMetGlnPheArgTyr 202
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Matches:
Conservative:
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45
135
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70715

70775

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71006

CDS

	REMARK	JOURNAL	AUTHORS	JOURNAL	REFERENCE AUTHORS	MEDLINE MEDLINE	TITLE	AUTHORS	PUBMED	JOURNAL	TITLE				AOLDORO	REFERENCE	ORGANISM	KEYWORDS	RESULT 23 U32753 LOCUS DEFINITION ACCESSION VERSION	,	Ş			QY Db 7	Db 7	Q	Db 7		Ş
improved, and a number of frame shifts have been corrected. We gratefully acknowledge the work of Tatusov et. al. We have incorporated their annotation into the /notes fields of the	le, MD 20850, USA has been updated h assigned product	Submitted (27-SEP-1997) The Institute for Genomic Research, 9712	4 (Dases 1 to 11435) White, O., Clayton, R.A., Kerlavage, A.R. and Fleischmann, R.D.	ubmitted edical Ce	3 (bases 1 to 11435) White,O., Clayton,R.A., Kerlavage,A.R. and Fleischmann,R.D.	Curr. B101. 6 (3), 2/9-291 (1996) 96398784 8805245	Metabolism and evolution of Haemophilus influenzae deduced from a whole-genome comparison with Escherichia coli	Tatusov, R. L., Mushegian, A.R., Bork, P., Brown, N.P., Hayes, W. Borodovsky, M., Rudd, K.E. and Koonin, E.V.		Science 269	Whole-genome random sequencing and assembly of Haemophilus	Geoghagen, N.S., Gnehm (C.L., McDonald, L.A., Small, K.V., Fraser, C.M., Smith H.O. and Venter, J.C.	Netrey,J.W., Wetuman,J.F., FILLIDS.C.A., Spr1998.T., Hedblom,E., Cotton,M.D., Utterback,T., Hanna,M.C., Nguyen,D.T., Saudek,D.M., Brandon R C Fine I. D Fritchman I I Whirmann I I.	Gocayne, J.D., Scott, J.D., Shirley, R., Liu, L.I., Glodek, A., Vollor, I.M. Wijdman, I.B. Dhilling, C. D. Coulogo, W. W. Wijdman, J. B. Dhilling, C. D. Coulogo, W. W. Wijdman, J. B. Dhilling, C. D. Coulogo, W. W. Wijdman, J. B. Dhilling, C. D. Coulogo, W. W. Wijdman, J. B. Dhilling, C. D. Coulogo, W. W. Wijdman, J. B. Dhilling, C. D. Coulogo, W. W. Wijdman, J. B. Dhilling, C. D. Coulogo, W. W. Wijdman, J. B. Dhilling, C. D. Coulogo, W. W. Wijdman, J. B. Dhilling, C. D. Coulogo, W. W. Wijdman, J. B. Dhilling, C. D. Coulogo, W. W. Wijdman, J. B. Dhilling, C. D. Coulogo, W. W. Wijdman, J. B. Dhilling, C. D. Coulogo, W. W. Wijdman, J. B. Dhilling, C. D. Coulogo, W. W. Wijdman, J. B. Dhilling, C. D. Coulogo, W. W. W. Wijdman, J. B. Dhilling, C. D. Coulogo, W. W. W. W. W. W. W. W. W. W. W. W. W.		Haemophilus. 1 (bases 1 to 11435)	Haemophilus Bacteria; Pi	us influenzae	U32753 N Haemophilus influenzae Rd section 68 of 163 of the complete genome. U32753 L42023 U32753 G1:1573701	71397 GTGAAACTTCACTTTGAAGTGCGCCGCAACGGTAAGCCTGTCGATCCGATGCGTTTCCTT 71456	302 AlaLeuPheGluPheArgIleSerArgAsnGlyValTyrValAspProLeuThrValLeu 321	CAATCCACGGTCAAGAAAGGGCAGAAGATCGCCGAAATGGGCAGTACCGATGCGGACCGC	GlvAspThrValArgThrGlvGlnArgIleAlaSerMetLvsAsnGlnProSerGlvAla	262 GlnHisThrAsnGlyPheValSerSerTyrIleHisIleLysAspAlaGlnValLysThr 281 	71217 GATGACGGAAAAGTGATCCACGTTGGACCCTTGCGTGGGTACGGGAATCTTGTCATCATC 71276	AlaGlYThrVallleGlnAlaAspHisAsnMetAspGlYAlaSerI	223 INTVALINESEASHGLYMECIEPPRESETGLYAEGASGGLYASDLEULLEASHALASEE 242	CCCGCGCATGGCCAGGTGATCGGCCGCTTCGAC	203 ProValGlyAlaThrAsnProValValArgArgPheGlyThrAlaThrValAlaGlySer 222
	*	CDS	gene			- 1				CDS	gene						CDS	gene		• ••			CDS	gene	FEATURES	REMARK	JOURNAL	AUTHORS	BEFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF
by sequence	to GB:U00096 PID	/gene="HI0702" 23573106	NYTEE" 23573106	TEQRYGROGUNTYQALRWAQOSTKYKORKKBSYLSAARSETEYLYVAARTEKSTINO VLPNDITOLAGSHSHYRKADRKEDLTJALQVRIENQDITLTJATDETENLEASETENSIV NQHSAPDPLMKQERMKAARRPLLMKAKGFSWAFEPEGLRLKFYLPAGSYATALVRELV	ALYVRKTDCNTLFVGEKLAKFAGVSERNMGYAGLKDRRAVTEQWFCLQMPGMETPDFS QFELDGVELLTVTRHNRKLRTGSLEGNYFDILLRGAEESDELKARLDFVANFGFPNYF	/protein id="AAC22360.1" /db_xref="GI:1573704" /translation="MLEOLPYLALKTPPKTTALLKAECADFIVKEHLGYEMSGDGEFV	<pre>/transl_table=11 /product="conserved hypothetical protein"</pre>	<pre>by sequence similarity; putative" /codon_start=1</pre>	/Journe arty of John John John John John John John John	/96:10="5147" 1328: -2347 /Gorge="HT0701"	1328 2347	/ traibiatilisming property of the library of the second o	/protein 1d="AACZ2359.l" /db xref="GI:1573703" /+-Targle-ics- westartorenershipsonoons	/product="conserved hypothetical protein"	<pre>sequence similarity; putative" /coon start=1 /troof table-1</pre>	/note="similar to SP:P37163 GB:U14003 PID:537096 GB:U00096 PID:1790704 percent identity: 54.20; identified by	/gene="nivvo" complement (7581219) /gene="HIO700"	complement (7581219)	/protein_id="AAC22358.1" /db_xxef="GI:1573702" /tb_xxef="GI:1573702" /translation="kkVEKNVVVSISYQVRTQDGVLVDEAPANQPLEYLQGHNNLVIG /translation="kkVEKNVVVVSISYQVRTQDGVLVDEAPANQPLEYLQGHNNLVIG LEKALEGKEVGDKFEVRVQPEEGYGAYSENMVQRVPKDVFQGVDELEVGMRFLADTDI GPVPVVITEIDGDEVVVDGNIHLAGQDELHFTVVAAREATLEEIAHGHVHGAHSHDD DERCHGCGCGCHHFEUNHENHGSCCCCGH"		similarity; putative" /codon_start=1 /trans1_table=11		complement (106678)			The whole genome was shifted by 588 nucleotides for a new start On Sep 30, 1996 this sequence version replaced gi:1221405.	Direct Submitseion Submitted (28-MAY-1998) The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD 20850, USA	White,O., Clayton,R.A., Kerlavage,A.R., Fleischmann,R.D., Peterson,J., Hickey,E., Dodson,R. and Gwinn,M.	corresponding H. influenzae genes

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3702. 3887
3702. 3887
3702. 3887
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GKSVDPVRYLPRH"
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putative"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="similar to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein; identified by GeneMark;
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CDS

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14

TKDLRAFGVEKSPLGLSAAGCLLQYAKETQRTALPHIQSISLIQNQDCIQLDAATRRN LELTQNIAGGTENTLASVLBKCVT PMGSRLLKRWIHQDVRDVEKLKQRQQSIABILNF DLVDELQPLJCLUGDMER ILARVLKASAR PRDLJTRLRTALEQIPALASIVQQKTPPFL TALFSQIADFSEQCDLLQRALIETPPLLIRDGGVIAEGYNAELDEWRMLSDGATQYLE MLEKRERESTGLDTIKKIGFNAVHGYYLQISQQQAHKAPIHYVRRQTLKNAERYIPEL KEYEDKYLKSKQALALSEQJYDTIKLIGFNAVHGYYLQISQQQAHKAPIHYVRACTLKNAERYIPEL KEYEDKYLKSKQALALSEQJYDLAGASITASIALSELDYVULAERADTLNYMPTFCDEVSVKIKNGRHPVVEQVLKDPFIANPVELNHNRHLLVITGPNMGGKST

Db 5	Ş	Ω γ 5	Qy Db 4	Оу .	Qy Db 4	Qy Db 4	Qy Db 4	Qy .	Qy Db 4	Qy Db 4	Qy Db 4	Qy Db 4	Qy Db 4	Qy Db 4	US-10-018-	Alignment So Pred. No.: Score: Score: Percent Simi Best Local S Query Match: DB:
078 CGCTATAAAGGTAAATCAGTGGATCCAGTACGTTACCTA 5116	309 SerArgAsnGlyValTyrValAspProLeuThrValLeu 321	289 GlnArgIleAlaSerMetLysAsnGlnProSerGlyAlaAlaLeuPheGluPheArgIle 308 	269 SerSerTyrIleHisIleLysAspAlaGlnValLysThrGlyAspThrValArgThrGly 288 :::	251 AspHisAsnMetAspGlyAlaSerIleValIleGlnHisThrAsnGlyPheVal 268	231 PheSerGlyArgAspGlyAspLeuIleAsnAlaSerAsnAlaGlyThrValIleGlnAla 250	216 ThralaThrValAlaGlySerThrValThrSerAsnGlyMetTrp. 230	196 GlyvalMetGlnPheArgTyrProValGlyAlaThrAsnProValValArgArgPheGly 215	176 GlnGlnProAlaProValAlaProProValThrGluAlaProPheAlaThrGlySerSer 195	161ProValValValValLysLysProThrProThrProProValVal 175	151 GlnHisProAlaValGlnLysProThrPro	131 ValasnThrAlaHisThrProSerProValAlaValGlnSerSerArgProProValGln 150	111 GlnTrpLeuThrLeuTrpSerGlyAspLeuLysValArgGluArgSerIleSerSerGly 130	91 ASNTYPAYGGIUIIEGIYHISIIEASNASNLEUASNSEYSEYTYYTTAYIETYYTTYGIY 110 	71 ASDARGTYRGINVAILYSGINGIYASPTHRVAISERLYSIIEAIAGIDARGTYRGIYLEU 90	706-2 (1-322) x U32753 (1-11435)	ment Scores: 0.00115 Length: 11435 No:: 0.00115 Matches: 76 s: 219.50 Matches: 76 ent Similarity: 44.69% Conservative: 46 Local Similarity: 24.46% Mismatches: 114 Local Similarity: 13.14% Indels: 37 Match: 13.14% Gaps: 10

SGS

gene

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REFERENCE
AUTHORS
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MEDLINE
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Comparison of the genomes of two Xanthomonas pathogens with differing host specificities
Nature 417 (6887), 459-463 (2002)
22022145
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Xanthomonas axonopodis pv. citri str. 306
Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the complete genome. AE011804 AE008923 AE011804.1 GI:21107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Brazil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sao Paulo,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kitajima,J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (28-NOV-2001) Departmento de Bioquimica, Universidade, Av. Prof. Lineu Prestes 748, Sao Paulo, SP 05508-900,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                            gene="pyrG"
note="identified by
                                                                                                                                                                                                                                                                                                                                                                                                                                     organism="Xanthomonas axonopodis pv. citri str. 306"
                                                                                                                  note="identified by sequence similarity; putative; ocated using Blastx/Glimmer/Genemark"
                                                                                                                                                                                                                                                     note="XAC1716"
                                                                                                                                                                                                                                                                                                                                                                                                            strain="306"
                                                                   codon_start=
                                                                                                                                                                                                                                                                                                                                                  note="pathovar:
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182 of 469 of
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Almeida
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transl_table=11
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transl_table=11
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gene="XAC1718"
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SdO

translation="MRNWRWLLLVLAVLLAWLQYRFWFGPGNSGEVMMLEAQVAHQTQ

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Best Local S:
Query Match:
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                                           ThrSerGlySerGlyGlyLeuAlaIleGlySerGlnValIleThrAspSerGlnGlyVal
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219.50
40.07%
27.27%
13.14%
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Deinococcus radiodurans.

Deinococcus radiodurans

Bacteria; Thermus/Deinococcus group; Deinococci; Deinococcales;

Bacteria; Thermus/Deinococcus.

1 (bases 1 to 14193)

White,O., Eisen,J.A., Heidelberg,J.F., Hickey,E.K., Peterson,J.D.

Dodson,R.J., Haft,D.H., Gwinn,M.L., Nelson,W.C., Richardson,D.L.

Moffat,K.S., Qin,H., Jiang,L., Pamphile,W., Corsby, M., Shen,M.,

Vamathevan,J.J., Lam,P., McDonald,L., Utterback,T., Zalewski,C.,

Makarova,K.S., Aravind,L., Daly,M.J., Fraser,C.M. et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GluAlaProPheAlaThrGlySerSerGlyValMetGlnPheArgTyrProValGlyAla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GACCAGTGGCTATCCGCATACGGTCATAACCGCAAGCGCCTGCTCAACGAAGGCCAGAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTGGTGTATTCGGGCGCCGGCCTGGTCGGCTACGGCGAACTGATCATCATCAAGCACAAC 11269
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ThrAsnProValValArgArgPheGlyThrAlaThrValAlaGlySerThrValThrSer
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Science 286
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White, O., Eisen, J.A., Heidelberg, J.F., Hickey, E.K., Peterson, J.D., White, O., Eisen, D.H., Gwinn, M.L., Nelson, W.C., Richardson, D.L., Dodson, R.J., Haft, D.H., Gwinn, M.L., Nelson, W.C., Richardson, D.L., Moffat, K.S., Qin, H., Jiang, L., Pamphile, W., Crosby, M., Shen, M., Vamathevan, J.J., Lam, P., McDonald, L., Utterback, T., Zalewski, C., Makarova, K.S., Aravind, L., Daly, M.J., Minton, K.W., Fleischmann, R.D., Ketchum, K.A., Nelson, K.E., Salzberg, S., Smith, N.O., Venter, J.C. and Fraser, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (08-NOV-1999) The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD 20850, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10567266
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RLGVENGCRSVAFPSISTGVYGYPLDRAAPIALATIQDFLRSHPDLSVRMVLYGADAL
                                                                                                                                                                                                                                            /note="similar to GB:U00096 PID:1787283 percent identity: 64.29; identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="MSGMVTAIVMVQAERHRIQETAEALAAVPSVREVYSVTGEWDIV
AIVKLAEYPRLDDVTGHLRRIDGIMRTQTMLAFRTYNBEVLDQGFGIGLDG"
complement (2232. .3733)
/gene="DRrrnaAl6S"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SGDDHRALITTEEDRAPGVPRLTREALVSLIEHARLAPLGALDLRGYWRAGDVDLDSA
ASVAELVSAHLAQRGTFTYVLLTLSQQPAQSLVNVSELAQRLGNGVSTDDMNAILDTL
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GSLTGRRTAPSGGRNLSGLGEERRPATGEEGEPRPSGLKPIAPAFTPQVPQPGRQELT
LPASLASFGTRSREAEPVAAPGAAESGPSDVPAALSPVPSGPVPAVQEVVSDPAPAPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MCCDNVPRPSHPSWRTARVNPTRYILTRSCIEEGSMRLLKFNEA
SFPESGPVQFVDDRGKEYPAVVDRTQMQVLGLGELYHDHNLGVNDVLTVTPTEPGRYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement (90. .1598).
/gene="DR2286"
                                                                                              /product="conserved hypothetical protein"
/protein_id="AAF11835.1"
/db_xref="GI:6460097"
                                                                                                                                                                                                                                                                                                                              complement (4055. .4567)
                                                                                                                                                                                                                                                                                                                                                                                     complement (4055. .4567)
                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="DRrrnaA16S"
/product-""'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="transcriptional
/protein_id="AAF11834.1"
/db_xref="GI:6460096"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ARPPFLAVTPLPNGQFLLRSTVTDLLADLADYAQGVRRRLRAPGGGTEGPRG'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                \QLGALEDQIVEFARLSGYRLTLLGRGLVRLTADLGPAYGYTVLLATDREALSSPEWD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="hypothetical protein"
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/db_xref="GI:6460106"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement (90. .1598)
/gene="DR2286"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="similar to GB:AE000782 percent identity: 64.18; dentified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'gene="DR2287"
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chromosome="1"
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|strain="R1"
                                                                                                                                                                                         transl
                                                                                                                                                                                                                                                                                                                                                                                                                   product="Ribosomal RNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       transl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene="DR2287"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="identified by Glimmer2; putative"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene
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/gene="DR2293"
/note="similar to GB:D12650 SP:P30865 PID:1208970
PID:216647 GB:U00096 percent identity: 45.69; identified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MDADPRLYAPPPGFTRLRLTVAWDGRDYAGWQEQRNAVSVQET
LQTALHALGGEGALRPVSAGRTDAGYHAEAWFLHWDVTTFRVDLVQLDRALIAWLPA
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AQSLIGLHDFAAFATREDRQTVRDLLRLEVQPQGELWDIHVAGESFLRHWVRGLVGTL
LLYQQGKLGAAEVEGILASRERARAGANVPPGGLYFAGAEYGVRRVEGRSGNGGEPGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="MGESQAPTGAAERGTGTDARTDDEAVSVAYSAGMMASAPQDRPA
GTPPQGTALIIVTGASGVCKGTLRERWLAGQDVFYSTSWTTEEPRPGEVNGRDYVDFN
SPAEPLAKAQQNGFLEHAQFVGHYGTPIEPIEAALERGDDVVLEIFVEGAMQVKORN
GEQAILVFIMPPSLTELRRRLTGRATETPERIEKRLTRARDEIQAAHDFRYVIVNDNL
                                                                                              /gene="DR2293"
7988. .8956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TAPARPAPARPAPARPSPAQPAPPRVAQATPEHHARVVVRQTSSHSLMQWPLPGYGRI
TSDFGWRVLDGEREKHQGIDVAAPPGTPVIAARSGRVIQAHLDETYGWGWTVVIQHPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HVFERALAQL"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement (4567.
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/cransl table=11
/product="guanylate kinase"
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/db_xref="GI:6460098"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="similar to PID:1651722 percent identity: 68.11; dentified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="DR2289"
                                                                                                                                                                                   trānslation="metaphtawpstvwyvelrgkeaeatlrqwleqlpgqagfagae
.bdspaqpglalvashwsgplpeltppagakhwtfrvlaqr"
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db_xref="GI:6460100"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      product="pseudouridylate synthase
protein_id="AAF11837.1"
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transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'gene="DR2290"
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transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="similar to PID:1653709 percent identity: 59.04;
dentified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        omplement (5351. .6193)
                                                                                                                                                                                                                                                                                                                                                                                                                          gene="DR2292"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              t rans lat ion="mlanvpllsIrlomksspfarpvlgpvtgIllagalllggagae
yrvkpgetlyrIalnaglseetvooanpvlrgghalyagomltippkplppgtfrvr
gedlkklaorlgvsegpirrdnpqIdrrgslnagovlrlparliaaoraaeoaaook
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225

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260

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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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                                                                                                                                                                                                                                        ThrValSerLy8IleAlaGlnArgTyrGlyLeuAsnTrpArgGluIleGlyHi8IleAsn 99
||| :::|||:::||||:::|||
ACCTTCTACAGCGTCGCGCGCGCTACGGCATCACCCCATCGCCCTACAGGAGTACAAC 69
                                                GlnLysProThrProProValValValValLysLysProThrProThrProProValVal 175
                                                                                          ĠŦĠĠĊĊ----CCAGCCĊĠĊĊĊĠGCĠĊĊĠĠTŦCGTCTGGTGGTGGCCCGAĊĊĊĠĊACCT
             GCATCACCCACGCCCGCACCTACCGCACCCGCCCGGCCCCCTGCGCGCGACCTGCTCCT 7175
                                                                                                                       ValAlaValGlnSerSerArgPro---ProValGln------GlnHisProAlaVal 155
                                                                                                                                                                                                    LeuLysValArgGluArgSerIleSerSerGlyValAsnThrAlaHisThrProSerPro 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="DR2294"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          translation="MGKMPRPFLPALFSSRLVNGMFGLVALGWALGAWVGERTLPTLL"
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Conservative:
Mismatches:
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AUTHORS
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Yersinia
AE013686
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Yersinia pestis KIM.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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2 (Dases 1 to 10592)
2 (Dases 1 to 10592)
Deng,W., Burland,V., Plunkett,G. III, Boutin,A., Mayhew,G.F.,
Deng,W., Perna,N.T., Rose,D.J., Mau,B., Zhou,S., Schwartz,D.C.,
Fiss,P., Perna,N.T., Rose,D.J., Mau,B., Zhou,S., Schwartz,D.C.,
Fetherston,J.D., Lindler,L.E., Brubaker,R.R., Plana,G.V.,
Straley,S.C., McDonough,K.A., Nilles,M.L., Matson,J.S.,
Blattner,F.R. and Perry,R.D.
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Deng,W., Burland,V., Plunkett,G. III, Boutin,A., Mayhew,G.F.,
Liss,P., Perna,N.T., Rose,D.J., Mau,B., Zhou,S., Schwartz,D.C.,
Fetherston,J.D., Lindler,L.E., Brubaker,R.R., Plana,G.V.,
Stralley,S.C., McDonough,K.A., Nilles,M.L., Matson,J.S.,
Blattner,F.R. and Perry,R.D.
Genome Sequence of Yersinia pestis KIM
J. Bacteriol. 184 (16), 4601-4611 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AE013686.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ThrValIleGlnAlaAspHisAsnMetAsp------GlyAlaSerIleVal
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AE009952
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                                                                                                                                                                                                    ocation/Qualifiers
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/translation="mknnbkldshtpmmqqylrlkaqhpeillpyrmgdfyelpysda (raasqlldisltrrgasageb) independents (raasqlldisltrrgasageb) independents (raasqlldisltrrgasageb) independents (rabetlyreatur) issgrrvab (rabetlyreatur) issgrrvab palletmaaelqrtnpaellypendepmsliehheiglrrrplmefeldtakqqlniqpg ardlefraaelqrtnpaellypendepmsliehheigltrrrplmefeldtakqqlniqpg tradicefromentaaildcsvtpmschukrwlhmeirdtrrqqdistrrn lettqnlsggsentlaaildcsvtpmsrbllkrhamentarqqlpethrltrqqaiggloi aaelqtelgloerilarlaalalatartrrrarendlaanharqqlpethrltrqqaiggloi aaelqtelgloerilarlaalatartrarendlaanharqqlpethrltradaalabratytdrl labetlgraggebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebendelgebende
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//note="synthesis of many growth plase related proteins;
residues 1 to 332 of 332 are 92.46 pct identical to
residues 1 to 330 of 330 from E. coli Kl2 : B2741;
residues 1 to 332 of 332 are 97.28 pct identical to
residues 1 to 332 of 332 are 97.28 pct identical to
residues 1 to 331 of 331 from GenPept : >gb|AAC43391.1|
(U16152) RpoS [Yersinia enterocolitica]"
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                                                                                                                                                                           EIREREKLGLDTLKVGFNGVHGYYIQVSRGQSHLVPIHYVRRQTLKNAERYIIPELKE
YEDKVLTSKGKALAIEKGLYEEIFDLLLPHLPELQLSANALAELDVLANLAERAETLN
YSCPTLSDKPGIKIMGGRHPVVEQVLKEPFISNPLTLSPQRRMLIITGPNMGGKSTYM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="residues 5 to 851 of 851 are 84.09 pct identical to residues 5 to 853 of 853 from E. coli KI2: B2733; residues 5 to 851 of 851 arom E. coli tidentical to residues 5 to 851 of 851 from GenPept:

>gb|AAG57842.1|AE005501_11 (AE005501) methyl-directed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DELLAQGYTQRVLDATQLYLGEIGYS PLLTAEEEVYFARRALRGDVSSRRRMIESNLR
LVVKIARRYSNRGLALLDLIEEGNLGLIRAVEKFDPERGFRFSTYATWWIRQTIERAI
MNQTRTIRLFIHIVKELNVYLRTARELSHKLDHEPSAEEIAEQLDKPVDDVSRWLRLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AKNNI AEPYSLNVGQSI QLGNGSGGGMLAATDATSSGI AQPPSNI QNTTTI QNTTTTV
DSQSTSAYSGNSGKQNVGKMLPSSGAVVATTAPVTAPSSSVSEPASNGGPVSGWRWPT
DGKTI DSFSASEGGNKGIDI AGSRGQPI LATASGRVVYAGNALRGYGNLI I I KHNDDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="residues 1 to 333 of 333 are 58.65 pct identical residues 1 to 379 of 379 from B. coli K12: B2742; residues 1 to 373 of 333 are 58.65 pct identical to residues 1 to 379 of 379 from GenPept;
                                                       GVVNVHLDALEHGET I AFMHS VQEGAASKS YGLAVAALAGVPRDV I KRARQKLKELES
                                                                                        NATEQSLVLMDEIGRGTSTYDGLSLAWACAENLASRIKAMTLFATHYFELTTLPEKME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mismatch
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/gene="muts"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement (2497. .5052)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ERITSVDTPLGGDSEKALLDILSDENENGPEDTTQDDDMKQSIVKWLFELNAKQREVL
ARRFGLLGYEAATLEDVGREIGLTRERVRQIQVEGLRRLREILQTQGLSIEALFRE"
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/protein_id="AAM84419.1"
/db_xref="GI:21957564"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              lsayahndtmlvreqqevkagqkiatmgstgtssvrlhfeirykgksvnplrylpqr"
                                                                                                                                      rQtalivllahlgsyvpadqatigpidriftrvgaaddlasgrstfmvemtetanilh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="mutS"
/note="y0835"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="methyl-directed mismatch repair protein"
/protein_id="AAM84420.1"
/db_xref="GI:21957565"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=1
/transl_table=
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function="enzyme;
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/transl_table=
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/protein_id="AAN84423.1"
/protein_id="AAN84423.1"
/db_xref="GI:21957568"
/translation="MCDKKPLKESSMSHENLKGAQMAEGIPETMRAVVAYGPRDYRFE
/translation="MCDKKPLKESSMSHENLKGAQMAEGIPETMRAVVAYGPRDYRFE
RYPVPTIDAKEILVKVEGCGICAGDTKAFEGAPSFWGDDKQPAYIKAPMIPGHEFIGH
VVGLGADVEGFELGDRVTSEQIVPCWGCRFCHMHQQYMCLGHVVVLAAGSGTLGLGMI
VKGTKEAINYHVPDHLPLEKAILIEFYACAFHAVQRAKIKLGDVVVLLAGSGTLGLGMI
GAIKKSGAAKLIVLDLSDDRLALAKKFGADLVLNPSRDDVNTLIKEMTGGYGCDIYID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="similar to 2,3-butanediol dehydrogenase; residues 30 to 375 of 382 are 34.00 pct identical to residues 1 to 375 of 545 from GenPept: -dbj|BAB60856.1| (AB063194) acetylacetoin reductase [Bacillus cereus]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="y0838"
6751. .7899
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/note="residues 1 to 147 of 151 are 44.21 pct identical residues 1 to 146 of 149 from E. coli K12: B4090; residues 1 to 146 of 151 are 54.36 pct identical to residues 2 to 150 of 151 from GenPept: >gb|AAK03729.1| (AE006201) RpiA [Pasteurella multocida]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="residues 1 to 42 of 44 are 39.53 pct identical to residues 84 to 126 of 698 from GenPept : 

>gb | AAF28325.1 | AF204952_3 (AF204951) ESV-1-144 [Ectocarpu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="y0836"
5549. .5683
/transl_table=11
/product="putative dehydrogenase"
/protein_id="AAM84424.1"
/protein_id="AAM84424.1"
/db_xref="Gi;21957569"
/translation="MPNDYKWFDTAFSLSGKVAAITGGATGIGHAIAELYLAKGARVV
LMDCADNVAEIAEQLDRDNAVGLHCDVSDSQSVRQAVAQAIGAFGQLDILVNSAGIAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /trānslation="MLSIAIGCDDAAIEMKNQIVIFLQSKNITVVDYSCDQHQEPTMY
PDIAIQVALAIKAGKHERGILICGTGIGMSISANKVFGVRAAQCHDTFSAQRARKSNN
AQIICLGARVIGPELAKTLIEAMLDAEFDGGGSTEKVERIRYYEQSLHD"
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                                                                                                                                                                                                                                                                                                                                                  /function="putative"
/note="residues 5 to 256 of 256 are 54.76 pct identical
/note="residues 5 to 254 from GenPept : >emb|CAC95595.1|
(AL596164) similar to dehydrogenase/reductase [Listeria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VIEGISNGDLPTEGVVTHILPLEKYAEGIELVKRGVDSLKVVLNPNLT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATGAQKAVEQGLTLLRKLGTFVEFSVFKDPVTVDWSIISDRKELDVLGSHLGPYCFPI
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/protein_id="AAM84422.1"
/db_xref="GI:21957567"
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/note="y0837"
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/protein_id="AAM84421.1"
/db_xref="GI:21957566"
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                                                             GlySerSerGly---ValMetGlnPheArgTyrProValGlyAlaThrAsnProValVal
                                                                                                            GCGGTTGTCGCTACAACAGCÁCCTGTTACCGCACCAAGCAGTTCTGTCAGTGAACCAGCC
                                                                                                                                                ProValValGlnGlnProAlaProValAlaProProValThrGluAlaProPheAlaThr
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                                                                                                                                                                                                                                                                                                   ---ValGlnGlnHisProAlaValGlnLysProThrProProVal------
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AYCASKFGVIGITKVLALEWGPLDIQVNAISPTVVLTALGQKAWSGQLAEDMKLKIPA
RRFRYPAEVAACALFLASDAANMITGENLVIDGGYTIQ"
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/function="putative"
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Submitted (04-OCT-2001) Submitted on behalf of the Yersinia
sequencing team, Sanger Centre, Wellcome Trust Genome Campus,
Hinxton, Cambridge CB10 1SA E-mail: parkhill@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Parkhill, J., Wren, B.W., Thomson, N.R., Titball, R.W., Holden, M.T.G., Prentice, M.B., Sebaihia, M., James, K.D., Churcher, C., Mungall, K.L., Baker, S., Basham, D., Bentley, S.D., Brooks, K., Cerdeno-Tarraga, A.M., Chillingworth, T., Cronin, A., Davies, R.M., Davis, P., Dougan, G., Celtwell, T., Hamlin, N., Holroyd, S., Jagels, K., Leather, S., Karlyshev, A.V., Moule, S., Oyston, P.C.F., Quail, M., Rutherford, K., Simmonds, M., Skelton, J., Stevens, K., Whitehead, S. and Barrell, B.G. Genome sequence of Yersinia postis, the causative agent of plague Nature 413 (6855), 523-527 (2001)
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Yersinia pestis strain CO92 complete genome;
AJ414156 AL590842
AJ414156.1 GI:15981150
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Yersinia pestis
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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Location/Qualifiers
                                                                                                                                                      /organism="Yersinia pestis"
/strain="CO92"
/db xref="taxon:632"
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/complement (191. 715)
/gene="YPO3215"
/note="aroL"
             complement(191...715)

/gene="YPO2215"
/gene="YPO2215"
/EC number="2.7.1.71"
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/note="sinilar to Escherichia coli shikimate kinase II
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/note="1.55.4" to Esch
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement (668. .691)
/gene="YPO3215"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement (470. .544)
/gene="YPO3215"
/note="PS01128 Shikimate kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="mlnivrrnfksqfsylqrfiasprtvgslvpsspwlcqamlnqi
DWTQNLNIAELGAADGVLTKRILSHMSANSSLQAYEIQPHFVHALHQLKDSRLQIADR
SAEQLDQEYDVVFCCLPLLSIPTKISIRILQQTQQRLRARNGVLVLFQYSHLSESLLS
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/gene="YPO3216"
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/gene="YPO3216"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement (209. .709)
/gene="YPO3215"
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VAEVVESEGWDGFRLRESMALQAVTAPKTVVATGGGAVLSSENKAFMRDHGRVIYLRA
SAAVLAKRLAEDPEEAQRPSLTGKPIVEBILDVLASREALYQDVAHHVLDGTQTPSLV
                                                                                                                                                                                                  /note="Similar to Escherichia coli hypothetical protein /note="Similar to Escherichia coli hypothetical protein vafE SW:YAFE ECOLI (B30866) (207 aa) fasta scores: E(): 0, 65.1% id in 169 aa, and to Pseudomonas aeruginosa YafE or PA3119 TR:O87011 (EMBE:U93274) (187 aa) fasta scores: E(): 0, 55.2% id in 172 aa"
                                                                                                                                                                                                                                                                                                                                            complement (2249. .2770)
/gene="YPO3218"
                                                                                                                                                                                                                                                                                                                                                                                                                        IKNIASPHVLSIVACSIKKAAAKMRLS"

complement (2249. .2770)
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787. ~~~
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,a) fasta scores: E(): 0, 63.7% id in 168 aa"
        translation="MQAAADKKLTNIEIQQGLAESLPFADQSFDIVISRYSAHHWHDV"
                                   product="conserved hypothetical protein"
protein id="cAC92453.1"
db xref="g1:15981154"
/db_xref="SPTREMBL:08ZC12"
                                                                                                                                                                                                                                                                                                                                                                                                      /gene="YP03218"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="hypothetical protein"
/protein_id="CAC92452.1"
/db_xref="GI:15981153"
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transl_table=11
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/protein_id="CAC92451.1"
/db_xref="GI:15981152"
/db_xref="GI:15981152"
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/transI_table=
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/db_xref="GI:15981151"
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/protein id="CAC92450.1"
                                                                                                                                                codon_start=1
table=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      translation="MIGTDVGIVVANVIMAETNDDRGRSISCHFFIQSSPNAHPLNVD"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   _xref="SPTREMBL:Q8ZC13"
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/note="Pfam match to entry PF00171 aldedh, Aldehyde dehydrogenase family, score -217.90, E-value 0.00013" complement (4776. .4841)
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complement (4572. .5744)
/gene="YPO3221"
                                                                                                                                                                                         /product="gamma-glutamyl phosphate reductase"
/protein_id="CAC92456.1"
/db_xref="gi_15981157"
/db_xref="SPTRRMBL.QBZCO9"
/translation="WNILEHMGKAAKQASWQLAMLSTAKKNQALAVIANLLESESQTILQAMERDMAARESGNSEALLDRILLTPARLAAIANDVRQVCRLNDPYGRVIDGSLLDLQAMERRRAVPLGUIGVIEARRAVILEGKETHYTNQATVNV
                                                        IREHGTSHSDAILTRSLSHAEYFVRAVDSSAVYVNASTRFTDGGQFGLGAEVAVSTQK
LHARGPMGLDALTTYKWIGYGDDLVRS"
                                                                                                             IQRALEQCGLPAAAVQAIESPDRQLVNELLRLDRYVDMLIPRGGASLHKLCREQSTIP
VITGGIGVCHTFVDENADFEKALLVIENAKIQRPSACNSLETLLVHQAVAKTFLPLLS
ARMHAFGVTLHASPLAMPYLADGKAKVVAVEAADYDDEWLSLDLNVDIVTDIDAAIDH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement (4554. .5813)
/gene="YPO3221"
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LPAFSSAIPEQLYFIQRREYFRVSIPQWPAYYCSGKFPDGTQYKYTLADISLGGMGLY
AMKGSEFPLQGCSVLRDAAVDLCGFGLFKLDLQFIRALDKQVVNNKGEMLTVQRLSFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="one of 2 probable for YPO3219 by TMHMM2.0"
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/gene="YPO3219"
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/protein id="CAC92454.1"
/db_xref="GI:15981155"
/db_xref="SI:15981155"
/db_xref="STERMBL:08ZC11"
/translation="MEGSVMGISEEESIRRLINEKNAVGHSAKWVAIISAVYFIIMLF
YKHELGVLTLAGGIFLVSFTTWMKKRQKVKSYKNQLQQIEEDKTV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(4554. .5813)
/gene="YPO3221"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FLRLSPIQEKGLQRAIFELEKQQTAKARKFQEGL"
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/gene="YPO3220"
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'product="conserved hypothetical protein"
'product="conserved hypothetical protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein_id="CAC92455.1"
/db_xref="GI:15981156"
/db_xref="SPTREMBL:Q8ZC10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="Similar to Escherichia coli hypothetical protein
CgR SW:YCGR_ECOLI (P76010) (244 aa) fasta scores: E():
0.7% id in 241 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                  codon start=1
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Best Local Similarity:
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Pred. No.:
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                                                                                                               AGCAATGGTGGTCAGTTAGTGGCTGGAGATGGCCAACCGAT-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CGCATAGTTTATAACCGCAGTTACGACAATATCCCCCAAAGGAAGCTACAGCGGTAATACC 166046
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ProlleLysArgLeuGlyLeuIlePheGly---VallleThrThrCysIleLeuAlaGly 32
                                                                                                                                              GlySerSerGly---ValMetGlnPheArgTyrProValGlyAlaThrAsnProValVal 211
                                                                                                                                                                                GCGGTTGTCGCTACAACAGCACCTGTTACCGCACCAAGCAGTTCTGTCAGTGAACCAGCC 165665
                                                                                                                                                                                                               ProValValGlnGlnProAlaProValAlaProProValThrGluAlaProPheAlaThr 192
                                                                                                                                                                                                                                                 AGCGCGTATTCTGGAAACTCGGGTAAACAGAATGTTGGCAAAATGTTGCCATCATCTGGT 165725
                                                                                                                                                                                                                                                                                                                 AATATTĆÁĠAACACAACTACTATTĆÁĠAACACAÁĊTACAACGGTTGATTCTCAATCAACT 165785
                                                                                                                                                                                                                                                                                                                                                                                GGAATA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LeuThrLeuTrpSerGlyAsp-----LeuLysValArgGluArgSerIleSerSer 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TATACCGTTAAGCGTGATACGCTGTTTTATATCGCTTGGATAACAGGAAATGACTTC
                                                                                                                                                                                                                                                                                                                                               ---ValGlnGlnHisProAlaValGlnLysProThrProProVal------
                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTCAATTGGGTAATGGGTCTGGTGGCGGTATGTTAGCCGCCACTGATGCCACATCAAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CGTGATTTGGCAGCAAAAAATAATATTGCAGAACCCTATAGCCTGAATGTGGGGCAATCT 165926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TyrGlnValLysGlnGlyAspThrValSerLysIleAlaGlnArgTyrGlyLeuAsnTrp 92
                                                                              ArgArgPheGlyThrAlaThrValAlaGlySerThrValThrSer----
                                                                                                                                                                                                                                                                                                                                                                                                             GlyValAsnThrAlaHisThrProSerProValAlaValGlnSerSerArgProPro--- 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="YPO3221"
/note="PS01223 Gamma-glutamyl phosphate reductase signature."
complement(5823. .6926)
/gene="YPO3222"
/note="pro8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="YP03222"
-AsnGlyMetTrpPheSerGlyArgAspGlyAspLeuIleAsnAlaSerAsn
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218.50
39.72%
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                 GGTAAAACGATCGATAGCTTCTCTGCTTCCGAA 165590
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REFERENCE
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KEYWORDS
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ORGANISM
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MEDLINE
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Bscherichia coli L-isoaspartyl methyltransferase (pcm) and katf
gene, partial cds and lipoprotein precursor (nlpD) gene, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           L07869.1 GI.433183
L-isoaspartyl methyltransferase;
Escherichia coli (strain MP180) [
Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ( (bases 1 to 1433) (chikawa, J.K., Li,C., Fu, J. and Clarke, S. gene at 59 minutes on the Escherichia colipoprotein with unusual amino acid repeat Bacteriol. 176 (6), 1630-1638 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTTAGATTGCATTTTGAAATTCGTTACAAGGGGAAATCCGTAAACCCGCTGCGTTACCTT
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/map="59 min o
<1. .57
/transl_table=11
/product="lipoprotein precursor"
/protein id="NAA17875.1"
/protein id="NAA17875.1"
/protein id="NAA17875.1"
/db xref="G1:433185"
/translation="MSAGSPKFTVRRIAALSLVSLMLAGCSDTSNPPAPVSSVNGNAP
/translation="MSAGSPKFTVRRIAALSLVSLMLAGCSDTSNPPAPVSSVNGNAP
ANTNSGMLITPPEMMGTTSTAQOPOIDPVQPVQDPQIQATQQPQIQPVQPPVAMQQPVQMENG
RIVVNRQYGNIFPFKGSYGSTYTVKKGDTLFYIAWITGNDFRDLAQRNNIQAPYALNVG
QTLQVGNASGTPITGGNAITQADAAEQGVVIKPAQNSTVAVASQPTITYSESSGEQSA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       organism="Escherichia/strain="MP180"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              location/Qualifiers
                                                                                                                                                                                                                                                                                           note="putative"
                                                                                                                                                                                                                                                                                                                                                  'groducT="L-isoaspartyl methyltransferase"
'grotein id="AAA17874.1"
'db_xref="GI:433184"
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Best Local Similarity:
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                                                                                                                TTACGTATTCTGAGTCTTCGGGTGAACAGAGTGCTAACAAAATGTTGCCGAACAACAAGC
                                                                                                                                                                                                                                                                                                                                                    CCGTGACCTTGCTCAGCGCAACAATATTCAGGCACCATACGCGCTGAACGTTGGTCAG--
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CTGTCAGCAGTACATCAACCAGTACGCCTATCTCCACCTGGCGCTGGCCCG-----ACTG 989
                         heAlaThrGly------SerSerGlyValMetGlnPheArgTyrProValGlyAlaT 207
                                                                                                                                                                                                  isProAlaValGlnLysPro-----ThrProProValValValValLysLysProThr-
                                                                                                                                                                                                                                 CACTGGCGGAAATGCCATTACCC
                                                                                                                                                                                                                                                            snThrAlaHisThrProSerProValAlaValGlnSerSerArgProProValGlnGlnH
                                                                                                                                                                                                                                                                                                                    pLeuThrLeuTrpSerGlyAsp-LeuLysValArgGluArgSerIleSerSerGlyValA
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                                                                                                                                                                                                                                                                                                                                                                                                                                   gTyrGlnValLysGlnGlyAspThrValSerLysIleAlaGlnArgTyrGlyLeuAsnTr 92
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                                                                                   roThrProProValValGlnGlnProAlaProValAlaProProValThrGluAlaProP 190
                                                                                                                                                                        AGGA-GTTGTGATCAAGCCTGCACAAAATTCCACCGTTGCTGTTGCGTCGCAACCGACAA
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GGNKGIDIAGSKGQAIIATADGRVVYAGNALRGYGNLIIIKHNDDYLSAYAHNDTWLV
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1399. .>1433
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/db_xref="GI:476826"
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25.74%
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                                                                                                                                                                                                                                                                                                                        Submitted (22-OCT-2000) Laboratory of Genetics, Un
Wisconsin, 445 Henry Mall, Madison, WI 53706, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                             2 (bases 1 to 10573)
Perna,N.T., Plunkett,G. III, Burland,V., Mau,B., Glasner,J.D.,
Perna,N.T., Plunkett,G. III, Burland,V., Mau,B., Glasner,J.D.,
Rose,D.J., Mayhew,G.F., Evans,P.S., Gregor,J., Kirkpatrick,H.A.,
Posfai,G., Hackett,J., Klink,S., Boutin,A., Shao,Y., Miller,L.,
Posfai,G., Hackett,J., Linn,A., Dimalanta,E., Potamousis,K.,
Grotbeck,E.J., Davis,N.W., Linn,A., Dimalanta,E., Potamousis,K.,
Apodaca,J., Anantharaman,T.S., Linn,J., Yen,G., Schwartz,D.C.,
Welch,R.A. and Blattner,F.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genome sequence of enterchaemorrhagic Nature 409 (6819), 529-533 (2001)
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Escherichia coli O157:H7 EDL933
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (bases 1 to 10573)
/gene="Z4048"
/function="putative regulator; Not classified"
/note="Residues 12 to 146 of 146 are 100.00 pc
                                                                                                                                 nomologous
                                                                                                                                                                                             /note="enterohemorrhagic"
                                                                                                                                 note="0-island #110; Region of the EDL933 nomologous to E. coli K-12 MG1655"
                                                                                                                                                                                                                                                              /organism="Escherichia
/strain="EDL933"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                         gene="Z4048"
                                                                                                                                                                                                                   db_xref="taxon:155864"
                                                                                                                                                                                                                                        serotype="0157:H7"
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3, section 121
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SG.

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/gene="nlpD"
/gene="nlpD"
/function="membrane; Macromolecule synthesis,
modification: Lipoprotein"
/note="Residues 1 to 379 of 379 are 99.73 pct identical to
residues 1 to 379 of 379 from Escherichia coli K-12 Strain
MG1655: B2742"
                                                                                                                                                                                                                                                                                                                                                                                                                                      /function="enzyme; Macromolecule synthesis, modification: Proteins - translation and modification" (note="Residues 1 to 208 of 208 are 100.00 pct identical to residues 1 to 208 of 208 from Escherichia coli K-12 translation MG165; B2743"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement (2982. .3608)
/gene="pcm"
/function="enzyme; Macro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QTLQVGNASGTPITGGNAITQADAAEQQVVIKPAQNISTVAVASQPTITYSESSGEQSA
NKMLENNKFTATTVTAPVTVPTASTTEPTVSSTSTSTPISTWRWPTEGKVIETFGASE
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RIVYNRQYGNIPXGSYSGSTYTVKKGDTLFYIAMITGNDFRDLAQRNNIQAPYALNYG
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/function="enzyme; Global regulatory functions"
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MG1655: B2741"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /trānslation="miaadslpgvymtlrnkafhQlfQQHtarwQhelpDltkpQ
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tasgekilaaaipigdsvdesplgrlsaeeQelfvQlvrkmmnt"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement (2982. .3608)
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/note="Z4051"
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/transl_table=
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(trans) at i one "mysrkyqallidolraqgijodqyunallaydrekryddaregoka
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                                                                                                                                                protein_id="AAG57850.1"
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                                                                                                                                                                                                                                                                                                       carboxylmethyltransferase
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CDS

CDS

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residues 1 to 236 of 236 from Escherichia
MG1655; B2747"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="survival protein"
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BGYVSITPLHVDLTCHSAQDVVSDWLNSVGVGTQW"
BGYVSITPLHVDLTCHSAQDVVSDWLNSVGVGTQW"
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complement(3602. .4363)
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to residues 1 to 159 of 159 from Escherichia cc
Strain MG1655: B2746"
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/note="Residues 1 to 349 of 349 are 99.42 por
residues 1 to 349 of 349 from Escherichia co
MG1655: B2745"
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/func+:-
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transl_table=11
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                                                            protein"
                                                                                                                                                                                  pct identical to
coli K-12 Strain
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coli K-12 Strain
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by correlating it with other data. Capricially upth with other data. Cappreciated. Updated information will genome Project's World Wide Web Site (http://www.genetics.wisc.edu). *** Tits annotations are periodically upda		Db 2004 AGGGATTGATATCGCAGGCAAAAGGAAATTATCGCAACACGAAATGATCGCCGAATGCCCGTG 1945 Qy 247 alileGlalaAspHisAspmetAspGlyAlaSer
Mary Berlyn. A public version of (http://cgsc.biology.yale.edu) ongoing task whose goal is to ma		Qy 227 snGlyMetTrpPheSerGlyArgAspGlyAspLeuIleAsnAlaSerAsnAlaGlyThrV 247
Stock Center (CGSC) database at Ya		Qy 207 hrAsnProValValArgArgPheGlyThrAlaThrValAlaGlySerThrValThrSerA 227
determined from E. coli K12 strain MG frames were determined using GeneMark Mark Borodovsky, Georgia Institute of		Qy 190 heAlaThrGlySerSerGlyValMetGlnPheArgTyrProValGlyAlaT 207 ::: ::: ::: 2103 CTGTCAGCAGTACATCAACCAGTACGCCTATCTCCACCTGGCCGCTGGCCGACTG 2050
This sequence was determ University of Wisconsin- Supported by NIH grants Droiset and NCHGDD Tho		Qy 170 roThrProProValValGlnGlnProAlaProValAlaProProValThrGluAlaProP 190
AL Submitted (13- Wisconsin, 449	COMMENT	Db 2223 TTACGTATTCTGAGTCTTCGGGTGAACAGAGTGCTAACAAAATGTTGCCGAACAACAAGC 2164
4 (bai	REFERENCE	2282 AGGA-GTTGTGATCAAGCCTGCACAAAATTCCACCGTTGCTGTTGCGTCGCAAACCGACAA
AL Submitt Univers Email:	ou	Db 2324 CACTGGCGGAAATGCCATTACCCAGGCCGACGCAGCAGCAGCA 2283 Qy 152 isProAlaValUysProThr- 169
HORS Blattner, F.R. TLE Direct Submission	AUTHORS TITLE	Qy 132 snThrAlaHisThrProSerProValAlaValGlnSerSerArgProProValGlnGlnH 152
		Qy 112 pLeuThrLeuTrpSerGlyAsp-LeuLysValArgGluArgSerIleSerSerGlyValA 132
	REFERENCE AUTHORS TITLE JOIRNAL	Qy 92 pArgGluIleGlyHi8IleAsnAsnLeuAsnSerSerTyrThrIleTyrThrGlyGlnTr 112
The complet Science 277 97426617	TITLE JOURN MEDLI	Oy 72 gTyrGlnValLysGlnGlyAspThrValSerLysIleAlaGlnArgTyrGlyLeuAsnTr 92
Blattner, F.R., Riley, M., Colla Gregor, J., Davi Mau.B. and Shac	AUTHORS	Qy 60 rGlnValIleThrAspSerGlnGlyValProAsnAr 72 ::::::::::::::::::::::::::::::::::::
# Escherichia coli Bacteria; Proteo Escherichia.	DRG ORG	Qy 41 SerThrSerGlySerGlySerHisArgThrSerGlySerGlyGlyLeu-AlaIleGlySe 60 ::: :::
ISION AE000358 U00096 ON AE000358.1 GI:2367156 NRDS Escherichia coli K12	ACCESSION VERSION KEYWORDS SOURCE	Qy 21 IlePheGlyVallleThrThrCyslleLeuAlaGlyCysAlaSerLysProThrTyrAsn 40
30 88/c	RESULT AE00035 LOCUS DEFINIT	12.78% Indels: 1 Gaps:) x AE005502 (1-10573)
64	Qy dd	Alignment Scores: 0.00238 Length: 10573 Pred. No.: 0.00238 Length: 10573 Score: 213.50 Matches: 87 Percent Similarity: 42.01% Conservative: 55 Best Local Similarity: 25.74% Mismatches: 137
285 alArgThrGlyGlnArgIleAlaSerMetLysAsn ::: ::: ::: 1824 TGAAGGCGGGCAAAAAATAGCAACCATGGTAAC	p 9	/gene="Z4056" complement(6598.
265 snGlyPheValSerSerTyrIleHisIleLysAsp :::::: :: 1884 ATGATTACCTGAGTGCCTACGCCCATAACGACACA	Ωy	LLAHPRVKRVVIAISPGDSRFAQLPLANHPQITVVDGGDERADSVLAGLKAAGDAQWV LVHDAARPCLHQDDLARLLALSETSRTGGILAAPVRDTMKRAEPGKNAIAHTVDRNGL WHALTPQFFPRELLHDCLTRALNEGAAITDEASALEYCGFHPQLVEGRADNIKVTRPE DLALAEFYLTRTIHQENT" Gene COmplement (5.588, 6909)

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** The E. coli K12 sequence and updated; this is version M54. No
                                                                   y of Genetics, University of m, WI 53706, USA ion replaced gi:1789096. he E. coli Genome Project at the Frederick R. Blattner, director). nd HG01428 (from the Human Genome equence was independently mG1655. Predicted open reading Mark software, kindly supplied by e of Technology, Atlanta, GA, edul. Open reading frames that loci are being annotated with CG genes in the E. coli Genetic ale University, kindly supplied by the database is accessible annotation of the genome is an e the genome sequence more useful comments to the authors are will be available at the E. coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ch,C.A., Perna,N.T., Burland,V.,
,J.D., Rode,C.K., Mayhew,G.F.,
H.A., Goeden,M.A., Rose,D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     t III, Laboratory of Genetics, Mall, Madison, WI 53706, USA. e: 608-262-2534 Fax:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             t III, Laboratory of Genetics, Mall, Madison, WI 53706, USA. e: 608-262-2534 Fax:
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248 of 400 of the complete
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Complement (4487. .5248)

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egyvsitplhvdltahsaodyvsdwlnsvgvgtqw"
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NKMLPNNKPTATTVTAPVTVPTASTTEPTVSSTSTPISTWRWPTEGKVIETFGASE
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RIVXNRQYGNIPKGSYSGSTYTVKKGDTLFYIAWITGNDFRI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 lement (3867. .4493)
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luPheArgIleSerArgAsnGlyValTyrValAspProLeuThrValLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTATACCGTGAAAAAAGGCGACACACTTTTCTATATCGCCTGGATTACTGGCAACGATTT
                                                                                                                                                                                                                                                                                                                                                                                                                CTGTCAGCAGTACATCAACCAGTACGCCTATCTCCACCTGGCGCTGGCCG-----ACTG
                                                                                                                                                                                                                                                                                                                                                                                                                                               heAlaThrGly-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CACTGGCGGAAATGCCATTACCC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pLeuThrLeuTrpSerGlyAsp-LeuLysValArgGluArgSerIleSerSerGlyValA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACGCATCGTCTATAACCGTCAGTATGGGAACATTCCGAAAGGCAGTTATAGCGGCAGTAC
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                                                       TTAAGGCGGGGCAAAAAATAGCGACCATGGGTAGCACCGGAACCAGTTCAACACGCTTGC
                                                                                       alArgThrGlyGlnArgIleAlaSerMetLysAsnGlnProSerGlyAlaAlaLeuPheG
                                                                                                                          ATGATTACCTGAGTGCCTACGCCCATAACGACACAATGCTGGTCCGGGAACAACAAGAAG
                                                                                                                                                          snGlyPheValSerSerTyrIleHisIleLysAspAlaGlnValLysThrGlyAspThrV
                                                                                                                                                                                             TIGITITATGCTGGTAACGCGCTGCGCGCGGCTACGGTAATCTGATTATCATCAAACATAATG
                                                                                                                                                                                                                               allleGlnAlaAspHisAsnMetAspGlyAlaSer----IleValIleGlnHisThrA
                                                                                                                                                                                                                                                                    AGGGGATTGATATCGCAGGCAGCAAAGGACAGGCAATTATCGCGACCGCAGATGGCCGCG
                                                                                                                                                                                                                                                                                                      snGlyMetTrpPheSerGlyArgAspGlyAspLeuIleAsnAlaSerAsnAlaGlyThrV
                                                                                                                                                                                                                                                                                                                                             AGGGCAAAGTGATCGAAACCTTTGGC---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rGlnValIleThrAspSerGln-----GlyValPro------AsnAr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACAACCGCAAATCCAGCCAGTGCAGCCAGTAGCTCAGCAGCCGGTACAGATGGAAAACGG
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                                                                                                                                                                                                                                                                                                                                             -GCTTCTGAGGGGGGC
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REFERENCE
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ORGANISM
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VERSION
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ECU29579/c
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                                                                                                                                                                                                                                                                                                                                     feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (20-JUN-1995) Guy P. Plunkett, University of Wisconsin, Laboratory of Genetics, 445 Henry Mall, Madison, WI 53706, USA This sequence was determined as part of the E. coli Genome Project (Frederick R. Blattner, director) at the University of Wisconsin-Madison. Supported by award HG00301 from the NIH Human Genome Project. The entire sequence was independently determined from E. coli WG1655; overlaps with other sequence determinations are annotated. This entry should be considered somewhat provisional; it will be updated and merged with others at a later
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Escherichia coli.
Escherichia coli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Escherichia coli K-12 genome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTTTGAAATTCGTTACAAGGGGAAATCCGTAAACCCGCTGCGTTATTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (bases 1 to 72221)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="this sequence comprises the following lambda
clones: DD609(EC30K446-3), DD612(EC19-195), DD615(EC27-
240), DD618(EC22-172), and DD620(EC18-1463); M13Janus
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GVGLTQSLALDLAEYGITVHSLMLGNLLKSPMFQSLLPQYATKLGIKPDQVEQYYIDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               240), DD618(EC22-172), and DD62 vector was used for subcloning"
DPLSQNALSLALKLKRG"
                                                                                                                                                                                                                                                                                                                                                        VPLKRGCDYQDVLNMLLFYASPKASYCTGQSINVTGGQVMF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="gutD" 39. .818
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phosphate 2-dehydrogenase)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                      function="glucitol
note="CG Site No. :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein_id="AAA692
/db_xref="GI:882597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="gutD"
/EC_number="1.1.1.140"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="similar to
(ECOGUT)"
                                                                                                                                                                                                                                                                                                              note="similar to GenBank Accession Number X13463"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="CG Site No. 153; alternate
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                                                                                                                              codon_start=1
                                                                                                                                                                                             gene="gutM"
                                                                                                                                                                                                                                          gene='
                                                                                                                                                                                                                                                                                    ECGUTMR) 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     codon_start=1
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note="alternate
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note="CG Site No. 152; alternate gen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(3610. .4668)
note="alternate name ygaB; ORF_f352"
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40873
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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Pred. No.:
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                                                                               21 IlePheGlyValIleThrThrCysIleLeuAlaGlyCysAlaSerLysProThrTyrAsn 40
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10433...14724
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="similar to GenBank Accession Number M73326 (ECOASCBFG)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    product="4Fe-4S iron-sulfur protein"
protein id="AAA69223.1"
(db_xref="GI:882606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          function="electron transport from formate to hydrogen"
note="CG Site No. 33521"
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213.50
42.01%
25.74%
12.78%
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Mismatches:
Indels:
Gaps:
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VERSION
KEYWORDS
SOURCE
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ACCESSION
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                                                                                  270365
Escherichia coli O157:H7 DNA,
APO02562 BA000007
Escherichia coli O157:H7 (strain:O157:H7, DNA.
                                                                   AP002562 BA000007
AP002562.1 GI:13
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                                                                                                                                                                                                                                     ATTTTGAAATTCGTTACAAGGGGAAATCCGTAAACCCGCTGCGTTATTTG 39931
                                                                                                                                                                                                                                                                     luPheArgIleSerArgAsnGlyValTyrValAspProLeuThrValLeu
                                                                                                                                                                                                                                                                                                                                                            alArgThrGlyGlnArgIleAlaSerMetLysAsnGlnProSerGlyAlaAlaLeuPheG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gTyrGlnValLysGlnGlyAspThrValSerLysIleAlaGlnArgTyrGlyLeuAsnTr
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                                                                                                                                                                                                                                                                                                                                   TTAAGGCGGGGCAAAAAATAGCGACCATGGGTAGCACCGGAACCAGTTCAACACGCTTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                ATGATTACCTGAGTGCCTÁCGCCCÁTAACGACACAATGCTGGTCCGGGAACAACAAGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       snGlyPheValSerSerTyrIleHisIleLysAspAlaGlnValLysThrGlyAspThrV
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                                                                     GI:13362858
                                                                                                                bp DNA complete
                                                                                                                linear
genome, sec
                 sub_strain:RIMD 0509952)
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Ohnishi,M., Kurokawa,K., Makino,K.,
Hayashi,T.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             enterohemorrhagic Escherichia coli 0157:H7 Sa
Escherichia coli K-12 strain MG1655
Syst. Appl. Microbiol. 23 (3), 315-324 (2000)
20557356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (26-JUN-2000) Ken Kurokawa, Osaka University, Information Research Center; 3-1, Yamadaoka, Suita, Osa Japan (E-mail:ken@gen.info.osaka-u.ac.jp,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Complete genome sequence of enterchemorrhagic 0157:H7 and genomic comparison with a laborato DNA Res. 8 (1), 11-22 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Complete nucleotide sequence of the prophage VT1-Sakai carrying Shiga toxin 1 genes of the enterohemorrhagic Escherichia coli O157:H7 strain derived from the Sakai outbreak Gene 258 (1-2), 127-139 (2000)
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Yutsudo,C.H., Kurokawa,K., Ishii,K., Hattori,M., Abe,H., Iida,
Yamamoto,K., Hayashi,T., Yasunaga,T., Honda,T., Sasakawa,C. ar
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Kurokawa,K., Ishii,K., Hattori,M., Tatsuno,I., Abe,H., Iida,T.,
Yamamoto,K., Ohnishi,M., Hayashi,T., Yasunaga,T., Honda,T.,
Sasakawa,C. and Shinagawa,H.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         URL:http://www.gen-info.osaka-u.ac.jp/,
Fax:81-6-6879-2047)
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Kurokawa,K., Yasunaga,T., Yokoyama,K., Makino,K.,
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                                                                                                                                                                                                                                                      complement (435. .1220)
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                                                                                                                                                                                                                                                                                                      complement (435. .1220)
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98 in 261 aa (Conserved in E
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                                                                                                                                                                                                                                                                                                                                                     /sub_strain="RIMD 0509952"
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                                                                db_xref="GI:13362859"
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                                                                                                                                                                                                                                                                                                                                                                                                       organism="Escherichia coli O157:H7"
strain="O157:H7"
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O157:H7 Sakai strai
                                                                                                                sensitivity'
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a laboratory strain K-12
                                                                                                                                                                                                              gi|1788871
.coli K-12)'
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K., Shinagawa,H.
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complement (3364. .5214)
/gene="EC83392"
complement (3364. .5214)
/gene="EC83392"
complement (3364. .5214)
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100 in 616 as (Conserved in E.coli K-12)"
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DAQRQGTKDAARLAGIHVLRLNEFTAAAIAXCILDSGQDGVIAVDLGGGTDISIL
RLSRGVFEVLATGGDASLGGDDFDHLADYIRSGAGIDLGSDNRYQRELDAAIAKI
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RLSRGVFEVLATGGDASLGGDDFDHLADYIRSGAGIDLGSDNRYQRELDAAIAKI
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PIDICQVKKGEKGISHFITEHLAPFYERRWGGFLRDFKQNRII"
complement (1354...2724)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement (3027. .3362)

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/gene="EC83391"
/note="similar to FER ECOLI gi|119999|sp|P25528 percent identity 100 in 111 aa (Conserved in E.coli K-12)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement (3027. .3362)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement (2815. .3015)
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VGGSTRADELVREKVGEEFGREPELTSIDEDKVVALGAAIQADILVGNKPDSSMLLLDVI
PLSILGLETMGGLVEKVIERNTTIPADAQDETTFKDGQTAMSIHVMQGRERELVQDCRS
LARFALRGIPALPAGGAHIRVTFQVDADGLLSVTAMEKSTGVEASIQVKPSYGLTDSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="identical to YFHJ_ECOLI gi|1788873 (Conserved g.coli K-12)"
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Best Local Similarity:
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DB:
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                                                                                                                                                                                                                 214655 ACAACCGCAAATCCAGCCAGTGCAGCCAGTAGCTCAGCAGCCGGTACAGATGGAAAACGG 214596
      214535 CTÁTACCGTGAÁAAAAGGCGACACGCTTTTCTATATCGCCTGGATTACTGGCAACGATTT 214476
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gene

SdC

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rGlnValIleThrAspSerGln-----GlyValPro-----

-----AsnAr 72

ACGCATCGTCTATAACCGTCAGTATGGGAACATTCCGAAAGGCAGTTATAGCGGCAGTAC 214536

gTyrGlnValLysGlnGlyAspThrValSerLysIleAlaGlnArgTyrGlyLeuAsnTr 92

SerThrSerGlySerGlySerHisArgThrSerGlySerGlyGlyLeu-AlaIleGlySe 60

IlePheGlyValIleThrThrCysIleLeuAlaGlyCysAlaSerLysProThrTyrAsn 40

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Alignment Scores: Pred. No.:
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complement (5231. .5746)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement (6182. .6568)
/gene="ECs3395"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement (5842...6165)

complement (5842...6165)

/gene="BC83394"

/note="similar to ISCA_ECOLI gi|1788877 percent identity

100 in 107 aa (Conserved in E.coli K-12)"

/codon_start=1
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/gene="EC83394"
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                                                                                                                                                                                                                                                                                                                                 /evidence=not_experimental
/transl_table=11
                        0.0852
213.50
42.01%
25.74%
12.78%
Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
        270365
87
55
137
60
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RESULT 33
AL627276/c
                                                                                                                         REFERENCE
AUTHORS
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VERSION
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1 (bases 1 to 274050)
Parkhill, J., Dougan, G., James, K.D., Thomson, N.R., Pickard, D., Parkhill, J., Dougan, G., James, K.D., Bentley, S.D., Holden, M.T.G., Wain, J., Churcher, C., Mungall, K.L., Bentley, S.D., Holden, M.T.G., Sebaihia, M., Baker, S., Basham, D., Brooks, K., Chillingworth, T., Sebaihia, M., Bavis, P., Davise, R.M., Dowd, L., White, N., Farrar, J., Feltwell, T., Hamlin, N., Haque, A., Hien, T.T., Holroyd, S., Jagels, K., Krogh, A., Larsen, T.S., Leather, S., Moule, S., O'Gaora, P., Parry, C., Quail, M., Rutherford, K., Simmonds, M., Skelton, J.,
                                                                                                                                                                                                                                                                                                AL627276 274050 bp DNA linear BCT 06-C Salmonella enterica serovar Typhi (Salmonella typhi) strain complete chromosome; segment 12/20.
                                                                                                                                                                                               Salmonella enterica subsp. Salmonella enterica subsp.
                                                                                                                                                                                                                                                                               complete chromosome; segment AL627276 AL513382
                                                                                                                                                                Salmonella.
                                                                                                                                                                               Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                 AL627276.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCGTGACCTTGCTCAGCGCAACAATATTCAGGCACCATACGCGCTGAACGTCGGTCAG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                    luPheArgIleSerArgAsnGlyValTyrValAspProLeuThrValLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                         ATTTTGAAATTCGTTACAAGGGGAAATCCGTAAACCCGCTGCGTTATTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGAAGGCGGGCAAAAAATAGCAACCATGGGTAGCACCGGAACCAGTTCAACACGCTTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTGTCAGCAGTACATCAACCAGTACGCCTATCTCCACCTGGCGCTGGCCG-----ACTG
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    enterica serovar Typhi
    enterica serovar Typhi
    gamma subdivision; Enter

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MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL
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                    feature
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Nature 413 (6858), 848-852 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E-mail: parkhill@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequencing team, Sanger Centre, Hinxton, Cambridge CB10 1SA, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (25-OCT-2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Details of S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hinxton,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (bases 1 to 274050)
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             World Wide Web.
                                                       /product="putative RNA methyltransferase"
/product="cands832.1"
/protein_id="CADD5832.1"
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/db_xref="G1:16503807"
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DGARETRVGENACQALFQSRPDAIVRAMFIQSVTPRFKGALRWMAANRKAYHVVDEA
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AHFGVKGVVVQDAALLESGAAIRTABGGAEHYGPITGESIUVLDDFRQAGYTYVTGS
SDRQQALFSTTLPEKMVLVLGREYDYLPEAAREPDDLCVKINGTGNVESLNVSVATGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="uraci1-DNA glycosylase"
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/db_xref="G1:16503806"
/db_xref="SPTREMEL:Q8XGK6"
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FVRPAHGYLESWARQGVLLNTVLTVRAGQAHSHASLGWETFTDKVISLINQHEEGVV
FLLWGSHAQKKGAIIDPQRHHILKAPHPSPLSAHRGFFGCNHFALTNQWLEQHGEKTI
                      complement (1040.
                                         LLAEWWRQNKA"
                                                                                                                                                                                                                                                                                                                                                                                                             /gene="STY2840"
/note="PS00130 Uracil-DNA
complement (1013. .2050)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             glycosylase, score 376. .405
                                                                                                                                                                                                                                                                                                                                                       complement (1013.
                                                                                                                                                                                                                                                                                            /note="Orthologue of E. coli yfif (YFIF_ECOLI); Fasta hit
to YFIF_ECOLI (345 aa), 88% identity in 345 aa overlap"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="Pfam match"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Orthologue of
UNG_ECOLI (228 aa), 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="STY2840"
/EC_number="3.2.2.-"
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                                                                                                                                                                                                                                                                                                                                                                                note="yfif"
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transl_table=
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                                                                                                                                                                                                                                                                                                                                         gene="STY2841"
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9e-132"
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YFIP_ECOLI (232 aa), 88% identity in 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /genne="SY72842"
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/note="Pfam.match to entry PF00085 thiored, Thioredoxin,
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TRNA Methylase family, score 181.50, B-value 1.4e-50"
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3480. .6140
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/note="PS00194 Thioredoxin family active site"
2746. .3426
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AsnAsnLeuAsnSerSerTyrThrIleTyrThrGlyGlnTrpLeu----
                                                                                                                                       AspThrValSerLysIleAlaGlnArgTyrGlyLeuAsnTrpArgGluIleGlyHisIle
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US-10-018-706-2 (1-322) x AL627276 (1-274050)
TATGGGAATATTCCGAAAGGTAGCTATACGGGCGGCAGTACTTACACCGTGAAAAAGGGT
                                                        -----GlyValPro---
                                                                                                                   CHACCGGTCACGGAACAACCCGTGCAGATGGAAAATGGGCGAATCGTATACAATCGCCAG 214948
                                                                                                                                                                                                                                              CCGCAACAAGCGCCGCAAATTCAACCCGTTCAGCGTCCTGTAACGCAGCCCATGCAAACT 215008
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SEFTALIVTILDIA PEDGDNESSLLAVRPY PHQLEEWVENKNGDRCLFR PILPEDEPQLR
GETALVYTKEDLYYRY VESETUBETHEDLANMTQIDYDREMAFVAVRRMDNAEEILGVTR
QEIAQVTKEDLYYRY VESETUBETHEDLANMTQIDYDREMAFVAVRRMDNAEEILGVTR
AISDPDNVDAEFAVLVRSDLKGLGLGRRLMEKLIAYTRDHGLKRLNGITMPNNRGMVA
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Matches:
Conservative:
Mismatches:
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                                             ----AsnArgTyrGlnValLysGlnGly
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84
56
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138
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2 (bases 1 to 1290)
Paesold,G. and Krause,M.
Analysis of rpoS mRNA in Salmonella dublin: identification multiple transcripts with growth-phase-dependent variation transcript stability
J. Bacteriol. 181 (4)
                                                                                                                                                                                                                          nlpD gene.
Salmonella enterica subsp. enterica serovar Dublin.
Salmonella enterica subsp. enterica serovar Dublin
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                             Submitted (18-MAY-1998)
Swiss Federal Institute
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                                                                                                                                                                                                                                                                                                                              Salmonella dublin nlpD gene, AJ006131
                                                                                                                                                                                                                         Salmonella.
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                                                                     IleSerSerGlyValAsnThrAlaHisThrProSerProValAlaValGlnSerSerArg
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Potter, A.A., Rioux, C. and Schryvers, A.B.
Vaccine compositions comprising Haemophilus somnus transferrin-binding proteins and methods of use Patent: US 6391316-A 4 21-MAY-2002;
                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4 from
AR210638
AR210638.1 GI:2
                                                                                                                                                                                                                                                                                                                                                                           Unknown
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           TyrGlnValLysGlnGlyAspThrValSerLysIleAlaGlnArgTyrGlyLeuAsnTrp 92
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McClelland, M., Sanderson, K.E., Spieth, J., Clifton, S.W., McClelland, M., Sanderson, K.E., Porwollik, S., Ali, J., Dante, M., Du, I Latreille, P., Courtney, L., Porwollik, S., Scott, K., Holmes, A., Hou, S., Layman, D., Leonard, S., Nguyen, C., Scott, K., Holmes, A., Hou, S., Ngu, H., Florea, L., Miller, W., Sroneking, T., Nhan, M., Waterston, R. and Wilson, R. K. Stoneking, T., Nhan, M., Waterston, R. and Wilson, R. K. Complete genome sequence of Salmonella enterica serovar Typhim.
                                                                                                                                                                                          Salmonella typhimurium LT2.
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gene	PEATURES SOURCE Gene CDS	AUTHORS TITLE JOURNAL COMMENT
/gene="STM2912" /gene="STM2912" /gene="STM2912" /gonde="start=1 (304 aa), 32% identity in aa 6 - 289" /codon start=1 /codon start=1 /product="putative LysR family transcriptional regulators" /product="putative LysR family transcriptional regulators" /product="putative LysR family transcriptional regulators" /protein id="pal2192.1" /protein id="pal2192.1" /protein id="pal2192.1" /protein id="pal2192.1" /protein id="pal2192.1" /protein id="pal2192.1" /protein id="pal2192.1" /protein id="pal2192.1" /protein id="pal2192.1" /protein id="pal2192.1" /protein id="pal2193.1" /gene="STM2913" /gene="STM2913" /gene="similar to E. coli putative transport protein (pac75782.1); Blastp hit to AAC75782.1 (454 aa), 33% /complement(10452541) /protein id="pal2193.1" /product="putative permease" /protein id="pal2193.1" /product="putative permease" /protein id="pal21103.1" /protein id="pal21703.1" /protein id="pal21703".1" /protein id="pal21703".1" /protein id="pal21715LIPIVARALAKSGKRSLITLGVALAGGLVGHHTUP PTGGPLGVAGIFNVDIGAMLITGMALAVECVIGIVFYAGMILERTRYDEFTILAGGLIG RALAITGYIVSIPIFVDSAFVILAYTTUPIVILTELEGLOSAGIILLVTGAGGALAGA ILRDSGAGQQLAEQVANLPISPILIPFIVATLAEEGLOGAGIILLVTGASGIILLYTGAGGALGA ILRDSGAGQQLAEQVANLPISPILIPFIVATLAEEGLOGAGIILLVTGASGRABIILLQTBABAIGG PGINNLLAAQAATWGSLFFGYFNDSLFWVVNRMMGVSDVKQGMVVWSVPTTIAWAIGG PGINNLLAAQAATWGSLFFGYFNDSLFWVVNRMMGVSDVKQGMVVWSVPTTIAWAIGG **TITTE *	and Pedro Romero and Peter Karp at Ecocyc; http://ecocyc.PangeaSystems.com/ecocyc/ The analyses of ribosome binding sites and promoter binding sites were kindly provided by Heladia Salgado, Julio Collado-Vides and ReguonDB; ReguonDB; ReguonDB; This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistries or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one mil subclone. Location/Qualifiers 1. 20984 /organiem="Salmonella typhimurium LT2" /db_xref="HATCC:700720" /db_xref="Laxon:99287" 71. 1003 /gene="STM2912" 71. 1003	The Salmonella typhimurium Genome Sequencing Project. Direct Submission Submitted (29-MAR-2001) Genome Sequencing Center, Department of Genetics, Washington University School of Medicine, 4444 Forest Park Boulevard, St. Louis, MO 63108, USA COMMENT Supported by NIH grant 5U 01 A143283 Coding sequences below are predicted from manually evaluated computer analysis, using similarity information and the programs, GLIMMER; http://www.tigr.org/softlab/glimmer/glimmer.html and GeneMark; http://opal.biology.gatech.edu/GeneMark/ EC numbers were kindly provided by Junko Yabuzaki and the Kyoto Encyclopedia of Genes and Genomes; http://www.genome.ad.jp/kegg/,
gene CDS RBS CDS	RBS RBS 	gene CDS

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/gene="STM2914"
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ACRRQPKIREVESSSLAVYGGTLPECVTDTTALTERSSYGAQKAACELLVNDYTRKG
YVDGLALRLDTICVREGKERNRAASESVSAIREPLQGETTVCPVSESSLRUMISSPATV
IHNLSLAATLPAPGEASSINLPGISVTVGEMLETLCQAGGQAARDRVTHQRDEGVEKI
VASWFGRI DNQRALALGFVADKRFDDIIERFRQDDMEGRS"
complement (2543. 2548)
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(AAC75779.1); Blastp hit to AAC75779.1 (388 aa), 79%
identity in aa 1 - 384"
                                                                                                                                                                                                /note="putative RBS for ygbM; RegulonDB:STMS1H002972"
complement(4944. .6217)
                                                                                                                                                                                                                                                                          complement (4313. .4318)
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LLANHGPVVCGENLQEAANNTEELEETAKLIFILGERPIRYLTTEEIAQLRR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement (4309. .4947)
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complement(4309. .4962)
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                                                                                                                      complement (4944. .6206)
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(AAC75780.1); Blastp hit to AAC75780.1 (212 aa), 85%
identity in aa 1 - 211"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="similar to E. coli orf, hypothetical protein
(AAC75781.1); Blastp hit to AAC75781.1 (258 aa), 79%
identity in aa 1 - 258"
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                                                                                                                                                 'note="STM2917"
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note="STM2915"
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transl_table=11
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12414

12453

12513

12573

237

12363

275

12255

12195

257

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Percent Similarity:
Best Local Similarity:
Query Match:
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                                                                                      ValLysGlnGlyAspThrValSerLysIleAlaGlnArgTyrGlyLeuAsnTrpArgGlu
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                                                                                                                                            IleGlyHisIleAsnAsnLeuAsnSerSerTyrThrIleTyrThrGlyGlnTrpLeu---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---IleGlySerGlnValIleThrAspSerGln----
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RDVDVARCLSSSTREAVAEALAGGITRFIVAGGETSGVVTQSLGITGFHIGPCISPGVPWVNAL
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/note="putative RBS for ygbL; RegulonDB:STMS1H002973"
complement 6200. .7134)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="3-hydroxyisobutyrate dehydrogenase"
/protein id="AALZ1798.1"
/protein id="AALZ1798.1"
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/translation="MTTGTDFHVGIVGHAARSCLRAGLS"
/translation="M
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/note="similar to E. coli putative dehydrogenase
/AAC75778.1; Blastp hit to AAC75778.1 (302 aa),
identity in aa 1 - 299"
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/note="STM2918"
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/transl_table=11
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209.00
38.25%
22.95%
12.51%
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-ThrLeuTrpSerGlyAspLeuLysValArgGluArgSer ::: ::: :::
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Matches:
Conservative:
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88
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VERSION
KEYWORDS
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AE004139
LOCUS
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MEDLINE
PUBMED
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AUTHORS
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AUTHORS
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                                                                                                                                                                                                                               Batteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.

1 (bases 1 to 10104)

1 (bases 1 to 10104)

Heidelberg, J. F., Eisen, J.A., Nelson, W.C., Clayton, R.A., Gwinn, M.L.,
Dodson, R.J., Haft, D.H., Hickey, E.K., Peterson, J.D., Umayam, L.,
Gill, S.R., Nelson, K.E., Read, T.D., Tettelin, H., Richardson, D.,
Ermolaeva, M.D., Vamathevan, J., Bass, S., Qin, H., Dragoi, I.,
Ermolaeva, M.D., Vamathevan, J., Bass, S., Qin, H., Dragoi, I.,
Sellers, P., McDonald, L., Utterback, T., Fleishmann, R.D.,
Nerman, W.C. and White, O.

DNA sequence of both chromosomes of the cholera pathogen Vibrio
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Vibrio cholerae
      2 (bases 1 to 10104)
Heidelberg.J.F., Eisen,J.A., Nelson,W.C., Clayton,R.A., Gwinn,M.L., Bodson,R.J., Haft,D.H., Hickey,E.K., Peterson,J.D., Umayam,L.A., Gill,S.R., Nelson,K.E., Read,T.D., Tettelin,H., Richardson,D.,
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Vibrio cholerae
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AE004139 AE003852
AE004139.1 GI:9654953
                                                                                                                                                                                Nature 406 (6795),
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|||:::|||:::||| ::: :::::|||:::|| |||
GTAATCTTATTATCATCAAACATAACGATGATTACCTGAGTGCCTACGCCCATAATGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AsnGlnProSerGlyAlaAlaLeuPheGluPheArg[]eSerArgAsnGlyValTyrVal 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACGATGCTGGTCCGGGAACAACAGGAAGTTAAGGCGGGGCAAAAAATCGCTACTATGGGT 12135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AspAlaGlnValLysThrGlyAspThrValArgThrGlyGlnArgIleAlaSerMetLys 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ProProVal-----------GlnGlnHisProAlaValGlnLysProThr 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGCACCGGCACCAGCTCTACACGCTTGCATTTTGAAATTCGTTACAAGGGGAAATCCGTA 12075
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ermolaeva, M.D., Vamathevan, J., Bass, S., Qin, H., Dragoi, I., Sellers, P., McDonald, L., Utterback, T., Fleishmann, R.D., Nierman, W.C., White, O., Salzberg, S.L., Smith, H.O., Colwell, Mekalanos, J.J., Venter, J.C. and Fraser, C.M.
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                                                                                 /translation="MTDILSPLAYLCGKPTAKAKLKALPEHFQVNEVLGYSLTGHGEH
LMVRIRKTGENTSFVANELAKACGVPSRAVSWAGLKDRHAVTEQWLSVHLPNGETPDF
SAFLAQYPSIEILEVTRHDKKLRPGDLQGNEFVVTLSEVSDVAAVLSRLETVAELGVP
                               NYFGSQRFGRHGNNLSEARRWGRDNVRSRNQNQRSLYLSAARSWIFNQIVSKRIEQGC
FARFIEGDIALAEQQMFNVDGDLALWDQRLQAGEVAISAALAGDNALFTSGQALFLEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PLIEHYVVAVSADDPYFANLPLAHHPRVIRVDGGKERADSVLSALEYVCQHRLSEWVL
VHDAARPCVTHADITQLITTALAHPIGAILASPVRDTMKRGDHLQQIVHTVDRTALWH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="similar to GB:L42023 PID:1005557 PID:1220756 PID:1204923 PID:1573673; identified by sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALTPOMFRAQSLRERLFAALQQQVTITDEASAFEWRGEKPALVAGRADNLKITQPEDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /trānslation="mvmrvfaltlslllvwllytlmmgkngvmdfravqabievqqqv
Nanlhlrnqemfabiddlrqgldaieerarnelgmvkdgetfyriigeesrq"
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                                                                                                                                                        product="conserved hypothetical protein"

protein id="AAF93698.1"

(db xref="GI:9654957"
                                                                                                                                                                                                                                                                                                                               1573. .2658
/gene="VC0530"
                                                                                                                                                                                                                                                                                                                                                           /gene="VC0530"
573. .2658
                                                                                                                                                                                                                                                                                                                                                                                                                                       APKMAPYIQAMCAAIAEDLETDLGNINVKATTTEKLGFTGRKEGIACEAVVLLRKA"
                                                                                                                                                                                                                                                   codon_start=1/
transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      product="conserved hypothetical protein"
protein id="AAF93697.1"
db_xref="GI:9654956"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LAEFYLSRNKEKS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  product="CDP-ribitol pyrophosphorylase-related
protein_id="AAF93696.1"
db_xref="GI:9654955"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    product="conserved hypothetical protein"
protein_id="AAF93695.1"
db_xref="GI:9654954"
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                                                                                                                                                                                                                                                                                                   note="identified
                                                                                                                                                                                                                                                                                                                                                                                                                    573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SDALLGATAAGDIGRHFPDTDDKWKGADSRELLKDVYRRVKAQGYVLGNADVTITAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       codon_start=1
transI_table=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene="VC0527"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             chromosome="I"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       translation="MIRIGHGFDVHRFGGEGPIIIGGVKIPYEQGLIAHSDGDVALHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="identified by Glimmer2; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene="VC0529"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene="VC0529"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         translation="MNNMTAIVPAAGVGSRMQADRPKQYLTLLDKTVLEHTVEHLLEH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene="VC0528"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="identified by Glimmer2; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="biotype:
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                                                                                                                                                                                                                                                                                                   Glimmer2; putative"
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                                                                                                                                                                                                                                                                                                                      /codon_start=1
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QLAEGGRMYIPVGBDEQYLYKIVRQGGQFISERVEAVRFVPLVAGDLA"
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GINHGANLGDDVLYSGTVAAAMEGHFLGVQSIAFSLAGTTHFASAAHFVRQLVEQHLA
NPIPTNRLLNVNIPDRPLELIQGIEVTRLGARHHAESMIKQKDPRGHDIYMLGPPGKE
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nqtrtirlpihvvkelniylrtarelsqrldheptpebialeldrpvddvtkmlrlne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GOKIATMGSSGTNSVRLHFEIRYQGKSVNPKRYLP"
5040. .6047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGGAATVAVASSTSASVAKAATTATVAQTVSKSSNTKNVQNGSTNSQNLTKKD PVKTV
DQTKTKEYVEPVGKQNVNVNVAKAKPSDEKIAKMLMPTKGRVIKNFSAGDQGNKGIDI
AGQRGQAVVATADGTVVYSGNALRGYGNLIIIKHNEHYLSAYAHNDQLLAKEGQTVQA
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GSYYEVKKGDTLYFIAYLTDKDVNDLISYNDLAPPYTIHPGQKIKLMLPNYTPPAYGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4031. .4966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="similar to GB:M63493 SP:P24206 PID:147115
PID:882636 GB:U00096; identified by sequence similarity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QDAGPGTDFHAIERGWVSLTPLQVDLTAHESLRSMDHWLKEKVNG"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="lipoprotein NlpD"
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dentified by sequence similarity; putative"
note="similar to GB:M64730 SP:P23909 PID:146906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="similar to GP:2897902; identified by sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'gene="VC0534"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene="\
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transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'gene="VC0532"
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transl_table=11
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                                                                                                                                                                 ISSVDTPIGGDGDKALLDILPDSHNADPEFSTQDDDIRESLLNWLDELNPKQKEVLA
RFGLLGYEPSTLEEVGREINLTRERVRQIQVEGLRRLREILVKQGLNWEALFNVEYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 imilarity; putative"
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                                                                                                              .8728)
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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         AlaValGlnLysProThrProProValValValLysLysProThrProThrProPro
                                                               GTGAGCAAAAGCTCTAATACCAAAAATGTACAAAATGGGTCAACGAATAGTCAAAATTTG 448
                                                                                                                     ValAlaValGlnSerSerArgProProValGln----
                                                                                                                                                                           GCTTCAAGCACAAGTGCAAGTGTTGCCAAAGCGGCGACGACGGCAACAGTTGCTCAAACC
                                                                                                                                                                                                                              -----ArgGluArgSerIleSerSerGlyValAsnThrAlaHisThrProSerPro
                                                                                                                                                                                                                                                                                    TTACCTAATTATACTCCTCCTGCTTATGGTGGAACGGGCGGTGCAGCTACCGTGGCTGTG
                                                                                                                                                                                                                                                                                                                                                                                                 AGTTACAACGATCTCGCTCCACCTTACACCATTCATCCTGGGCAAAAAATTAAGCTCTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAAGGCGACACGCTCTATTTATTGCCTTACCTCACAGATAAAGATGTAAATGATCTGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TACCGCGGAAGTTAC----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AlaIleGlySerGlnValIleThrAspSerGlnGlyValProAsnArgTyrGlnValLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCTACGCCAGCACCAGTCTCTGGATTGGGTAAAGATTACAACAAAGTTGAGCGTGGTAGT 4156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CGACTGGGCTTATTA-----TTGTTTTTGCAGCTTATTATTCGGCTGTACTGCA---
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KLQQLELLSSQPAETRKFSRVDIANQLSLIPEFSAVEQALAGVDDDLTFRQALDMLY
CLKKILT.
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8735. .8836
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PID:882626 GB:U00096; identified by sequence similarity; putative"
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Submitted (06-SEP-1993) Hideo Takahashi, The University of Tokyo, Inst. of Mol. & Cell. Biosci., Yayoi 1-1-1, Bunkyo-ku, Tokyo 113,
                                                            Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tanaka,K., Takayanagi,Y., Fujita,N., Ishihama,A. and Takahashi,H. Heterogeneity of the principal sigma factor in Escherichia coli: the rpoS gene product, sigma 38, is a second principal sigma factor of RNA polymerase in stationary-phase Escherichia coli Proc. Natl. Acad. Sci. U.S.A. 90 (8), 3511-3515 (1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Escherichia coli (strain:0H1) DNA, clone:pKTF106
Escherichia coli
Bacteria; Proteobacteria; gamma subdivision; Ente
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1612 bp DNA linear BCT 10-SEP-1999
Escherichia coli gene for RNA polymerase sigma factor, ORF-X
protein, L-isoaspartyl protein carboxy methyltransferase, partial
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A gene at 59 minutes on the Escherichia coli chromosome
lipoprotein with unusual amino acid repeat sequences
J. Bacteriol. 176 (6), 1630-1638 (1994)
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 ---CTAATTCTGGTATGTTACGCCGCCGCCGAAAATGGGGACGACGTCTACAGCGC 392
                                  GlyValileThrThrCysIleLeu----
                                                                                                      ValThrIleAlaIleAsnSerGlnAsnGlnLysProIleLysArgLeuGlyLeuIlePhe
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/LISQGATQRVLDATQLYLGEIGYSPLLT"
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Location/Qualifiers
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FWRWPTEGKVIETFGASEGGNKGIDIAGSKGQAIIATADGRVVYAGNALRGYGNLIII
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'db_xref="taxon:562"
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Direct Submission

Submitted (13-NOV-2001) Institute of Molecular Biology and Medicine, University of Scranton, Scranton, PA 18510, USA

3 (bases 1 to 12362)

8 Elzer, P.H. and Hagius, S.

Direct Submission

Submitted (13-NOV-2001) Department of Veterinary Science, LSU Ag Center, 111 Dalrymple Building, Baton Rouge, LA 70803, USA

4 (bases 1 to 12362)

Kapatral, V., Los, T., Ivanova, N., Anderson, I., Bhattacharyya, A., Iykidis, A., Reznik, G., Jablonski, L., Larsen, N., D'Souza, M., Eryhides, N., and Overbeek, R.

Bernal, A., Mazur, M., Goltsman, E., Selkov, E., Haselkorn, R., Burect Submission, and Overbeek, R.

Direct Submission

Birect Submission

Losdin, USA

Park Drive, II. 60612, USA

Forbases 1 to 12362)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Letesson, J.-J.

Direct Submission

Direct Submission

Submitted (13-NOV-2001) Unite de Recherche en Biologie Moleculaire,

Laboratoire d'Immunologie et de Microbiologie, Universite of Namur,

61 rue de Bruxelles, Namur 5000, Belgium

6 (bases 1 to 12362)

O'Callaghan,D.

Direct Submission

Submitted (13-NOV-2001) Faculte de Medecine, INSERM U431, Avenue

Yannadv. Nimes 30900, France
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 12362)
DelVecchio, V.G., Kapatral, V., Redkar, R.J., Patra, G., Mujer, C.,
DelVecchio, V.G., Kapatral, V., Redkar, R.J., Patra, G., Mujer, C.,
Los, T., Ivanova, N., Anderson, I., Bhattacharyya, A., Lykidis, A.,
Reznik, G., Jablonski, L., Larsen, N., D'Souza, M., Bernal, A.,
Reznik, G., Jablonski, L., Larsen, N., D'Souza, M., Bernal, A.,
Razur, M., Goltsman, E., Selkov, E., Elzer, P.H., Hagius, S.,
O'Callaghan, D., Letesson, J.-J., Haselkorn, R., Kyrpides, N. and
Overbeek, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Brucella melitensis
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Brucellaceae; Brucella.
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AE009547.1 GI:17983036
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DelVecchio, V.G., Redk
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Proc. Natl. Acad. Sci. U.S.A. 99 (1), 443-448 (2002)
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ProAsnArgTyrGlnValLysGlnGlyAspThrValSerLysIleAlaGlnArgTyrGly 89
                                                                                                                                                                      ATCGCTGGCGTTCCGCAAGCACCTGCTGTCAACGGCAAGAAATCCTCGCCGACCAATATG 11594
                                                                                                                                                                                                                    LeuAlaGlyCysAlaSerLysProThrTyrAsnSerThrSerGlySerGlySerHisArg 49
                                                                                                                   ThrSerGlySerGlyGlyLeuAlaIleGlySerGlnValIleThrAspSerGlnGlyVal 69
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/gene="BMEI1077"
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VLSTLHDVVILSGMFIVFRMEFNLWSVAAILTIIGYSLNDTVVIYDRVRENLRRYKSA
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/protein_id="AAL52257.1"
/db_xref="GI:17983044"
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/gene="BMEI1076"
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HGWEPKNPPLLSRADLGAILEEASDIEILLVGTGMDLRRIPEDVRALLRQHHISSDPM
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/protein_id="AAL52256.1"
/db_xref="GI:1/983043"
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/db_xref="GI:17983045"
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LMDVRVKGEPVADNKNK"
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Neisseria meningitidis Z2491
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTGGAA 10859
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                                                                                                                                            (bases 1 to 329861)
                                                                                                                                                                                                Proteobacteria; beta
                                                                                                                                                                                                                                                                                                 GI:7380091
                                                                                                                                                                                                                                                                                                                                                                                           329861 bp
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Parkhill, J., Achtman, M., James, K.D., Bentley, S.D., Churcher, C., Klee, S.R., Morelli, G., Basham, D., Brown, D., Chillingworth, T., Davies, R.M., Davies, P., Devlin, K., Feltwell, T., Hamlin, N., Holroyd, S., Jagels, K., Leather, S., Moule, S., Mungall, K., Quail, M.A., Rajandream, M.A., Rutherford, K.M., Simmonds, M., Skelton, J., Whitehead, S., Spratt, B.G. and Barrell, B.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Neisseria meningitidis serogroup A strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GACAATGGCCTTGTGACCGTCTATGGCCATAACAGCCAGATAATGGTGCAGCGCGGCCAG 10979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTTGTGATCTATGCGGGCGATGGTTTGAAGGAATTTGGCCAGACCGTTCTGATCCGCCAC 11039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---CGTGGGCGCATTCTGGCAAGCTTCGGCCAGCGTGAG------GGCACCTCGGTC 11159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTCCCTGTCGACCAGTTGAAGGCGGCAAACGGCCTGACCAGTGGC---GCCATTCGCGTC 1143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAGGTTCGCCGTGGCGAGGAAATCGCC-----AAGTCGGGCATGAGCGGCAACGCCAAG 10925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ThrValIleGlnAlaAspHisAsnMetAsp-----GlyAlaSerIleValIleGlnHis 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGCGACGGTATCGATATCATGGTGCCGGAAAGGCCACGCCGGTCAAAGCCGCCGAAAACGGT 11099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AlaThrAsnProValValArgArgPheGlyThrAlaThrValAlaGlySerThrValThr 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAGGATCAGGCCGCAGCGCCATCCTCAACCGGCATCTCGCAGATGCGTTGGCCGGTT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ThrGluAlaProPheAlaThrGlySerSerGlyValMetGlnPheArgTyrProValGly 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LysLysProThrProThrProProValValGlnGlnProAlaProValAlaProProVal 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ArgProProValGlnGlnHisProAlaValGlnLysProThrProProValValValVal 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGTGCGCCGACACAGGTGGCCGCAATCACGCCGCCAGCCGGCCAAACCCCGGCCAAAGCAGCC 11345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GlyValAsnThr-----AlaHisThrProSerProVal---AlaValGlnSerSer 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ThrValArgThrGlyGlnArgIleAlaSerMetLysAsnGlnProSerGlyAlaAla---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ThrAsnGlyPheValSerSerTyrIleHisIleLysAspAlaGlnValLysThrGlyAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SerAsnGlyMetTrpPheSerGlyArgAspGlyAspLeuIleAsnAlaSerAsnAlaGly 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GlyGlnTrpLeuThrLeuTrpSerGlyAspLeuLysValArgGluArgSerIleSerSer 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LeuAsnTrpArgGluIleGlyHisIleAsnAsnLeuAsnSerSerTyrThrIleTyrThr 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----LeuPheGluPheArgIleSerArgAsnGlyValTyrValAspProLeuThrVal 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----GTAATCGAGGATGCGGAA-----
                                                                                                                                                                                                                                                                                                                                        subdivision;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
Z2491 co
                                                                                                                                                                                                                                                                                                                                            Neisseriaceae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complete genome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BCT 04-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11264
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REFERENCE
AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMMENT
4.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JOURNAL
MEDLINE
PUBMED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (30-MAR-2000) Submitted on behalf of the Neisseria sequencing team, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA E-mail: parkhill@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491
Nature 404 (6777), 502-506 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Details of N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Notes:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Details of N. meningitidis sequencing at the Sanger Centre are available on the World Wide Web.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Parkhill
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (bases 1 to 329861)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     http://www.sanger.ac.uk/Projects/N_meningitidis/).Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label=DUS
592. .601
/note="Core DNA uptake s
/label=DUS
638. .2047
                                                                      /product="putative threonine synthase"
/product="putative threonine synthase"
/product="putative threonine synthase"
/product="putative threonine synthase"
/product="putative threonine synthase"
/proteoninid="chap4661"
/db_xref="gol:738093"
/db_xref="sprewal:093U91"
/db_xref="sprewal:093U91"
/translation="MKXISTRGETAHKPESEVLLMGLAPDGGIMLPEHYPQIGREALD
KWRGLAYPELAFEINELFUYDIPEDDLRDLILMRTYTEAAFGTKEITPVRTLSDGIKIQ
KWRGLAYPELAFEINELFUYDIPEDDLRDLILMRTYTEAAFGTKAUQNDAAFKEKYHIG
TVNSINMGRIVAQVYYTFAGYFKATOSNDEGVJSCTCVPSGUFCANCHARDRDPG
TVNSINMGRIVAQVYYTFAGYFKATOSNDEGVJSCTCVPSGUFCANGHAFKEKYFDLMDRDPG
RLIVATNENDYLDEFFKTGAYRAFRNSAHTYYTSSENDISKASNTATTOTAVETDEG
RLIVATNENDYLDEFFKTGAYRAFRNSAHTYYTSSENDISKASNTATTOTAVETDEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="NMA1439, possible lipoprotein, len: 123 aa; unknown, contains a probable N-terminal signal sequence and an appropriately positioned PS00013 Prokaryotic membrane lipoprotein lipid attachment site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="P800013 prokaryotic membrane lipoprotein lipid
attachment site"
complement (571. .580)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="sptreme1:093U92"
/translation="makthistilphaillggCaagggntfgSildggTgmggsIvkmave
SQCRAELNKRSEWRLTALAMSAEKQAEWENKICACVAQEAPNQLTGNDVMQMLDPSTR
                                                                                                                                                                                                                                                                                                                                                                     /note="NMA1440, thic, probable threonine synthase, len:
485 aa; similar to many e.g. SW:"HRC METGL (EMBL:14071),
485 ab; similar to many e.g. SW:"HRC METGL (EMBL:14071),
thrc, Methylobacillus glycogenes threonine synthase (EC
4.2.99.2) (475 aa), fasta scores; E(): 0, 61.9% identity
11 475 aa overlap. Contains Pfam match to entry PF00291
S T dehydratase, Pyridoxal-phosphate dependent enzymes"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NQALAALTAKTVSACFKHLYR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'gene="thrC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="Core DNA uptake
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="NMA1439"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="putative lipoprotein"
/protein_id="CAB84675.1"
/db_xref="GI:7380092"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'gene="NMA1439"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene="NMA1439"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                strain="Z2491"
|db_xref="taxon:122587"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organism="Neisseria meningitidis Z2491"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             transl_table=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="serogroup:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          _number="4.2.99.2"
                                                                                                                                                                                                                                                                                                                                                   _table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             _table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence: gccgtctgaa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gccgtctgaa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene
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                                                                                                                                                                                                                                        misc_feature
                                                                                                                                                                                                                                                                                                                                                                        misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        misc_feature
                                                                               repeat_unit
                                                                                                                                                            repeat_unit
                                                       complement (3984. .4038)
/note="RS103"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(2923. .2932)
/note="Core DNA uptake sequence: gccgtctgaa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="Stem loop containing DNA uptake sequences: gccgtctgaa gccc ttcagacggc atata" 2909. 2918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Pfam match to
Pyridoxal-phosphate
E-value le-65"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QTVPNSADAVKGIIEQTLA"
875. .1780
                                                                                                                                      3964. .3983
/note=">= 9
                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="maarntokvlsvhhwtdayftftctrdeslrfenggfvnvglmv
Dlavekhyklstgtrefftlyag
Dlavekhyklstgtrefftlyagdelyrgtrefftlyagthykkublaydrffkel
Dlavekhyklstgtrefftlypetlyrgdfikertelhkvgdkylktrefterfkel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /noTe="NMA1442, fpr, probable ferredoxin--NADP reductase, len: 258 aa; similar to many e.g. Sw:FENR AZOVI (RMBL:L16319), fpr, Azotobacter vinelandii ferredoxin--NADP reductase (EC 1.18.1.2) (257 aa), fasta scores; E(): 0, 69.8% identity in 255 aa overlap. Similar to NMA1664, fasta scores; E(): 1.3e-30, 34.6% identity in 257 aa overlap. Contains Pfam match to entry PP00175 oxidored fad, Oxidoreductase FAD/NAD-binding domain"
                                                                                                    /note=">= 90% match to ATTCCCNNNNNNNNNGGGAAT"
/label=dR83
                                                                                                                                                                                                                                                                                                  Oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /trānslation="MTVPMQETHFSILLDELAAKQEAAIAPHLLADGTKVWIRKAGRH
NAKWRYALLGMVARYLKLGVLKPVPSLGGEBAIATESKRLYELRAAGIAVPELLAVRK
NALWEGNLEGIPLDTQIROBABAGKADAWLAGLEAIARVHKOQFLSQAFARNUMSDG
KNISFLDFEDDPSEVLTIAQCQARDWLCYIHSTALILKNGGILEAAAEKWGGVLSDQP
                                                                                                                                                                                                                                                                                         /note="Pfam match to entry PF00175 oxidored_fad, xidoreductase_FAD/NAD-binding domain, score 20.00,
                                                                                                                                                                                                                                                                                                                                                                                                    CGSPAMLKDTCKVLDDFGLTVSPKTGVRGDYLIERAFVDQ'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /producE="putative ferredoxin--NADP reductase"
/protein id="CAB84678.1"
/db_xref="G17380995"
/db_xref="SPTREMBL:Q9JRE3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AEIQKLIAATVKPILPIRRLEHPRWGRDALRLAASISLISLADMPP"
                                                                                                                                                                                                .866. .3875
'note="Core DNA uptake sequence: gccgtctgaa"
                                                                                                                                                                                                                                                                       -value
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="Core DNA uptake sequence: gccgtctgaa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'product="hypothetical protein NMA1441"
'protein_id="CAB84677.1"
'db_xref="GI:7380094"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   codon_start=1
transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  codon start=1
transl_table=11
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gene="NMA1441"
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                                                                                                                                                                                          label=DUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                076. .3852
gene="fpr"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       _number="1.18.1.2"
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                                                                                                                                                                                                                                                                    8.4e-05"
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Percent Similarity:
Best Local Similarity:
Query Match:
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                                                                                                                                                                                                           283280
                                                                                                                                                                                                                                                                                              283313
                                                                                                                                                                                                                                                                                                                                                                             283367 GACGATTTCCGTGCGTGGAACGGCATGACCGACAAT---ACGTTGAGCATCGGTCAG--- 283314
                                                                                                                                                                                                                                                    133
                                                                                   173
                                                                                                                                                      153 ProAlaValGlnLysProThrProProValValValValLysLysProThrProThrPro 172
184 ProValThrGluAlaProPheAla-----ThrGlySerSerGlyValMetGln 199
                                                                                                                                                                                                                                                                                                                                                                                                                      93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                73 TyrGlnValLysGlnGlyAspThrValSerLysIleAlaGlnArgTyrGlyLeuAsnTrp 92
                                                                                                                          GCTGCCGTGCAAACCCCTGTG----
                                                                                                                                                                                                                                                ThrAlaHisThrProSerProValAlaValGlnSerSerArgProProValGlnGlnHis 152
                                                                                                                                                                                                                                                                                                                                                                                                                    ArgGluIleGlyHisIleAsnAsnLeuAsnSerSerTyrThrIleTyrThrGlyGlnTrp 112
                                     CCTGTGCAGTCCGCGCGCAACCTGCCGCGCCCCCTGCGGAAAATAAAGCGGTTCCCGCG 283143
                                                                                LeuThrLeuTrpSerGlyAspLeuLysValArgGluArgSerIleSerSerGlyValAsn 132
                                                                                                                                                                                                         ------CCGAAAGCCGCAGCCGTAAAA---AGCAGGCCCGCCGTACCG----- 283242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="NMA1444, probable P-type cation-transporting ATPase, len: 823 aa; similar to many e.g. SW:COPA_ENTHR (EMBL:1213292), copA, Enterococcus hirae copper/potassium-transporting ATPase A (EC 3.6.1.36) (727 aa), fasta scores; E(): 0, 34.0% identity in 744 aa overlap. Similar to NMA1539, fasta scores; E(): 0, 34.4% identity in 735 aa overlap. Contains hydrophobic, probable membrane-spanning regions. Contains two Pfam matches to entry PF00122 E1-E2_ATPase, E1-E2_ATPases and PS00154 [E1-E2_ATPases phosphorylation site"]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement (4509. .6980)
/gene="NMA1444"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="putative P-type cation-transporting ATPase"
/protein_id="CAB84680.1"
/db_xref="GE1:7380097"
/db_xref="SPTREMBL:Q9JU88"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="NMA1444"
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'protein_id="CAB84679.1"
'db_xref="GI.738096"
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f unusually low GC content"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    159. .4320
gene="NMA1443"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 codon_start=1
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43.46%
27.31%
12.16%
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Matches:
Conservative:
Mismatches:
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97
50
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Search completed: July 3, 2003, 21:18:47 Job time: 2677 secs

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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-Q=/cgn2 1/USPTO spool/US10018706/runat 30062003 091104 23784/app_query.fasta_1.519
-DB=N_Geneseq_101002 -QFMT=fastap -SUFFTX=rng -MTNMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=40
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MILLEN=0 -MAXLEN=2000000000
-USER=US10018706_GCGN 1 1 20R0=ext -HEAPSIZE=500 -MILLONG-0-CUPU=3
-NO_MAAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Perfect score:
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Ygapop 10.0 , 1
Fgapop 6.0 , 1
Delop 6.0 , 1
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2: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*

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3662.341 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

conflict

Location/Qualifiers replace(310,G)

Moraxella catarrhalis.

vaccine; ss.

BASB110; infection; otitis media; pneumonia; gene therapy; diagnosis; antibacterial; antimicrobial; genetic immunisation;

Moraxella catarrhalis DNA encoding BASB110 protein.

RESULT 1
AAF30046
ID AAF3
XX AAF3
XX AAF3
XX AAF3
XX More
XX More
XX More
XX Wacc
XX Wacc
XX Wacc
XX Yacc
XX Yacc
XX Yacc
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AAF30046 standard; DNA; 969 BP.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                          No.:
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16-JUN-2000; 2000WO-US16649.
                                                                                                                                                 Genomic library; bacteria; human upper airway; otitis media; bronchopulmonary; endocarditis; meningitis; ss.
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Best Local Similarity:
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Novel BASB110 polypeptides of Moraxella catarrhalis, vaccine for treating Moraxella catarrhalis infections
                                                                           WPI; 2001-112459/12.
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Claim 10; Page 83; 88pp; English.

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                             Haemophilus influenzae Rd genome recorded on computer readable medium - useful for identifying commercially important nucleic fragments by homology searching
                                                                                                                                                                                                             Genome; bacterium; Haemophilus influenzae; computer readable medium; expression modulating fragment; regulation; gene expression; vector; organism; open reading frame; ORF; ds.
                 Claim 1; Page 77.2-77.1091; 1291pp; English
                                                                                                                                                                                                                                            Haemophilus influenzae complete genome sequence.
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Alignment Scores Pred. No.:

1.93e-06 209.00

Length: Matches:

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Sequence 2179

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390 G; 677 T;

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                                          The present sequence encodes the Haemophilus somnus lipoprotein LppB. CR Recombinant vaccines containing H. somnus lipoproteins LppA, LppB cand LppC have been described. H. somnus transferrin-binding proteins Tbpl and Tbp2 have also been found to be effective in vaccines against cand Tbp2 have also been found to be effective in vaccines against careening a genomic expression library of H. somnus strain HS25 in E. coli with polyclonal antiserum raised against affinity-purified Tbp1 CC and Tbp2 of H. somnus. The genes coding for Tbp1 and Tbp2 were obtained by inverse PCR. The nucleotide sequence encoding Tbp1 and Tbp2 may be used for the recombinant production of Tbp1 and Tbp2, which may then be used for the recombinant production of Tbp1 and Tbp2, which may then be used to manufacture vaccine compositions for immunising against H. somnus infections. The antibodies raised against the transferrin binding proteins may also be used diagnostically to identify the presence of that causes a number of diseases in cattle such as thromboembolic meningencephalitis (TEME), myocarditis, septicaemia, arthritis and
                                                                                                                                                                                                                                                                                                                                                                          Nucleic acids encoding Haemophilus somnus transferrin binding proteins useful for vaccinating against and diagnosing H. somnus infections e.g. myocarditis and pneumonia in cattle -
                                                                                                                                                                                                                                                                                                                                           Disclosure; Fig 11; 67pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                               P-PSDB;
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24-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Haemophilus
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99US-0405728
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             Neisseria meningitidis; Neisseria gonorrheae; antigen; vaccine; antigenic; diagnosis; immunogenic; infection; meningitis; septicaemia; antibacterial; gene therapy; ds.
                                                                              Neisseria meningitidis ORF 025 partial DNA sequence SEQ ID NO:111-1
                                                                                                                   21-MAR-2000
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                                                                                                                                                                                                                                                                                                     GlyGlnArgIleAlaSerMetLysAsnGlnProSerGlyAlaAlaLeuPheGluPheArg 307
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                                                                                                                                                                                                                                             ATTCGTTATAAAGGTCAATCAGTAGATCCAATGAGATATTTA 1897
                                                                                                                                                                                                                                                                       IleSerArgAsnGlyValTyrValAspProLeuThrValLeu 321
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Mismatches:
Indels:
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02-SEP-1998;
09-OCT-1998;
09-OCT-1998;
09-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                         AAZ53015 to AAZ54536, AAZ54577 to AAZ54615, and AAY74253 to AAY75941 represent novel Neisseria meningitis and N. gonorrheae polynucleotides and polypeptides. AAZ54377 to AAZ54576 and AAZ54616 to AAZ54737 represent PCR primers used in the exemplification of the present invention. The polypeptides, the polynucleotides, antibodies and compositions of the invention can be used as vaccines, as diagnostic respents, and as immunogenic compositions. The polypeptides can be used in the manufacture of medicaments for treating or preventing infection due to Neisserial bacteria (e.g. meningitis and septicaemia), to detect the presence of Neisseria bacteria, or to raise antibodies. They may also be used to screen for agonists or antagonists, which may themselves have use as antibacterial agents. The polynucleotides of the invention may also be used in gene therapy protocols.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fraser C, G
Petersen J,
Tettelin H,
                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1248 BP; 277 A; 387 C;
                                                                                                                                                                                                                                                                                                                                                                      No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 7; Page 206-207; 1453pp; English.
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31-JUL-1998;
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                ThrAlaHisThrProSerProValAlaValGlnSerSerArgProProValGlnGlnHis
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                                                                                                                           GACGATTTCCGTGCGTGGAACGGCATGACCGACAAT---ACGTTGAGCATCGGTCAG---
                                                                                                                                                       ArgGluIleGlyHisIleAsnAsnLeuAsnSerSerTyrThrIleTyrThrGlyGlnTrp
                                                                                           LeuThrLeuTrpSerGlyAspLeuLysValArgGluArgSerIleSerSerGlyValAsn
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, Pizza M, Rappuoli
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98US-0094869.
98US-0098994.
98US-0099062.
98US-0103774.
98US-0103794.
98US-0103794.
98US-0121528.
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CCGAAAGCCGCAGCCGTAAAA---AGCAGGCCCGCCGTACCG--
                                                             ----ATTGTTAAAGTCAAACCGGCAGGATATGCCGCA---
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Scalato E, Scarselli M;
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02-SEP-1998;
02-SEP-1998;
  Praser C, (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Neisseria meningitidis; Neisseria gonorrheae; antigenic; diagnosis; immunogenic; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-NOV-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9957280-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Neisseria gonorrheae
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                                                                                      (GENO-)
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                                                                                                                   CHIRON CORP.
                                                                                      INST GENOMIC RES.
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Galeotti C, Grandi G,
Pizza M, Rappuoli R,
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98US-0094869

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  Hickey E,
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meningitis; septicaemia;
Masignani V, Mora M;
Scalato E, Scarselli
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AAZ53015 to AAZ54536, AAZ54577 to AAZ54615, and AAY74253 to AAY75941 represent novel Neisseria meningitis and N. gonorrheae polynucleotides and polypeptides. AAZ54537 to AAZ54576 and AAZ54616 to AAZ55473 represent PCR primers used in the exemplification of the present invention. The polypeptides, the polynucleotides, antibodies and compositions of the invention can be used as vaccines, as diagnostic reagents, and as immunogenic compositions. The polypeptides can be used in the manufacture of medicaments for treating or preventing infection due to Neisserial bacteria (e.g. meningitis and septicaemia), to detect the presence of Neisseria bacteria, or to raise antibodies. They may also be used to screen for agonists or antagonists, which may themselves have use as antibacterial agents. The polynucleotides of the invention may also be used in gene therapy protocols.
Sequence 1014
                                                                                                                                                                                                                                                                                                                          Claim 7; Page 205-206; 1453pp;
                                                                                                                                                                                                                                                                                                                                                                    Novel Neisserial polypeptides predicted to be useful antigens for vaccines and diagnostics
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DB; AAY74311.
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BP; 209 A; 318
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271 G;
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Query Match: DB: US-10-018-706-2 (1-322) x AAZ53073 3.63e-06 200.00 44.05% 26.19% 11.98% 21 (1-1014)

Percent Similarity: Best Local Similarity:

Alignment Scores:

Pred. No.:

Length: Matches: Conservative: Mismatches: Indels:

Q	73 TyrGlnValLysGlnGlyAspThrValSerLysIleAlaGlnArgTyrGlyLeuAsnTrp 92	
дb	313 CATACTATTGTGCGTGGACACGGTGTACAACATTTCCAAACGCTACCATATCTCTCAA 372	
Ą	93 ArgGluIleGlyHisIleAsnAsnLeuAsnSerSerTyrThrIleTyrThrGlyGlnTrp 112	
Db	373 GACGATTTCCGTGCGTGGAACGGCATGACCGACAATACGTTGAGCATCGGTCAG 426	
Ş	113 LeuThrLeuTrpSerGlyAspLeuLysValArgGluArgSerIleSerSerGlyValAsn 132	
Db	427ATTGTTAAAGTCAAACCGGCAGGATATGCCGCACCGAAAACC 468	
Ş	133 ThrAlaHisThrProSerProValAlaValGlnSerSerArgProProValGlnGlnHis 152	
Db	469 GCAGCCGTAGAAAGCAGGCCCGCCGTACCGGCTGCCGCGCAAACCCCCTGTGAAA 522	
S.	153 ProAlaValGlnLysProThrProProValValValLysLysProThrProThrPro 172	
DЬ	523 CCCGCCGCGCAACCGCCCGTTCAGTCCGCGCGCAACCTGCCGCG 567	
γ	173 ProValValGlnGlnProAlaProValAlaProProValThrGluAla 188	
Db	568 CCCGCTGCGGAAAATAAAGCGGTTCCCGCCCCCCCCCCC	
γŞ	189ProPheAlaThrGlySerSerGlyValMetGlnPheArgTyrProValGlyAlaThr 207	
дb	628 TCGCCTTCCGGCACGCGTTCGGTCGGCGGCATTGTTTGGCAGCGTCCGACCCCAA 681	
Qγ	208 AsnProValValArgArgPheGlyThrAlaThrValAlaGlySerThrValThrSerAsn 227	
В	682 GGTAAAGTGGTTGCCGATTTCGGCCGGCGCAACAAG 717	
Qy .	228 GlyMetTrpPheSerGlyArgAspGlyAspLeuILeAsnAlaSerAsnAlaGlyThrVal 247	
Db	718 GGTGTCGATATTGCCGGCAATGCCGGGACAACCCGTTTTGGCGGCGGCGGCTGACGGCAAAGTG 777	
Ą	248 IleGlnAlaAspHisAsnMetAspGlyAlaSerIleValIleGlnHisThrAsn 265	

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  AAZ53015 to AAZ54536, AAZ54577 to AAZ54615, and AAY74253 to AAY75941 represent novel Neisseria meningitis and N. gonorrheae polymucleotides and polypeptides. AAZ54577 to AAZ54576 and AAZ54616 to AAZ5473 represent PCR primers used in the exemplification of the present invention. The polymeptides, the polymucleotides, antibodies and compositions of the invention can be used as vaccines, as diagnostic reagents, and as immunogenic compositions. The polypeptides can be used in the manufacture of medicaments for treating or preventing infection due to Neisserial bacteria (e.g. meningitis and septicaemia), to detect the presence of Neisseria bacteria, or to raise antibodies. They may also be used to screen for agonists or antagonists, which may themselves have use as antibacterial agents. The polymucleotides of the invention
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09-OCT-1998;
09-OCT-1998;
09-OCT-1998;
25-FEB-1999;
                                                                                                                                                                                                                                                                                              Claim 7; Page 206- ; 1453pp; English.
                                                                                                                                                                                                                                                                                                                                           Novel Neisserial polypeptides predicted vaccines and diagnostics -
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P-PSDB; AAY74312.
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31-JUL-1998;
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INST GENOMIC RES.
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, Pizza M, Rappuoli R,
, Venter JC;
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Scalato E, Scarselli
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                                                        SerMetLysAsnGlnProSerGlyAlaAlaLeuPheGluPheArgIleSerArgAsnGly 312
                                                                                                                        HisIleLysAspAlaGlnValLysThrGlyAspThrValArgThrGlyGlnArgIleAla
ValTyrValAspPro
                              TTGATGGGCAATACCGATGCTTCCAGAACGCAGCTTCATTTCGAGGTGCGTCAAAACGGC
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                                                                                          CACAACCAAAAATTGCTGGTCGGCGAGGGGGCAGCAGGTCAAACGCGGTCAGCAGGTTGCT
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AAA81766;

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Query Match:
DB:
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Best Local Similarity:
                                                                                                         Alignment Scores:
                                                                                                                                                                         AAAB1452 represent Neisseria meningitidis Menis polymorlocation of the present sequences, which are all used in the exemplification of the present invention. The nucleic acid sequences, protein sequences, and antibodies against them, can be used in the manufacture of a composition. The medicament for treating, preventing or diagnosing infection due to medicament) for treating, preventing or diagnosing infection due to Meisserial bacteria. For example, some of the identified proteins could be components of vaccines against Meningococcus B; against all serotypes, and/or against all pathogenic Neissariae. Identification of sequences from the bacterium will also facilitate production of biological probes, particularly organism-specific probes. Attempts to make efficacious Meningococcus B vaccines have failed mainly due to antigen tolerance. Multivalent vaccines have failed mainly due to antigen tolerance. Multivalent vaccines have also been tried but none have successfully overcome antigenic variability. The provision of further, complete exposed proteins that may be presumed targets for the immune system and which are not antigenically variable or at least more conserved than other more variable regions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes methods of obtaining immunogenic proteins from Neisseria genomic sequences. AAA81453 to AAA82414 represent specifically claimed Neisseria meningitidis genomic DNA sequences, AAA81260 to AAA81303 and AAB25620 to AAB25663 represent Neisseria DNA sequences and their corresponding proteins, AAA81254 to AAA81259 and AAA81304 to AAA81321 represent PCR primers used in the isolation of Neisseria meningitidis DNA sequences; and AAA81322 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isolated nucleotide sequences of Neisseria meningitidis which can be used in the diagnosis and treatment of N. meningitidis infection and other Neisserial infections, for example, N.gonorrhoea -
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Masignani V, Galeott
Rappuoli R, Pizza M;
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30-APR-1999;
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                                                                                                                                            Sequence 6100 BP; 1552 A; 1757
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, Galeotti
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99US-0132068.
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C, Mora
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Ratti G, So
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Scarselli
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US-10-018-706-2 (1-322) x AAA81766 (1-6100)

ARESU ID ARF2: AC AC AC AC AC AC AC AC AC AC AC AC AC	8 8 8 8	. B & B & B	P & B &	음	B & B &	D
SSULT 10 RP21610/c AAP21610 standard; DNA; 349980 BP. AAP21610; AAP21610; Neisseria meningitidis B nucleotide sequence SEQ ID NO:111. Neisseria meningitidis; Neisseria gonorrheae; immunogenic; vaccine; diagnosis; antigen; detection; infection; gene therapy; antibacterial; ds. Neisseria meningitidis.	293 SerMetLysAsnGlnProSerGlyAlaAlaLeuPheGluPheArgIleSerArgAsnGly 312	255 ABDGIYALASerIleVallleGlnHiBThrABnGlyPheValSerSerTyrIle 272 259 AGGGATACGGAAACTTGGTCATCCATCCAGCATAATTCTTCCTTGCCTGACCGCATACGGG 520 259 AGGGGATACGGAAACTTGGTCATCCAGCATAATTCTTCCTTTCCTGACCGCATACGGG 520 273 HiBIleLyBABDAlaGlnValLyBThrGlyABpThrValArgThrGlyGlnArgIleAla 292 273 HiBIleLyBABDAlaGlnValLyBThrGlyABpThrValArgThrGlyGlnArgIleAla 292 274	215 GlyThrAlaThrValAlaGlySerThrValThrSerAsnGlyMetTrpPheSerGlyArg 234	168 ProThrProThrProProValValGlnGlnProAlaProValIAlaPro	ValAsnThrAlaHisThrProSerProValAlaValGlnSerSerArgPro 147	73 TyrGlnValLysGlnGlyAspThrValSerLysIleAlaGlnArgTyrGlyLeuAsnTrp 92 ::::::::

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                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes the full length genome of CC Neisseria meningitidis B (NMB). The sequences in AAF21644 and AAF21607 CC to AAF21613 represent fragments of the NMB genomic sequence, as the CC sequence was too long to go in a record on its own it was split into 8 CC sequence which overlap each other at the beginning and end of each CC sequence by 49980 bp (i.e. the last 49980 bp of AAF21647 are repeated at CC the beginning of AAF21607, the last 49980 bp of AAF21547 are repeated at CC the beginning of AAF21608, and so on). AAF21545 to AAF221589 to CC AAF21606 represent pCR primers which are used in the exemplification of CC AAF21606 represent invention. The NMB genome and fragments from it have cC Neisseria putcleic acids, proteins and/or antibodies which binds to the present invention. The NMB genome and tragments and gene therapy. CC Neisseria nucleic acids, proteins and/or antibodies which binds to the present invention are sead in vaccines and gene therapy. CC Neisserial bacteria or as a diagnostic reagent for detecting the CC pretains can be used in compositions for treating or preventing infection due to Neisserial bacteria or as a diagnostic reagent for detecting the CC pretain CC more seed in a search to identify open reading frames (ORF8) CC atabases can be used in a search to identify open reading frames (ORF8) CC more effective in vaccines than the outer membrane proteins which are CC more effective in vaccines than the outer membrane proteins which are CC used.
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Galeotti C, Mora M,
Frazer CM, Grandi G;
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28-FEB-2000; 2000GB-0004695.
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-----ValAsnThrAlaHisThrProSerPro---ValAlaValGlnSerSerArgPro 147
                                                        TTCCGTGCGTGGAACGGC-----ATGACCGACAATATGTTGAGCATCGGTCAGATT 330831
                                                                                                                                                                                                          CATACTATTGTGCGCGGCGACACGGTGTACAACATTTCCAAACGCTAC------
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                                                                                           LeuThrLeuTrpSerGlyAspLeuLysValArgGluArgSerIleSerSerGly-----
                                                                                                                                                                ArgGluIleGlyHisIleAsnAsnLeuAsnSerSerTyrThrIleTyrThrGlyGlnTrp 112
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, Scarselli M,
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Conservative:
Mismatches:
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   Pizza M, Hickey E,
Galeotti C, Mora M,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Y Match:
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The present invention describes methods of obtaining immunogenic proteins from Neisseria genomic sequences. AAA81453 to AAA82414 represent specifically claimed Neisseria meningitidis genomic DNA sequences; AAA81260 to AAA81303 and AAB256620 to AAB25663 represent Neisseria DNA sequences and their corresponding proteins; AAA81254 to AAA81259 and AAA81304 to AAA81321 represent PCR primers used in the isolation of Neisseria meningitidis DNA sequences; and AAA81322 to
                                                                                                                                                                                                                                                                              Isolated nucleotide sequences of Neisseria meningitidis which can used in the diagnosis and treatment of N. meningitidis infection other Neisserial infections, for example, N.gonorrhoea -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Frazer CM, H
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Best Local Similarity:
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Sequences, which are all used in the exemplification of the present
invention. The nucleic acid sequences, protein sequences, and antibodies
capainst them, can be used in the manufacture of a composition. The
composition can be used in the manufacture of a composition due to
medicament) for treating, preventing or diagnosing infection due to
Neisserial bacteria. For example, some of the identified proteins could
be components of vaccines against Meningococcus B; against all serotypes;
and/or against all pathogenic Neissariae. Identification of sequences
from the bacterium will also facilitate production of biological probes,
particularly organism-specific probes. Attempts to make efficacious
Meningococcus B vaccines have failed mainly due to antigen tolerance.
Multivalent vaccines have also been tried but none have successfully
overcome antigenic variability. The provision of further, complete
sequences may provide an opportunity to identify secreted or surface
caposed proteins that may be presumed targets for the immune system and
contained that may be presumed targets for the immune system and
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contained than the provision of further, complete
sequences may provide an opportunity to identify secreted or surface
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AspGlyAlaSer-----IleValIleGlnHisThrAsnGlyPheValSerSerTyrIle
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04-JUN-1992;
04-JUN-1992;
04-JUN-1993;
29-MAR-1993;
                                                                                         Sequence 1885
                                                                                                                                        The DNA sequence is that of the Haemophilus somnus lppB gene LppB can be used in vaccines for preventing or treating H. s infections, which cause thromboembolic meningo-encephalitis, septicaemia, arthritis and pneumonia in vertebrates. See also AAQ51080-6.
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                                                                                                                                                                                                                                                                                Claim 8; Fig 9; 119pp; English.
                                                                                                                                                                                                                                                                                                                                and corresp. DNA
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                      Antibacterial; Listeria; infection; ds.
 Listeria innocua
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TACAAAGTACGCAAAGGCGATACCATGTTTCTTATTGCTTATATTTCAGGCATGGATATA 1288
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                                                                                                                                                                                                                                                                                                                                                                                                       ATTATTCAAGGATTTTCCAGTGCTGATGGAGGC------AATAAAGGTATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 684707 BP; 213423 A; 126375 C; 133438 G; 211468 T; 3 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New genomic sequences from Listeria species, useful for detection treatment and prevention of infection, also related polypeptides, antibodies and modulators -
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                                                                                                                                                                                         11-APR-2000;
                                                                                                                                                                                                                                11-APR-2001;
                                                                                                                                                                                                                                                                                                                                                          Listeria monocytogenes
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The present sequence is the genome sequence of Listeria monocytogenes EGD-e. This sequence and fragments of this sequence are useful for selecting probes and primers for detecting genes in L. monocytogenes and related organisms, and to study genetic polymorphisms and other genomes. Proteins (ABB47297-ABB50149) expressed from the present sequence are useful for raising specific antibodies, identification of L. monocytogenes and related organisms, and for biosynthesis and biodegradation, especially biosynthesis of Vitamin B12. This sequence and proteins encoded by it are also useful for selecting compounds that regulate gene expression and cell replication and modulate L. monocytogenes-related diseases. In addition, this sequence and proteins encoded by it are useful in pharmaceutical and vaccines compositions for the treatment or prevention of infections by L. monocytogenes and related organisms.
                                                       Note: The sequence data for this patent did not form part of the specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genomic sequence for listeria monocytogenes, useful e.g. for and prevention of Listeria and related bacterial infections, related polypeptides
       Sequence 2944528 BP; 914202 A;
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                                                                                                                                      The present invention relates to nucleic acid sequences (ABQ67188-ABQ71212) from Listeria sp. The sequences are useful as probes and primers for identification and/or detection of Listeria (e.g. as contaminants in foods, or mutational analysis) and for analysis of gene expression. Proteins encoded by the nucleic acid sequences can be used to screen for compounds that modulate gene expression, replication and pathogenicity of Listeria (potential therapeutic agents), also for treating infections by Listeria, and are useful as immunogens in
                   anti-Listeria vaccines, Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New genomic sequences from Listeria species, useful for detection, treatment and prevention of infection, also related polypeptides,
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    LeuAlaIleGlySerGlnValIleThrAspSerGlnGlyValProAsnArgTyrGlnVa

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Note: The sequence data for this patent is based on equivalent patent w0200177334 (published 18-OCT-2001) which is available in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2365589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New nucleotide sequence useful in the identification or Lactococcus lactis and related species -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID 1; 2504pp; French.
                                                                                                                                                                                                                                                         Match:
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Coryneform bacterium; amino acid synthesis; vitamin; organic acid synthesis; ds.
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Corynebacterium glutamicum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       particularly L-lysine. The present sequence is a nucleic acid described in the exemplification of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel polymucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
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P-PSDB; AAG92487.
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                                                                                                                                                                                                                                                                                                     146
                                                                                                                                                                                                                                                                                                                                                                       107
                                                                                                                                                                                                 192 ThrGlySerSerGlyValMetGlnPheArgTyrProValGlyAlaThrAsnProValVal
                                                                                                                                                                                                                                     194
                                                                                                                                                                                                                                                                                                                                                                                              137 ProSerProValAlaValGlnSerSerArgProProValGlnGlnHisProAlaValGln 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8; SEQ ID NO:
HisAsnMetAsp---GlyAlaSerIleValIleGlnHisThrAsnGlyPheValSerSer
                                  GCAAACTCAATCGGCACCCCAATCTACGCCGTCATGGCCGGCACTGTCATCAGCTCTGGC
                                                                SerGlyArgAspGlyAspLeuIleAsnAlaSerAsnAlaGlyThrValIleGlnAlaAsp
                                                                                                   CCACGTTGGGGAACC-
                                                                                                                                ArgArgPheGlyThrAlaThrValAlaGlySerThrValThrSerAsnGlyMetTrpPhe 231
                                                                                                                                                                                                                                   AAGCTGCAGGAGTCGCAACCACCGCCGTC-GCACCAGCCGCCACCGTAGCGCGCCCAGCA
                                                                                                                                                                                                                                                                   ProValValGln---GlnProAlaProValAlaProProValThrGluAlaProPheAla
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                                                                                                                                                                                                                                                                                                                                                                    CCGCAACCGCTACCG-----CCACCATGCCATGCCATCCG-----CGC
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; 2000JP-0159162.
; 2000JP-0280988.
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Senoh A, Ikeda
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Ozaki A;
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Alignment Scores:

Sequence 349980 BP; 80900 A;

98397 C; 92139 G;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nakagawa S,
Tateishi N,
                                                                                           analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a nucleic acid described in the exemplification of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
                                                                                                                                                                                                                                                                                                                                                     The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-DEC-1999; 99JP-0377484.
07-APR-2000; 2000JP-0159162.
03-AUG-2000; 2000JP-0280988.
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da M, Ozaki A;
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                                                                                                                                                                                                                                                                             Actinobacillus actinomycetemcomicans; microbial; infection; vaccine; identification; localised juvenile periodontitis; antibacterial; antinflammatory; ds.
                                                                                                      04-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                               Actinobacillus actinomycetemcomitans clone nucleotide sequence #8.
                                                                                                                                                                                                                                                                                                                                                                                                              02-MAY-2001
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                      (IVIG-) IVIGENE CORP
                                                              06-AUG-1999;
                                                                                                                                                     15-FEB-2001.
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Best Local Similarity:
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                                                           GGCGTAGGTACTGCTGCACCGGCAACCAATCAGCCGATAACCCAAGCGGGCACCGCACCG
                                                                                         ArgPheGlyThrAla--
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                                                                                                                                                GGCACA-----CAATATGGTTCCGACGGCACGATTACCGGCCCGATTAAAGCC
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                                                                                                      ThrValAlaGlySerThr---
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Query Match:
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                      AAX20500-21243 represent polynucleotide sequences from the genome of Treponema pallidum. The sequences can be used for detection, diagnosis, characterisation, prevention and therapy for T. pallidum infections, particularly syphilis. They can also be used for detecting diseases related to Borrelia infections in animals, and for the production of biosynthetic products such as enzymes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated Treponema pallidum nucleic acids - used to develop products for the detection, diagnosis, characterisation, prevention and therapy of T. pallidum infections, particularly syphilis
                                                                                                                                                                                                                                                                                                       No . .
                                                                                                                                                                                                                                                                                                                                                         Sequence 14063
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to nucleic acid sequences (ABG67188-ABG71212) from Listeria sp. The sequences are useful as probes and primers for identification and/or detection of Listeria (e.g. as contaminants in foods, or mutational analysis) and for analysis of gene expression. Proteins encoded by the nucleic acid sequences can be used to screen for compounds that modulate gene expression, replication and pathogenicity of Listeria (potential therapeutic agents), also for treating infections by Listeria, and are useful as immunogens in anti-Listeria vaccines.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New genomic sequences from Listeria species, useful treatment and prevention of infection, also related antibodies and modulators -
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                                                                                                                                                                             Genome; bacterium; Haemophilus influenzae; computer readable medium; expression modulating fragment; regulation; gene expression; vector; organism; open reading frame; ORF; ds.
07-JUN-1995;
                                 22-APR-1996;
                                                                     24-OCT-1996
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                                                                                                                                             Haemophilus influenzae.
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Best Local Similarity:
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                                                          ---ATTTTGCATACTTTTGGT----TCTATCCAAGCAGGCGAAGTACGTTGGAAAGGT
                                                                                                                  ProvalValArgArgPheGlyThrAlaThrValAlaGlySerThrValThrSerAsnGly 228
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95US-0476102.
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children, pneumonia in elders, sinusitis, nosocomial infections, invasive diseases, chronic otitis media with hearing loss, fluid accumulation in the middle ear, auditive nerve damage, delayed splearning, infections of the upper respiratory tract and inflammat the middle ear. The present sequence is a version of the uncertainty.

spiratory tract and inflammation of is a version of the BASB201 coding

speech ç,

The present invention provides the protein and coding sequences of several versions of the BASB201 protein from non-typeable Haemophilus influenzae. These can be used in the production of vaccines against H. influenzae infection, which can cause otitis media in infants and

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RESULT 24
                                                                               New isolated non-typeable Haemophilus influenzae BASB201 polypeptides, useful as components of vaccines for treating bacterial infection such as otitis media, delayed speech learning and inflammation of middle ea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     H influenzae
  Claim 13; Page 88;
                                                                                                                                                                                                                                                                                        Thonnard
                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-OCT-2001; 2001WO-EP11561.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200230967-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BASB201; otitis media; pneumonia; sinusitis; nosocomial infection; auditive nerve damage; delayed speech learning; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-AUG-2002
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DB; AAO17658.
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90pp; English.
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US-10-018-706-2 (1-322) x AAL46626
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Pred. No.:
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Best Local Similari
H influenzae BASB201 coding sequence
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                                                                                                       AAL46624 standard;
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                                                                                                                                                                                              PheArgIleSerArgAsnGlyValTyrValAspPro 317
                                                                                                                                                                                                                                           GGCAGGTTATTGCTCAAGTAGGAAATACAGGGGAAATATCACGTTCTGCGCTTTAT---
                                                                                                                                                                                                                                                                                GlyGlnArgIleAlaSerMetLy8Asn-----GlnProSerGlyAlaAlaLeuPheGlu 305
                                                                                                                                                                                                                                                                                                                TTAAGTTTATATGGCTTCAATCAAGCGGTATCAGTGAAAGTTGGTCAGCTTGTTTCAGCA
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Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated non-typeable Haemophilus influenzae BASB201 polypeptides, useful as components of vaccines for treating bacterial inflection such as otitis media, delayed speech learning and inflammation of middle ear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1233 BP; 466 A; 224 C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BASB201; otitis media; pneumonia; sinusitis; nosocomial infection; auditive nerve damage; delayed speech learning; vaccine; antibacterial; auditory; antiinflammatory; gene; ds.
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                                                134
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DB; AAO17656.
                                                                                                                                                                                        94 GluIleGlyHisIleAsnAsnLeuAsnSerSerTyrThrIleTyrThrGlyGlnTrpLeu 113
                                                                                                                                                                                                                                                             74 GlnValLysGlnGlyAspThrValSerLysIleAlaGlnArgTyrGlyLeuAsnTrpArg
                                                                                                           ThrLeuTrpSerGlyAspLeuLysValArgGluArgSerIleSerSerGlyValAsnThr 133
                  AlaHisThrProSerProValAlaValGlnSerSerArgProProVal----GlnGlnHis 152
                                                                                                                                                                                                                             CAAAAAAAACAACAACAAGCATTGCAAAAAGCACAGCAAGAGCATCAA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of the invention.
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/product= "BASB201"
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                                                                                     - TTGAATGCACTAAAAGCAAACGAACAAGCACTTCGTCAAGAAATTCAACGA
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Matches:
Conservative:
Mismatches:
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RESULT 26
AAQ51086
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See also AAO51080-
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                                                               GATATTAGCGGTTCTCGTGGACAAGCTGTTAATGCAGCAGCTGCATGGACGCAGTTGTAT 3537
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                                                                                                                                                                                                                                                                    In situ production of a homologous autolysin or a heterologous autolysin from a food grade Gram positive bacteria, can be used in a process for the lysis of a culture of lactic acid bacteria. The process can be used in the manufacture of products containing cultures of lactic acid bacteria e.g. cheese, where the culture is lysed following the completion of fermentation. The enhanced induction of the autolysin is performed some hours after the fermentation is finished. No extra lysin needs to be added and the lysin does not need to be isolated or encapsulated. The time of lysis can be precisely controlled.
                                                                                                                                                                                                                                  Sequence 1929 BP; 619 A; 378 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 14; Page 51-54; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lysis of a culture of lactic acid bacteria in, e.g. cheese production - by in situ prodn. of an auto:lysin, regulated by inducible promoter.
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26 ThrThrCysIleLeuAlaGlyCysAlaSerLysProThrTyrAsnSerThr----
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                                                                                                                                                                                                         GlnProSerGlyAlaAlaLeuPheGluPheArgIleSerArgAsnGlyValTyrVal
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inhibition activity. The proteins may be administered to patients as vaccines, and the nucleotides may be used as part of a gene therapy regime. Diseases or conditions that may be treated using the proteins or nucleotides of the invention include autoimmune diseases; genetic disorders; haemophilia; cardiovascular diseases; cancer; bacterial, fungal and viral infections, especially HIV; multiple sclerosis; rheumatoid arthritis; pulmonary inflammation; Guillain-Barre syndrome; insulin dependent diabetes mellitus; and allergic reactions such as asthma and anaemia. They may also be used for treating wounds, burns, ulcers, osteoporosis, osteoarthritis, periodontal diseases, Alzheimer's
                                                                                                                                                                                                                                                                                                           cytokine activity; cell proliferation; differentiation; immune modulation; haematopoiesis regulation; tissue growth activity; activin/inhibin activity; chemotactic/chemokinetic activity; h
                                                                                                                                                                                                                                                                                                                                                           The invention relates to 40 human secreted proteins (AAY9498i-Y95020), and cDNA sequences encoding them (AAA23423-A3462). The secreted proteins of the invention include those that are thought to be only partially secreted, i.e., transmembrane proteins. The proteins of the invention may exhibit one or more activities selected from the following:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New secreted or transmembrane proteins and polynucleotides encoding them, useful for treating neurodegenerative disorders, autoimmune diseases and cancer -
                             additionally be useful as contraceptives. Nucleic acid sequences invention may be used in chromosome mapping, and as a source of diagnostic primers and probes. The present sequence represents concoding one of the 40 proteins of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; secreted protein; cancer; tumour; cardiovascular disorder; blood disorder; haemophilia; autoimmune disease; diabetes; inflam infection; fungal; bacterial; viral; HIV, allergy; arthritis; neurodegenerative disease; asthma; contraceptive; ss.
Sequence 4093
                                                                                            disease, Parkinson's disease, Huntington's disease and amyotrophic lateral sclerosis (ALS). Proteins with activin/inhibin activity may
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 72; Page
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 11115 BP; 1521 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel isolated gene cluster encoding polypeptides involved in everninomicin biosynthesis useful for construction of everninomicin overproducing strains, and to allow chemical modifications of everninomicin to enhance certain properties -
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DB; ABB06922, AF
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TCGGTGACCTCGCCGACCCCGGACCCACCACCCCCCCC
                      HisThrProSerProValAlaValGlnSerSerArgProProValGlnGlnHisProAla
                                                     TGGAGCGGCAGCAACCCCGTGCCGAAGTCGTTCGCGCTCAACGGCACGACCTGCACCGGC
                                                                             TrpSerGlyAspLeuLysValArgGluArgSerIleSerSerGlyValAsn---ThrAla 134
                                                                                                              ĠĠĀTCGCTGGGCACGGGCGGAŤĊĠACCACGATCGGCTTCAACĠĠĊTCG---
                                                                                                                                        GlyHisIleAsnAsnLeuAsnSerSerTyrThrIleTyrThrGlyGlnTrpLeuThrLeu
                                                                                                                                                                           CAGTCCGGCACGAGCGTCTCGGCCGCCAGC----
                                                                                                                                                                                                     LysGlnGlyAspThrValSerLysIleAlaGlnArgTyrGlyLeuAsnTrpArgGluIle
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Streptomyces venezuelae vep ORF1 (AAT68715) comprises the polyketide synthase (PKS) gene cluster encoding a polyene of 12 carbons (see also AAM16829-30 and AAW00918). It contains 5 PKS modules, with a 5' loading module and a 3' end domain. Each of the sequenced modules includes a keto-ACP, an acyltransferase, a dehydratase, a keto-reductase and an acyl carrier protein domain. He gene cluster was cloned using a heterologous hybridisation strategy from a genomic DNA library. A novel expression cassette encoding the first module
                                                                                                                                         Claim 54; Fig
                                                                                                                                                                                       Expression cassettes for production provide wide range of biodegradable
                                                                                                                                                                                                                                      P-PSDB;
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DB; AAW19629-30 AND AAW00918.
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14148..15827
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                                                                                                                                                                                       of polyhydroxyalkanoate(s) polymers for medical or
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gene cluster has polyhydroxyalkanoate (PHA) monomer synthase
activity and can be used for PHA prodn. in host (esp. insect) cell
for use as a biodegradable polymer.
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GCGGAGACCGCCGTGGCGGCCTCCTGGTCGCGTACGGAGTCCGCCGCCATCGCGGAGCAG
                            AlaGlyThrValIleGlnAlaAsp---HisAsnMetAspGlyAlaSerIleValIleGln
                                                                                           Ser----AsnGlyMetTrpPheSerGlyArgAspGlyAspLeuIleAsnAlaSerAsn
                                                                                                                                                         ArgArgPheGlyThrAlaThrValAlaGlySer-----ThrValThr
                                                                                                                                                                                           CCGTCGAACCAGTGGCGTTCGCGCTGGAAGGCGTAGGTCGGCAGGGGCACCCTGACCGTG
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The invention relates to an isolated and purified nucleic acid segment CC comprising a desosamine biosynthetic gene cluster, a fragment or its biologically active variant, where the nucleic acid sequence is not CC biologically active variant, where the nucleic acid sequence is not CC derived from the eryC gene cluster of Saccharopolyspora erythraea or CC Streptomyces antibioticus. The invention also relates to a macrolide CC biosynthetic gene cluster encodes proteins which synthesise methymycin, pikromycin, neomethymycin, narbomycin or a combination of these CC compounds. Recombinant or augmented cells comprising the desosamine CC compounds. Recombinant or augmented cells comprising the desosamine CC and/or macrolide biosynthetic gene clusters are useful for the CC production of biologically active macrolides. The macrolide biosynthetic proteins are useful for synthesis of methymycin, pikromycin, compounds are useful for synthesis of methymycin, pikromycin, pikromycin, pikromycin, pikromycin, pikromycin, pikromycin, pikromycin, pikromycin, pikromycin, pikromycin, pikromycin, pikromycin, pikromycin, pikromycin, pikromycin, pikromycin, pikromycin, pikromycin, pikromycin, pikromycin, pikromycin, pikromycin, pikromycin, pikromycin, pikromycin, pikromycin, pikromycin, pikromycin, pikromycin, pikromycin, pikromycin, pikromycin, pikromycin, pikromycin, pikromycin, pikromycin, pikromycin, pikromycin, pikromycin, pikromycin, pikromycin, pikromycin, pikromycin, pikromycin, pikromycin, pikromycin, pikromycin, pikromycin, pikromycin, pikromycin, pikromycin, pikromycin, pikromycin, pikromycin, pikromycin, pikromycin, pikromycin, pikromycin, pikromycin, pikromycin, pikromycin, pikromycin, pikromycin, pikromycin, pikromycin, pikromycin, pikromycin, pikromycin, pikromycin, pikromycin, pikromycin, pikromycin, pikromycin, pikromycin, pikromycin, pikromycin, pikromycin, pikromycin, pikromycin, pikromycin, pikromycin, pikromycin, pikromycin, pikromycin, pikromycin, pikromycin, pikromycin, pikromycin, pikromycin, pikromycin, pikrom
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neomethymycin; narbomycin; polyhydroxyalkanoate monomer synthase
biopolymer; antibiotic; chemotherapeutic; immunosuppressant; ast
chronic obstructive pulmonary disease; respiratory inflammation;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            biomedical applications, to engineer PHA monomer synthases or to prepare biologically active agents, such as chemotherapeutics, immunosuppressants, agents to treat asthma, chronic obstructive pulmonary disease as well as other diseases involving respiratory inflammation, cholesterol-lowering agents or macrolide-based antibiotics which are active against a variety of organisms, e.g., bacteria, including multi-drug resistant pneumococci and other respiratory pathogens, as well as viral parasitic pathogens, or as crop protection agents (e.g., fungicides or insecticides) via expression of polyketides in plants. The present sequence represents a Streptomyces venezuelae ATCC 15439 DNA sequence, designated vep ORF 1 in the specification, which actually contains 3 open reading frames, which encode proteins AAY77177-Y77178 and AAY77199. The vep ORF 1 protein is defined in the specification as a PHA monomer armthese.
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                                                 CCGTCGAACCAGTGGCGTTCGCGCTGGAAGGCGTAGGTCGGCAGGGGCACCCTGACCGTG
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                                                                                 ---SerGlyValMetGlnPheArgTyrPro-----ValGlyAlaThrAsnProValVal
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                                                                                                                                                                                                                                                                                                                                                                          The present invention is related to a Lactococcus lactis nucleotide sequence (ABA90521) and related proteins (ABB33300-ABB55621). The nucleic acid sequence is useful in the detection and/or amplification nucleic acid sequence, particularly to identify Lactococcus lactis or related species. The proteins of the invention are useful for the blosynthesis or biodegradation of a composition of interest. The invention helps research in lactic bacteria, particularly useful in the production of yogurt and cheese.

Note: The sequence data for this patent is based on equivalent patent W0200177334 (published 18-OCT-2001) which is available in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID 1; 2504pp; French.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to evaluating strain variation within and between different populations of the tuberculosis bacterial pathogen, Mycobacterium tuberculosis or related Mycobacterium by determining the nucleotide sequence of the first strain at positions in the complete sequence of the genome that correspond to positions that differ in the nucleotide sequences of M. tuberculosis strains CDC 1551 (AAI99683) and H37RV (AAI99682). The method is useful for evaluating strain variation of M. tuberculosis and has valuable application in the fields of tuberculosis genetics, epidemiology, patient treatment and epidemic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Note: The sequence data for this patent did not form specification, but was obtained in electronic format at seqdata.uspto.gov/sequence.html?DocID=6294328B1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Evaluating strain variation of Mycobacterium tuberculosis, comprise determining the nucleotide sequence of the strain at positions in the genome corresponding to positions where M. tuberculosis strains CDC 1551 and H37Rv differ -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to evaluating strain variation within and between different populations of the tuberculosis bacterial pathogen, Mycobacterium by determining the mucleotide sequence of the first strain at positions in the complete sequence of the genome that correspond to positions that differ in the nucleotide sequences of M. tuberculosis strains CDC 1551 (AA199683) and 137Rv (AA199682). The method is useful for evaluating strain variation M. tuberculosis and has valuable application in the fields of tuberculosis genetics, epidemiology, patient treatment and epidemic monitoring.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               monitoring.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at sequence.html?DocID=6294328B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Evaluating strain variation of Mycobacterium tuberculosis, computetermining the nucleotide sequence of the strain at positions igenome corresponding to positions where M. tuberculosis strains 1551 and H37Rv differ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4411529 BP; 758565 A; 1449983 C; 1444602 G;
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ValGln-SerSerArgProProValGlnGlnHisProAlaValGlnLysProThrProPr 161
                                                                                                                                           GGCGACATGGGCAACGGCGCCTTCTGGCGCGGCGAC------CAGCAGGGCCTATTC 430898
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                                                                                                                                                                                                                                                                                                          GGCGACACCAACACCGGCATCGCCAACCTGGGCGACTTCAACACGGGCTTCTACAACACC 431009
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                                                             AGCGCGGGCTATCGGGTCCATGTTCCCGAAATACCCGCACACGTCACCGTGGAAGTTCCC 430838
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  H influenzae
                              (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS
                                                                          13-OCT-2000; 2000GB-0025169
                                                                                                                              05-OCT-2001;
                                                                                                                                                                               18-APR-2002
                                                                                                                                                                                                                             WO200230967-A2
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                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention provides the protein and coding sequences of several versions of the BASB201 protein from non-typeable Haemophilus influenzae. These can be used in the production of vaccines against H. influenzae infection, which can cause otitis media in infants and children, pneumonia in elders, sinusitis, nosocomial infections, or invasive diseases, chronic otitis media with hearing loss, fluid accumulation in the middle ear, auditive nerve damage, delayed speech
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated non-typeable Haemophilus influenzae BASB201 polypeptides, useful as components of vaccines for treating bacterial infection such as otitis media, delayed speech learning and inflammation of middle ea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   learning, infections of the upper respiratory tract and inflammation the middle ear. The present sequence is a version of the BASB201 codi
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DB; AAO17657.
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ValileGlnAlaAspHis---AsnMetAspGlyAlaSerIleValileGlnHisThrAsn 265
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                                                                          AAAGGTATGGTAATTGGCGCATCAGCAGGCACGCCTGTTAAAGCAATTGCTGCTGGACGC 996
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                                                                                                                      AsnGlyMetTrpPheSerGlyArgAspGlyAspLeuIleAsnAlaSerAsnAlaGlyThr
                                                                                                                                                                                                                                                                         CTTAATAGTACAÁGCGGTTTAGGGGGCGCAAAAAAAACÁÁTATTCCTTACCÁGTTTCTGGT
                                                                                                                                                                                                                                                                                                                       AlaThrGlySerSerGlyVal------MetGlnPheArgTyrProValGlyAla 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ThrLeuTrpSerGlyAspLeuLysValArgGluArgSerIleSerSerGlyValAsnThr 133
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                                                                                                                                                                         TCA----ATTITGCATACTTTTGGT-----TCTATCCAAGCAGGCGAAGTACGTTGG
                                                                                                                                                                                                                                                                                                                                                                           -----TCAAAACCTTATCAACCAACTGTGCAAGAACGCAATTA
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                                                                                                                                                                                                                        ThrAsnProValValArgArgPheGlyThrAlaThrValAlaGlySerThrValThrSer
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Alignment Scores 
Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Achromobacter lyticus beta-lytic protease gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAZ49721;
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                                                                                                                                                                                                                                                                                                                                                                      22-JUN-1998;
21-JUN-1999;
                                                                            The present sequence is a Achromobacter lyticus DNA encoding the present sequence is used in the production of altered genes which The present sequence is used in the production of altered genes which allow expression and preferably secretion of active protein in mammalian allow expression and preferably secretion of active protein in mammalian allow expression and preferably secretion of active protein in mammalian betea-lytic protease coding sequence with mammalian promoter, signal betea-lytic protease coding sequence with mammalian promoter, signal betea-lytic protease rowing sequences. The modified sequence paptide and translation initiation sequences. The modified sequence ruminants, e.g. goats, sheep, and cows. It is also used to produce transgenic animals which are resistant to staphylococcal infections.
                                                                                                                                                                                                                                                                                                                                                                                                              22-JUN-1999;
                                                                                                                                                                                                                                                                                                                        Bramley JA,
                                                                                                                                                                                                                                                                                 WPI; 2000-147208/13.
P-PSDB; AAY44646.
                                                                                                                                                                                                                                                                                                                                              (UYVE-) UNIV VERMONT & STATE AGRIC
                                                                                                                                                                                                                   Disclosure; Fig 14A; 61pp; English
                                                                                                                                                                                                                                              Treatment of Staphylococcal infections, animals, especially cows
                                                         Sequence 1520
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                                                                                                                                                                                                                                                                   AAX20248 to AAX20402 represent polynucleotide sequences isolated from Borrelia burgdorferi (Bb). Products derived from Bb can be used for the detection, diagnosis, characterisation, prevention and therapy of Bb infections, e.g. Lyme disease. They can also be used for the production of biosynthetic products, e.g. enzymes. Borrelia belongs to a family of motile, spiral-shaped bacteria called Spirochetes are pathogenic in humans and Borrelia causes epidemic and endemic relagsing fever, and Lyme borreliosis, more commonly known as
                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated Borrelia burgdorferi nucleic acids - used to develop products for the detection, diagnosis, characterisation, prevention and therapy of infections, particularly Lyme disease
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20-JUN-1997;
22-JUL-1997;
22-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAX20248 to AAX20402 represent polynucleotide sequences isolated from Borrelia burgdorferi (Bb). Products derived from Bb can be used for the detection, diagnosis, characterisation, prevention and therapy of Bb infections, e.g. Lyme disease. They can also be used for the production of biosynthetic products, e.g. enzymes. Borrelia belongs to a family of motile, spiral-shaped bacteria called Spirochetes. Spirochetes are pathogenic in humans and Borrelia causes epidemic and sendemic relapsing fever, and Lyme borreliosis, more commonly known as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated Borrelia burgdorferi nucleic acids - used to develop products for the detection, diagnosis, characterisation, prevention and therapy of infections, particularly Lyme disease
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                                                                                    GTATTAGGGGAGACTTTTATTTATCCTGTGCAGGGTGTTATTACTTCGGGGTATGGCTAT
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TyrProValGlyAlaThrAsnProValValArgArgPheGlyThrAlaThrValAlaGly
                                                                                                                                                                                                                              ArgSerIleSerSerGlyValAsnThrAlaHisThrProSerProValAlaValGlnSer 144
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                        Peptidase was purified from Achromobacter lyticus by a Sepharose CL-4B column, a Sephadex G-75 column, and by reverse phase HPLC. The first 25 N-terminal amino acids were found to be identical to those of the beta-lytic protease from Lysobacter enzymogenes. The beta-lytic protease from Lysobacter enzymogenes. The beta-lytic protease for he L. enzymogenes beta-protease. The full length sequence of the L. enzymogenes beta-protease. The full length sequence of the gene encoding the A. lyticus enzyme was determined by dideoxy sequencing. The beta-lytic protease is expected to be an enzyme which can decompose not only Gram-positive See also AAQ25084-6.
                                                                                                                                                                                            Claim 1; Fig 1; 13pp; Japanese.
                                                                                                                                                                                                                        Beta-lytic protease gene and DNA encoding it Gram-positive and some Gram-negative bacteria
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AsnAlaGlyThrValIleGlnAlaAspHisAsnMetAspGlyAlaSerIleVallleGln
                                                                                                         AAGCACTCGGAAGATCTCGCAC-----
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                             GACATGTCGCGCGGGGGCTGGGGCAGCAACCAGAACGGCAACTGGGTGTCGGCCTCG
                                                                                                                          AlaThrGlySerSerGlyValMetGlnPheArgTyrProValGlyAlaThrAsnProVal
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                                                                                      ValArgArgPheGlyThrAlaThrValAlaGlySer------
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                                               ThrValThrSerAsnGlyMetTrpPheSerGlyArgAspGlyAspLeuIleAsnAlaSer
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                                                                   US-10-018-706-2 (1-322) x AAZ00266 (1-7277)
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                                                                                                                                                                                               Sequence
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GlySerGlySerHisArgThrSerGlySerGlyGlyLeuAlaIle-

ACGACGGTGGTTGATGGCCCATCTTGAAGCGAATGGCCCTGAGGAGTATGTTCTGTCA 1814

-AlaSerLysProThrTyrAsnSerThrSer 43

ThrCysIleLeuAlaGlyCys-----

Search completed: July 3, 2003, 22:55:31 Job time: 8697 secs

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Result
No.
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-Q=Cgm2 1/USPTO. Eppool/USL0018706/runat 30062003 091105 23816/app query.fasta_1.519
-DB=ISSUEd Patents NA -QPMT=fastap -SUFFTX=rri -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DCCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALICN=40
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10018706 @CGN 1 1 32 @TUNAT 30062003 091105 23816 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-PGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*
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Listing first 45 summaries
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US-09-405-728-4
US-08-619-812-3
US-08-619-812-7
US-08-737-716-1
US-08-737-716-11
US-09-103-840A-1
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ALIGNMENTS

RESULT

PCT-US96-05320A-707

APPLICANT:

720

Rutland Avenue

Johns Hopkins University

United States of America

APPLICANT:

9410 Key West Rockville, MD Sequence 707, Application PC/TUS9605320A GENERAL INFORMATION:

Human

Genome Sciences

Avenue

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APPLICANT:
APPLICANT:
TITLE OF II
NUMBER OF S
                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
               CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                          SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
                                                                                                                                             COUNTRY: USA
ZIP: 20003-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT
                                                                                                          MEDIUM TYPE: Diskette, 3.50 inch, 1
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
APPLICATION NUMBER:
                                                FILING DATE:
                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                               ADDRESSEE:
                                                                                                                                                                                                                                                                                                 ANT: J. Craig Venter
OF INVENTION: Nucleotide Sequence of the
OF SEQUENCES: 48
                                                                                                                                                                                                                              Washington
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1100 New York Avenue,
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Owen White
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                                                                                                                                                                                                                                                                                                                                                                                                  United States of America
                                               April22,
                                                              PCT/US96/05320A
08/476,102
                                                                                                                                                                                                                                                  Goldstein & Fox
e, Suite 600
                                                                                                                                             inch, 1.4Mb storage
                                                                                                                                                                                                                                                                                                                  Haemophilus Influenzae
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FILING DATE:

June

7, 1995 08/487,429 , 1995

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TELEFAX: (202) 371-2600

TELEFAX: (202) 371-2600

INFORMATION FOR SEQ ID NO: 707:
SEQUENCE CHARACTERISTICS:
LENGTH: 1215 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
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Best Local Similarity:
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APPLICATION NUMBER: 08/487,42

FILING DATE: JUNE 7, 1995

ATTORNEY/AGENT INFORMATION:

NAMB: Eric K. Steffe

REGISTRATION NUMBER: 36,688

REFERENCE/DOCKET NUMBER: 1488
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GGCAATGCTTTACGTGGTTACGGTAATTTAATTATCATCAAACATAATGATGATTTTTTTA 1047
                           AspHisAsnMetAspGlyAlaSer-----IleValIleGlnHisThrAsnGlyPheVal 268
                                                                                       PheSerGlyArgAspGlyAspLeuIleAsnAlaSerAsnAlaGlyThrVallleGlnAla 250
                                                                                                                         ACTTCAGGTAATATCATCCAAGGTTTCTCAAGCACAGATGGCGGTAACAAAGGAATTGAT 927
                                                                                                                                                                                        AATGTCGTTGCG-----CCAATC---GCTCAAAT---GTTGTGTGGCAATGGCCG
                                                                                                                                                                                                                                                                                     GlnGlnProAlaProValAlaProProValThrGluAlaProPheAlaThrGlySerSer 195
                                                                                                                                                                                                                                                                                                                   GGTACTATTATTGGCCCAATTAAATCAGAGGCTGGCACATCGCCTAGTGTACCTGTGGCA 762
                                                             ATTAGTGGTTCACGAGGACAAGCTGTAAAAGCGGCTGCAGCAGGGCGAATAGTGTATGCA
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Sequence 4, Apprised Sequence 4, Appricant No. 6391316 |
Patent No. 6391316 |
Patent No. 6391316 |
PAPPLICANT: NEOTHER, Andrew A.
APPLICANT: Schryvers, Anthony B.
APPLICANT: Schryvers, Anthony B.
ITILE OF INVENTION: CLONING AND EXPRESSION OF HARMOPHILUS SOMNUS FITLE OF INVENTION: TRANSFERRIN-BINDING PROTEINS FITLE OF INVENTION: TRANSFERRIN-BINDING PROTEINS FILLE REPERENCE: 9000-00492-00
CURRENT APPLICATION NUMBER: US/09/405,728 |
CURRENT FILING DATE: 1999-09-24 |
EARLIER APPLICATION NUMBER: US 09/267,749 |
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; Sequence 4, Septiment No. 6391316
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US-08-619-812-3
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                                                                                                                                TELEFAX: (415) 327-323
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICANT: POTTER
APPLICANT: THEISE
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CORRESPONDENCE ADDRESS:
ADDRESSEE: REED & ROBINS
                                                                                                                                                                                          REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 90
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
                                     MOLECULE TYPE:
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     NAME/KEY:
                                                           STRANDEDNESS: si
TOPOLOGY: linear
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STATE: CALIFORNIA
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THEISEN, MICHAEL
HARLAND, RICHARD J.
RIOUX, CLEMENT R.
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                                                     Sequence 7, Application US/08619812
Patent No. 6100066
GENERAL INFORMATION:
 APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                 heValSerSerTyrIleHisIleLysAspAlaGlnValLysThrGlyAspThrValArgT 287
                                                                                                                                                                                                                                                                                                                                                                                                                                lnAlaAspHisAsnMetAspGlyAlaSer-----IleValIleGlnHisThrAsnGlyP
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                                                                                                                                                                                                          rg 307
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POTTER, ANDREW A. THEISEN, MICHAEL HARLAND, RICHARD
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43.80%
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   RICHARD J
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Matches:
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Indels:
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APPLICANT: RIOUX, CLEMENT R.
TITLE OF INVENTION: VACCINES FOR HAEMOPHILUS SOMNUS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:

ADDRESSEE:

REED & ROBINS

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; FEATURE:
; NAME/KEY:
; LOCATION:
US-08-619-812-7
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      red. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/619,812
FILING DATE: 15-MAR-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/038,719
FILING DATE: 29-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: ROBINS, ROBERTA L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 9000-0019:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
TELEPAX: (415) 327-328
TELEFAX: (415) 327-328
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
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MEDIUM TYPE: Floppy COMPUTER: IBM PC com
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LOCATION:
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                                                            TCAGAGGTGACACAAAATACAGTCAATGAG---ACATGGAATGCTAATAAACCAACAAAT 332
                                                                                                                                                                                              AAAGAATTGGCCACACTAAATAATATGTCTGAGCCATATCATCTGAGTATTGGACAAGTA 3210
GlnGlnHisProAlaValGlnLysProThrProProValValValValLysLysProThr 169
                                                                                             GlyValAsnThrAlaHisThrProSerProValAlaValGlnSerSerArgProProVal 149
                                                                                                                                                                                                                                                                                             ŢŢŗĠlnValLysGlnGlYAspThrValSerLysIleAlaGlnArgTyrGlYLeuAsnTrp
                                                                                                                              TTGAAAATTGCAAATAATATTCCCGATAGCAATATGATACCAACACAGACAATAAATGAA 3270
                                                                                                                                                                 LeuThrLeuTrpSerGly------AspLeuLysValArgGluArgSerIleSerSer 129
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7.84%
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Matches:
Conservative:
Mismatches:
Indels:
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US-08-737-716-1
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                                 MOLECULE TYPE: DN
ORIGINAL SOURCE:
ORGANISM: Lacto
STRAIN: MG1363
IMMEDIATE SOURCE:
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APPLICANT: Jan KOK
APPLICANT: Jan KOK
APPLICANT: Adrianus Marinus LEDEBOER
APPLICANT: Adrianus Marinus LEDEBOER
TITLE OF INVENTION: Process for the lysis of a culture of lactic
TITLE OF INVENTION: acid bacteria by means of a lysin, and uses of the lysin of the lysin of the lysin of the lysin of the lysin of the lysin of the lysin of the lysin of the lysin of the lysin of the lysin of the lysin of the lysin of the lysin of the lysin of the lysin of the lysin of the lysin of the lysin of the lysin of the lysin of the lysin of the lysin of the lysin of the lysin of the lysin of the lysin of the lysin of the lysin of the lysin of the lysin of the lysin of the lysin of the lysin of the lysin of the lysin of the lysin of the lysin of the lysin of the lysin of the lysin of the lysin of the lysin of the lysin of the lysin of the lysin of the lysin of the lysin of the lysin of the lysin of the lysin of the lysin of the lysin of the lysin of the lysin of the lysin of the lysin of the lysin of the lysin of the lysin of the lysin of the lysin of the lysin of the lysin of the lysin of the lysin of the lysin of the lysin of the lysin of the lysin of the lysin of the lysin of the lysin of the lysin of the lysin of the lysin of the lysin of the lysin of the lysin of the lysin of the lysin of the lysin of the lysin of the lysin of the lysin of the lysin of the lysin of the lysin of the lysin of the lysin of the lysin of the lysin of the lysin of the lysin of the lysin of the lysin of the lysin of the lysin of the lysin of the lysin of the lysin of the lysin of the lysin of the lysin of the lysin of the lysin of the lysin of the lysin of the lysin of the lysin of the lysin of the lysin of the lysin of the lysin of the lysin of the lysin of the lysin of the lysin of the lysin of the lysin of the lysin of the lysin of the lysin of the lysin of the lysin of the lysin of the lysin of the lysin of the lysin of the lysin of the lysin of the lysin of the lysin of the lysin of the lysin of the lysin of the lysin
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EDNESS: double
Fig.4 (publ.1) -acmA and ORFA
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                                                                                                     Lactococcus lactis
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US-10-018-706-2 (1-322) x US-08-737-716-1 (1-1930)
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US-08-737-716-1
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                                                                                                                                     AlaGlyThrValIleGlnAlaAspHisAsnMetAspGlyAlaSerIleValIleGlnHis 263
                                                                                                                                                                                                                                                                                                                          ValGlyAlaThrAsnProValValArgArgPheGlyThrAlaThrValAlaGlySerThr 223
                                                                                                                                                                                                                                                                                                                                                                        TGGAATCATTTAAGTTCAGATACCATTTATATTGGTCAAAATCTTATTGTTTCACAATCT 127
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  ACTTCTTCTAACTCAAATGCCTCAATTCAT---
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                                           ThrAsnGlyPheValSerSerTyrIleHisIleLysAspAlaGlnValLysThrGlyAsp 283
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 94
FILING DATE: 12-MAY-1994
INFORMATION FOR SEQ ID NO: 11
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                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
ORIGINAL SOURCE:
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APPLICATION NUMBER: PCT/NL95/00170
FILING DATE: 12-MAY-1995
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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TITLE OF INVENTION:
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CLONE: Fig.4
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                                                                                                                                                                                                                                                                                   NAME/KEY:
LOCATION:
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DEDNESS: double
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                                                        ThrVal------ArgThrGlyGlnArgIleAlaSerMetLys 295
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VENTION: Process for the lysis of a culture of lactic
VENTION: acid bacteria by means of a lysin, and uses of
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Indels:
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Matches:
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Sequence 1, Application US/09105537A
; Patent No. 6265202
; GENERAL INFORMATION:
APPLICANT: Sherman, D.H.
APPLICANT: Sherman, D.H.
APPLICANT: Xue, Y.
APPLICANT: Zhao, L.
TITLE OF INVENTION: DNA encoding methymycin and FILE REFERENCE: 600.438US1
; CURRENT APPLICATION NUMBER: US/09/105,537A
; CURRENT APPLICATION NUMBER: US/09/105,537A
; CURRENT APPLICATION NUMBER: 05.26
NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
; SEQ ID NO 1
; SEQ ID NO 1
; LENGTH: 15872
TYPE: DNA | CURRENT Streptomyces venezuelae
US-09-105-537-1
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3195 GCGTCGCGCCCC------TCGGCGAGCGAGCCGCACAGGTCCTCGGGGGAG 311
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    282 GlyAspThrValArgThrGlyGlnArgIleAlaSerMetLysAsnGlnProSerGlyAla 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT PFLICATION UMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
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APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: FLEISCHMAN, Robert APPLICANT: WHITE, Owen R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
FEATURE:
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                                                                          US-10-018-706-2 (1-322) x US-09-103-840A-1 (1-4411529)
                                                                                                                                    Query Match:
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Best Local Similarity:
                                                                                                                                                                                                              Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                      ; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1
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SOFTWARE: PatentIn Ver.
SEQ ID NO 1
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APPLICANT: VENTER, John C.
TITLE OF INVENTION: DIA SEQUENCES FOR STRAITILE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT PEPLICATION UNDERS: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
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APPLICANT: WHITE, Owen R.
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431224 AACTCGGGCAACTGGGGTATCGGCAACTCCGGCAGCGGCAACACCGGCATCGGC 431165
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Matches:
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Mismatches:
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RESULT 10
US-09-103-840A-1
; Sequence 1, Application US/09103840A
; Patent No. 6294328
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                                                                                                             GATGTCGATGTTCAACCTCGGCCTGGGAAACATCGGCCAATTC
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APPLICANT: WHITE, Owen R.
APPLICANT: FRASER CLAire M.
APPLICANT: VENTER, JOHN C.
ITITLE OF INVENTION: TUBERCULOSIS .
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PATENTIN VET: 2.1
SEQ ID NO 1
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US-08-276-213-6
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Best Local Similarity:
Query Match:
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; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1
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Sequence 6, Application US/08276213 Patent No. 5536655
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                                                                                                                                                                                                                               HisIleLysAspAlaGlnValLysThrG|yAspThrValArgThrG|yGlnArgIleAla
                                                                                                                                                                                                                                                                                                                       AlaSerIleValIleGlnHisThrAsnGlyPheValSerSer-----
                                                                                                                                                                                           CAGGTTGTGCCATGGCGAGGTGCTCTCGGGAGCGTTATATCCGTCGGC----
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                                                                                                                                                SerMetLysAsnGlnProSerGlyAlaAla 302
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                                                                                                                                                                                                                                                                                 ------CAATGCCTCGGTGGGTTCGTTGATGAAACTGAGAATGTCCTGCTG
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Query Match:
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US-08-276-213-6
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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HYPOTHETICAL: NO
ANTI-SENSE: NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Laymon, Robert APPLICANT: Himmel, Michael
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: O'Connor, Edna
REGISTRATION NUMBER: 29,252
REFERENCE/DOCKET NUMBER: NR
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CLASSIFICATION:
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CITY: Golden
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TOPOLOGY: linear
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--GlnTrpLeuThrLeuTrpSer----
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                                                                                                                                                                                                                  GlnGlyValProAsnArgTyrGlnValLysGlnGlyAspThrValSer---LysIleAla 85
                                                    CGTGGCTGAAGACGCTCGTCCAGTACCTACGGCCGACCGCCAATACGGTGCGGACAGCT 1886
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(307) TD NO: 6:
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                                                                                   -AsnLeuAsnSerSerTyr---
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                                                                                                                  ---TGGGCGAATTCGGTACGAĆÁĆTGCÁÁTCCACGACCGACCAGA 1826
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Matches:
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US-09-136-574A-1
                                                                                                                                                                                                                                                                                                  Sequence 1, Application Patent No. 6294366 GENERAL INFORMATION:
                                                                                                                                                                                                                                                APPLICANT: Farrington, Grah
Anderson, Paige
Gibbs, Moreland
                                                                                NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
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                                                                                                                                                                     TITLE
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STATE: PA
COUNTRY: USA
ZIP: 19477
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                                                CITY: Spring
                                                                     STREET:
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                                                                                                                      Daniels, Roy
Daniels, Roy
Morgan, Hugh W.
Williams, Diane P.
Williams, Compositions and Methods for
INVENTION: Compositions Cellulose Containing
                                                                                                                                                                                                                                Bergquist, Peter
                                                                  Spring
                                                    House
                                                                  House
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                                                                                                                                                                                                                                                                                      Graham
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                                                                  Corporate Center, P.O. Box
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PRIOR APPLICATION NUMBER: US 08/932,571
FILING DATE: September 19, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Bak, MATY E.
REGISTRATION NUMBER: 1997US001/CIP
REFERENCE/DOCKET NUMBER: 1997US001/CIP
TELEPONMUNICATION: INFORMATION:
TELEPONE: 215-540-5200
TELEPONE: 215-540-5818
TRELEX: <UNKnown>
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 11707 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
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Best Local Similarity:
Query Match:
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Pred. No.:
9258 ACACCCACTCCGACTCCTTCTGTCACAGATGATACAAATGATGATTGGTTATTTTGCGCAG 9317
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                                                                        9198 ACACCAACAGCAACGCCAACACCTACACCTTCTATCACGATAACACCAGCGCCAACTGCA 9257
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/136,574A
FILING DATE: 19-Aug-1998
CLASSIFICATION: <Unknown>
                                                                                                                                                                                             159
                                                                                                                                                                                                                                                         140 ValAlaValGlnSerSerArgPro---ProValGlnGlnHisProAlaValGlnLysPro 158
                                                                                                              179 AlaProValAlaProPro----- 189
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119.50
32.62%
25.32%
7.16%
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US-09-462-606-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: DNA
; ORGANISM: Hepatitis
US-09-462-606-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 1
LENGTH: 5127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/09462606 Patent No. 6432408
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APPLICANT: Purcell, Robert H.
TITLE OF INVENTION: A SWINE HEPATITIS E VIRUS
FILE REFERENCE: 20264267US1
CURRENT APPLICATION NUMBER: US/09/462,606
CURRENT FILING DATE: 2000-66-12
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PRIOR FILING DATE: 1997-07-18
PRIOR PPLICATION NUMBER: PCT/US98/14665
PRIOR FILING DATE: 1998-07-17
NUMBER OF SEQ ID NOS: 65
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        TTTTGCAGTGCCCTTTATAGATATAATAGGTTCACCCAGCGGCATTCGCTGACCGGTGGG 200:
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Sequence 3, Application US/09462606
Patent No. 6432408
GENERAL INFORMATION:
APPLICANT: MENG, XIANG-JIN
APPLICANT: Emerson, Suzanne U.
APPLICANT: Emerson, Suzanne U.
APPLICANT: PURCELL, Robert H.
TITLE OF INVENTION: A SWINE HEPATITIS E VIRUS ANI
FILE REFERENCE: 20264267US1
CURRENT APPLICATION NUMBER: US/09/462,606
CURRENT ELLING DATE: 1997-07-18
PRIOR APPLICATION NUMBER: US 60/053069
PRIOR APPLICATION NUMBER: PCT/US98/14665
PRIOR FILING DATE: 1998-07-17
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Pred. No.:
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; ORGANISM: Hepatitis E virus
US-09-462-606-3
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SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 3
LENGTH: 7207
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                                                                                                      ValValValLysLysProThrProThrProProValValGlnGlnProAlaProValAla 182
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Indels:
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-TCCCGCACTCGTCGTCTCCTACACCTAT
                                                                                                                                                                                                                                                                                                                                                               -----TCTGGCTTTTCTAGCGAT 2148
2406
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PATEBLE NO. 5994099

APPLICANT: Lewis, Randolph V

APPLICANT: Hayashi, Cheryl Y

ITILE OF INVENTION: CENTREWELY ELASTIC SPIDER SILK PROTEIN AND DNA

TITLE OF INVENTION: CENTREWELY ELASTIC SPIDER SILK PROTEIN AND DNA

NUMBER OF SEQUENCES: 29

CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
STREET: 8110 GATEHOUSE RD. SUITE 500E

ITY: FALLS CHURCH
STATE: VURGINIA
COUNTRY: UNITED STATES OF AMERICA
                                                                                                                                                                                                                              COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: PC-DOS/MS-DOS
SOFTWARE: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.
CURRENT APPLICATION NUMBER: US/09/010,928B
FILING DATE: 22-JAN-1998
FILING DATE: 22-JAN-1998
CLASSIFICATION: 435
AFTORNEY/AGENT INFORMATION:
MAME: MUTPHY JT., Gerald M
REGISTRATION NUMBER: 28977
REFERENCE/DOCKET NUMBER: 1447-109P
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2830 base pairs
TYPE: nucleic acid
CTPANNERDNESS: not relevant
US-09-010-928B-1
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US-09-010-928B-1/c
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                                                                PRATURE:

NAME/KEY:

LOCATION:

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OTHER INFORMATION:

OTHER INFORMATION:

OTHER INFORMATION:
                 FEATURE:
NAME/KEY:
LOCATION:
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o. 5994099
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TIGITIGAATCAGACTGTAACIGG------CTGGTTAATGCCTCA 2475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AlaLeuPheGluPheArgIleSerArgAsn 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HisThrAsnGlyPheValSerSerTyrIleHisIleLysAspAlaGlnValLysThrGly 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AACCCCGGGC-----CTCTGC 2508
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCCGACGGGGA------AAGGTGTATGCGGGGTCA 2436
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ĊĂŤ-----GCTTTTŤĂĊCAACGTTTCCCAGAGĠĊĠTTTTACCCGĂĊŤGAG 2553
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            CDS
219..2830
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                                                                                                                                                                                                CDNA
                                                                  /note= "Flagelliform DNA sequence
taken from the 5' region. The putative start codon is
position 219"
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Percent Similarity:
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                                                                                                             SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/09125287B Patent No. 6114602
                                                                                                                                                                                                FILE REFERENCE: INTRO GENETIC PARTHENOCAPRI IN PLANTS CURRENT APPLICATION NUMBER: US/09/125,287B CURRENT HILING DATE: 1998-11-09.
EARLIER APPLICATION NUMBER: PCT/IL97/00051
                                                                                                                                                                                                                                                                TITLE OF INVENTION: METHOD FOR THE INTRODUCTION OF GENETIC PARTHENOCARPY IN TITLE OF INVENTION: PLANTS
FILE REFERENCE: INTRO GENETIC PARTHENOCAPRI IN PLANTS
                                                                                                                                                                                                                                                                                                                                                                           BENERAL INFORMATION:
                                                                                                                                                                           EARLIER FILING DATE: 1997-02-13
                                                                                                                                                                                                                                                                                                                                APPLICANT: BARG, Rivka
APPLICANT: SALTS, Tehiam
                                                                                                                                                      NUMBER OF SEQ ID NOS:
                                    TYPE: DNA
ORGANISM: TPRP-F1 PROMOTOR
                           FEATURE:
    NAME/KEY: unsure
                                                                                         ENGTH: 4518
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -GATCCTCCTGCTCCACCAGCACCTCCTGCTCCACCAGCACCTCTAGCT 1658
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Indels:
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US-10-018-706-2 (1-322) x US-09-125-287-1 (1-12839)
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; OTHER INFORMATION: "n"'s are any nucleic residue US-09-125-287-2
                                                                Query Match:
                                                                                      Best Local Similarity:
                                                                                                           Percent Similarity:
                                                                                                                                                      Pred. No.:
                                                                                                                                                                           Alignment Scores:
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US-09-125-287-1
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                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE:
SEQ ID NO 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: METHOD FOR THE INTRODUCTION OF GENETIC TITLE OF INVENTION: PLANTS FILE REFERENCE: INTRO GENETIC PARTHEMOCAPRI IN PLANTS CURRENT APPLICATION NUMBER: US/09/125,287B CURRENT FILING DATE: 1998-11-09 EARLIER APPLICATION NUMBER: PCT/IL97/00051 EARLIER FILING DATE: 1997-02-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: BARG, Rivka
APPLICANT: SALTS, Tehi
                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                      NAME/KEY: unsure LOCATION: (5)..(113 OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: TPRP-F1 GENOMIC CLONE
                                                                                                                                                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 12839
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       136 ThrProSerProValAlaValGlnSerSerArgProProValGlnGlnHisProAlaVal 155
                                                                                                                                                                                                                                                                                                                                                                                                                    PatentIn Ver.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACCATCACCACCAGC 3611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCCAATCCTCCCGTGGTAATACCACCACCCTACGTGCCAAGTCCTCCGGTTGTTACTCCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACTCCAACACCACCTATTGTC-----CATCCACCAGTCACTCCAAAACCA----- 3357
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116.00
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                                                                Conservative: Mismatches: Indels:
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Matches:
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/194,290
FILING DATE: 09-FEB-1994
CLASSIFICATION: 435
APPLICATION NUMBER: US 07/895,367
FILING DATE: 09-JUNE-1992
CLASSIFICATION: 435
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TELEPAX: 617-542-8906
INFORMATION FOR SEQ ID NO: (
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NAME: TSAO, Y. ROCKY
REGISTRATION NUMBER: 34053
REFERENCE/DOCKET NUMBER: 08
TELECOMMUNICATION INFORMATION:
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APPLICANT: Bingle, Wade H.
APPLICANT: NO. 5976844ellini,
                                                                                                                                                                                                                                                                                                                                      No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE:
ORIGINAL SOURCE:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ADDRESSEE: Fish & Richardson
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                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Can
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TYPE: nucleic acid
STRANDEDNESS: double
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                                  63 IleThrAspSerGlnGly--
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                                                                                                                                         GGCGCCCTGTCGACCGACAACGCGGCTGGCGTGAACCTGTTCACCGCCTATCCGTCGTCG
CTGACGGGCACCGCCAACAACGACACGTTCGTTGCGGGTGAAGTCGCCGGCGCTGCGACC 940
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POLYPEPTIDES FROM CAULOBACTER
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EXPRESSION AND SECRETION OF
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                               ValProAsnArgTyrGln 74
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APPLICANT: Smit, Jonn
APPLICANT: Bingle, Wade H.
APPLICANT: Bingle, Wade H.
APPLICANT: No. 6210946ellini, John F.
APPLICANT: No. 6210946ellini, John F.
TITLE OF INVENTION: EXPRESSION AND SECRETION
FILE REFERENCE: 08106/002002
CURRENT APPLICATION NUMBER: US/09/142,648B
CURRENT FILING DATE: 1999-03-30
PRIOR APPLICATION NUMBER: PCT/CA97/00167
PRIOR APPLICATION NUMBER: US 07/614,377
PRIOR APPLICATION NUMBER: US 07/614,377
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; PRIOR FILING DATE: 19; NUMBER OF SEQ ID NOS: SOFTWARE: FASTSEQ for SEQ ID NO 6; SEQ ID NO 6; LENGTH: 3300; TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 21
US-09-142-648B-6
                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 6, Application US/09142648B Patent No. 6210948
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SECRETION OF
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Pred. No.:
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lSerSerTyrIleHisIleLysAspAlaGlnValLysThrGlyAspThrValArgThrGl
                           GGCCGTGACGGTCACCCAAACCGCCGCCGCCGCCGCCGCGCGCTACGGTCGCCGT
                                                     ----IleValIleGlnHisThr-----
                                                                              CGTGAACACC---ACGTTGACGCAAGCCGAGCGTGACCGGTAACTCCAGCACCAC 146
                                                                                                         aSerAsnAlaGlyThrValIleGlnAlaAspHisAsnMetAspGlyAlaSer-----
                                                                                                                                      rAsnGlyMetTrpPheSerGlyArgAspGlyAspLeuIle-------AsnAl 241
                                                                                                                                                                                            CAACTCGGCCGCTTCGGGCACCGTGTCGGTGAGCGTCGCGAACTCGAGCACGACCACCAC 1347
                                                                                                                                                                                                                      aThrAsnProValValArgArgPheGlyThrAlaThrValAlaGlySerThrValThrSe 226
                                                                                                                                                                                                                                                                          rGluAlaProPheAlaThrGlySerSerGlyValMetGlnPheArgTyrProValGlyAl 206
                                                                                                                                                                                                                                                                                                       CTGACCG---CCACGACCGCCCCCTC----AAGCCGCGAACAACGTCGCCGTCGACGGG 1228
                                                                                                                                                                                                                                                                                                                                                             GCCCTGAACACCAACACCAGCGGCGCGCGCCCAAACCCGTCACCGCCGGCGCTGGCCAGAAC 1177
                                                                                                                                                                                                                                                                                                                                                                                  oProValGlnGlnHisProAlaValGln---LysProThrProProValValValValLy 166
                                                                                                                                                                                                                                                                                                                                                                                                                   AACGTGACGTCGGGCGGCTGCGATCACCCTGAACACGTCTTCGGGCGTGACGGGTCTGACC 1117
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                                                     ----AsnGlyPheva 268
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Best Local Similarity:
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US-09-311-626B-15
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113.50
35.04%
26.77%
6.80%
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Sequence 15. Application US/09311626B

Sequence 15. Application US/09311626B

Patent No. 6399347

GENERAL INFORMATION:
APPLICANT: Orgensen, Per Lina
APPLICANT: Schnorr, Kirk
APPLICANT: Andersen, Leren No. 6399347boe
APPLICANT: Schulein, Martin
APPLICANT: Ochttrup, Helle
TITLE OF INVENTION: No. 6399347el Rhamnogalacturonan Hydrolases
FILE REFERENCE: 5572.204-US
CURRENT APPLICATION NUMBER: US/09/311,626B
CURRENT APPLICATION NUMBER: 0608/98
PRIOR APPLICATION NUMBER: 60/084,358
PRIOR APPLICATION NUMBER: 60/084,358
PRIOR APPLICATION NUMBER: 60/084,358
PRIOR APPLICATION NUMBER: 50/084,358
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TYPE: DNA
ORGANISM: Streptomyces coelicolor
                                                                                                                                                        1420 GCGGGCGCCGAGTCCTGGTCGTCCGCGGAGAGCGGCATCCGCAACCCCCAAGGGCACCGTC 1479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1075 ACCAACTCCTCCACCAACAGGGCAAGGGCTACGACGGCCAGGGCAACCACCACCTCTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1240 GCCATGCACGTCGGCGACCTCGACCCGTCCCGGGCGGGCCTGGAGGAGTTCAAGGTCGAC 1299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1135 GTCGCGGACGTGGACGGTGACGGCCGGGACGAGATCGTCTACGGCGCGATGGCCGTCGAC 1194
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                                                    138 rProValAlaValGln-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                         113 LeuThr-----LeuTrpSerGlyAsp 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80 ThrVal-----SerLysIleAlaGlnArgTyrGlyLeuAsnTrpArgGluIleGly 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCCACCGGCGAGCGACCGACAACGGCCGCGGTGTCTCCGGGGACATCTGGTCGGGCAGC 1419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HisIleAsnAsnLeuAsnSerSerTyr-----ThrIleTyrThrGlyGln-----Trp 112
                                                                                                                                                                                                                                                       LeuLysValArgGlu---ArgSerIleSerSerGlyValAsn-ThrAlaHisThrProSe 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAC-----AACGGCTACGCCCTGTGGACCACCAGGAACGGCCACGGCGAC 1239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AspSerGlnGlyValProAspArgTyrGlnVal------LysGlnGlyAsp 79
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Matches:
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Indels:
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-SerSerArgProProValGlnGlnHisProAl 154
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Percent Similarity:
Best Local Similarity:
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US-09-308-375-1
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Patent No. 6300117
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/308,375
CURRENT FILING DATE: 1999-05-14
EARLIER APPLICATION NUMBER: EP9719636.4
EARLIER FILING DATE: 1997-09-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Genencor International, Inc.
TITLE OF INVENTION: Proteases From Gram-Positive Organisms
FILE REFERENCE: GC394-PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 3
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Bacillius subtilis
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                                                                                                                                                                                                                                            4423
                                                                                                                                                                                                                                                                                                                                                                                                                           4303 TACGGTATTGTAACCTCTACAACTTCTTCTGGTGGAACCCCCCTCCTCAACTGGTGGATCA 4362
                                                     4537 --- GTAAATAACGCTTACGATCCTTATCAAAATGTTATGGGTGGAACAAAGTACCTCGCC 4593
                                                                                                                                                                                                                                                                                                                                   4363 TATTCAGGCAAGTATTCAAGCTACATAAATTCAGCAGCTAGTAAATACAATGTTGACCCT 4422
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               221 ySerThrValThrSerAsnGlyMetTrpPheSerGlyArg
       111 GlnTrpLeuThrLeuTrpSerGlyAspLeuLysValArgGluArgSerIleSerSerGly 130
                                                                                                                                                                                                                                                                                     57 AlaIleGlySerGlnValIleThrAspSerGlnGlyValProAsnArgTyrGlnValLys 76
                                                                                                                                                                                                                                                                                                                                                                                 42
                                                                                                   97 HislleAsnAsnLeuAsnSerSerTyr---
                                                                                                                                                                                        GlnGlyAspThrValSerLysIleAlaGlnArgTyrGlyLeuAsnTrpArgGluIleGly 96
                                                                                                                                                                                                                                    GCCCTTATTGCAGCTGTAATTCAGCAAGAATCAGGGTTT-----AATGCTAAAGCACGA 4476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PheGlyValIleThrThrCysIleLeuAlaGlyCysAlaSerLysProThrTyrAsnSer 41
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                                                                                                                                             TCTGGTGTAGGTGCCATGGGATTAATGĆÁÁCTGATGCCAGCAACAGCAAAAAAGCTTAGGÁ 4536
                                                                                                                                                                                                                                                                                                                                                                            ThrserGlySerGlySerHisArgThrSerGlySerGlyGlyLeu-------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gTyrProValGlyAlaThrAsnProValValArgArgPheGlyThrAlaThrValAlaGl 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         aValGlnLysProThrProProValValValLysLysProThrProThrProProVa 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.36
113.50
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Matches:
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                                                                                                 -ThrileTyrThrGly 110
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ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATENETIR Release #1.0, Vers

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/878,546

FILING DATE: 19-JUN-1997

CLASSIFICATION DATA:

APPLICATION DATA:

APPLICATION UMBER: JP 158677/1996

FILING DATE: 19-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: KIKUCHI, NORIHISA
APPLICANT: ODA, KOHEI
TITLE OF INVENTION: NOVEL PROTEINASE INHIBITOR AND
TITLE OF INVENTION: GENE ENCODING THE INHIBITOR
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: STEINBERG, F
STREET: 1140 AVENUE OF
CITY: NEW YORK
                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5043
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gileSerArgAsnGlyValTyrValAspPro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGGCTACAGTAAAACTGCAGGTAACTGCGTTGTTATTAAACAGGATGATGGAACAGTTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTTTGCTGCAAAAGCAGGTACAGCAATTAAATCTCTTCAAAGTGGTAAAGTCCAAATTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ------CACAAAGGAACTGA 4863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      lValArgArgPheGlyThrAlaThrValAlaGlySerThrValThrSerAsnGlyMetTr 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCTTTTAGGGTAAGCTCCAAATATGGACAACAGGAATCTGGTCTCCGCTCC-TCCCCA-- 4848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----CCACTTCTTCAATCGCCAGCT-----
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                                                                                                                                                                     Version
                                                                                                                                                                     #1.30
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Best Local Similarity:
Query Match:
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REGISTRATION NUMBER: 32,728
REPERENCE/DOCKET NUMBER: 382.1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 768-3800
TELEPAX: (212) 382-2124
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 2186 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDNESS: A-...
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Pred. No.:
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MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGINAL SOURCE:
ORGINAL STREPTOMYCES PLATENSIS
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NAME: DAVIDSON, CLIFFORD
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APPLICATION NUMBER:
FILING DATE: 26-AUG-
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                                                                                                                                                                                                               194 rSerGlyValMetGlnPheArgTyrProValGlyAlaThrAsnProValValArgArgPh 214
                                 CAGTGCTCGGCGGCCGGTCGTCGGCGGGGGTCAGCGACCGGCGGGCCGTCCCAGCA 483
                                                                                                                                                                                                                                                     TTCGCGGCGGCCGGCAGCCGCACCTCCAGCGGCGGT-GCGCCGGTCAGCCGTGCCAG
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1477..1911
-AspGlyAspLeuIleAsnAlaSer---AsnAlaGlyThrValIle------
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03-MAR-1997
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112.50
33.61%
23.77%
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                                                                   -ThrValThrSerAsnGlyMetTrpPheSerGlyArg-----
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Indels:
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RESULT 25
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                                                                                                                                                                                                                                                                                                                    TELEPHONE: 309-685-401
TELEPAX: 309-685-4128
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LENGTH: 8438 base pair:
                                                                                                                                                                                                STRANDEDNESS: dou
TOPOLOGY: linear
MOLECULE TYPE: DNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                               FEATURE:
NAME/KEY:
LOCATION:
FEATURE:
NAME/KEY:
LOCATION:
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MEDIIM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/945,283
FILING DATE: 1930911
CLASSIFICATION: 424
CCLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Ribando, Curtis P
REGISTRATION NUMBER: 27976
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADUAL STREET: 10.
STREET: 10.
CITY: Peoria
TATE: IL
USA
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HITLE OF INVENTION: Pseudorabies Virus Deletion Mutants
HITLE OF INVENTION: Involving The EPO and LLT Genes
HUMBER OF SEQUENCES: 7
NAME/KEY:
                                 LOCATION:
                                                   NAME/KEY:
                                                                                                                                                                                    ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESPONDENCE ADDRESS:
LDDRESSEE: Curtis P. Ribando
STREET: 1815 No. 5352596th University Street
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variation
                             variation replace(1267, "t")
                                                                               variation replace (1099,
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622..6495
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                                                                                                                                                                                      Pseudorabies virus
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application Patent No. 6083716
                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                              APPLICANT: Wilson, CAPPLICANT: Farina, SAPPLICANT: Fisher, FITTLE OF INVENTION:
APPLIANCE
PILING DATE:
PILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 60/024,700
APPLICATION NUMBER: US 60/024,700
APPLICATION NUMBER: OS-CREP-1996
APPLICATION NUMBER: OS-CREP-1996
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FEATURE:
NAME/KEY:
LOCATION:
                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 5
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                                                                                                                                                                                                                                                        ADDRESSEE: Howson and Howson
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                                                                                                                                                                                                           T: Spring House Corporate Cntr.,
Spring House
Pennsylvania
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33.90%
6.74%
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Krishna J
                                                                                                                                                                                                                                                                                                                                        James M.
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Sequence 221, Application US;
Patent No. 6448043;
GENERAL INFORMATION:
APPLICANT: Gil H. Choi
TITLE OF INVENTION: Ente
NUMBER OF SEQUENCES: 496
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Best Local Similarity:
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 36519 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: GN
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9200
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                                                                      Application US/09071035
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US-10-018-706-2 (1-322) x US-08-923-137-2 (1-36519)
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                                                                                                                                                                                                                                                                                   lThrGluAlapropheAlaThrGlySerSer 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTCTACATGCTAGGCTCTTACCGTGCAGATCAGGACGGGTTCCCCCCTCGAAGAGTACTGG 7025
                                                                                                                                                                                                                                   -ACTCGCATGCCATTTTCCGCCAGATCGTCT
                                                                                                                                                                                                                                                                                                                                                                                                    lLysLysProThrProThrProProValValGlnProAlaProValAlaProProVa 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAGGGACAGCTCAAGTATGACATCATCCAGGAGACCCTCGACTACTGCGCTCTGGACGTC
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US-10-018-706-2 (1-322) x US-09-071-035-221 (1-867)
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/09/
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
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REFERENCE/DOCKET NUMBER: PB369P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
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MEDIUM TYPE: Diskette, 3.50 inch, 1.
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
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ADDRESSE: Human Genome Sciences,
STREET: 9410 Key West Avenue
CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 867 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
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REGISTRATION NUMBER: 36
144 SerSerArgProProValGlnGlnHisProAla---ValGlnLysProThrProProVal 162
                                                                                                                                                                                                                                                                                                                                                   133 -----GTTTTACCAGATGAACCGAATGTACCAACTGACCCAATAACGCCAAGTGAGCCA
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                                             ACGCCAAGTAAGCCAGAGCAACCAACAGAGCCAACAACGCCAAGT---
                                                                      uArgSerIleSerSer-GlyValAsnThrAlaHis-ThrProSerProValAlaValGln
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                                                                                                                                                     rTyrThrIleTyrThrGlyGlnTrpLeuThrLeuTrpSerGlyAspLeuLysValArgGl 124
                                                                                                                                                                                                                                                                      GAGCAACCAACAGGGCCAAGTACACCAGAGC-----AACCATCGGAACCGTCAACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTATTATTGCCTTATTCAGTACAAGCCTTTTAGCAGGGGAAGCAGTGTTTCTGCTTAT
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DB:
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                 Alignment Scores:
Pred. No.:
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US-09-134-001C-1165
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Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
ITTLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EDIDERWIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE GENERAL INFORMATION: EDIDERWIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR PRICE 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
PRIOR FILING DATE: 1997-08-14
SEQ ID NO 1165
LENGTH: 993
TWOTH. TWO
                                                          220
                                                                                                                          160 ATTGCTAAATTAAAATCACTTAATGGATTGACTTCCAATTTAATATTTCCCTAATCAAGTA 219
                    55
                                                                                 35 SerLysProThrTyrAsnSerThrSerGlySerGlySerHisArgThrSerGlySerGly 54
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  GlyLeuAlaIleGlySerGlnValIleThrAspSerGlnGlyValProAsnArgTyrGln 74
                                                          TTGAAA-----
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                                                 ---GTATCAGGCTCATCTTCAAGAGCAACGTCAACAAATAGT 264
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Matches:
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Pred. No.: Alignment Scores: US-09-071-035-221

Alignment Scores: 0.394 Length: 2077 Pred. No.: 0.394 Matches: 74	NAME/KEY: misc feature; LOCATION: 299.7632 OTHER INFORMATION: /function= "cellulose binding; OTHER INFORMATION: domain" US-08-217-327-7	FEATURE: Ayranase year Ains FEATURE: NAME/KEY: CDS LOCATION: 2992077 FEATURE: FEATURE:	CE ON	; LENGTH: 2077 base pairs ; TYPE: nucleic acid ; STRANDEDNESS: double ; TOPOLOGY: linear ; MOLECULE TYPE: DNA (genomic)	; TELEPHONE: 608-251-5000 ; TELEPAX: 608-251-9166 ; INFORMATION FOR SEQ ID NO: 7: ; SEQUENCE CHARACTERISTICS:	; NAME: Seay, Nicholas J ; REGISTRATION NUMBER: 27,386 ; REFERENCE/DOCKET NUMBER: 1122990831 ; TELECOMMUNICATION INFORMATION:	PRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/812,233 FILING DATE: 19-DEC-1991 ATTORNEY/AGENT INFORMATION:	LICATION DATA: ON NUMBER: US/08/217,327 TE: ATION: 435	TYPE: F1 %R: IBM F NG SYSTEN %E: Pater	STATE: WI COUNTRY: USA ZIP: 53701-2113 COMPUTER READABLE FORM:	21 21		m 3 0 W	397 GTTTCTGGTAAAGCGACGAGTTCCAGTCGTGCAAAAGCTAGTGGG	340 ATCATGCAACTTAATGGGTTAAATAACTATCTTATTTTCCCTGGACAAAAGTTGAAA	CTTCTATTGCTGCAAAATACGGTACAACTTAT snSerSerTyrThrIleTyrThrGlvGlnTro	Db 265 GGCACAGTT
264 rAsnGlyPheValSerSerTyrIleHisIleLysAspAlaGlnValLysThrGlyAspTh 	1057 CTGGCAAACCGAACTATCGATGTGGATTTGGTACAGGGCAATAATATTGTGCAGTTGTC 244 aGlyThrVallleGlnAlaAspHisAsnMetAspGlyAlaSerIleVallleGlnHisTh	OV 232 rGlyArgAngglyAsniculleAsnalasserasn	946 TATCCGCTATGCCAATGGTGGAACCGCCAATCGCAATGGCTACTGGTGAT	Qy 183 oProValThrGluAlaProPheAlaThrGlySerSerGlyValMetGl 199	Qy 169ThrProThrProProValValGlnGlnProAlaProValAlaPr 183	Qy 166 168	Qy 147 oProValGlnGlnHisProAlaValGlnLysProThrProProValValValVal 165	Qy 129SerGlyValAsmThr-AlaHisThrProSerProValAlaValGlnSerSerArgPr 147	Qy 115 LeuTrpSerGlyAspLeuLysValArgGluArgSerIleSer 128	Qy . 95 IleGlyHisIleAsnAsnLeuAsnSerSerTyrThrIleTyrThrGlyGlnTrpLeuThr 114	Qy 75 VallysGlnGlyAspThrValSerLysIleAlaGlnArgTyrGlyLeuAsnTrpArgGlu 94 ::: ::::::::::::::::::::::::::::::	Qy 55 GlyLeuAlaIleGlySerGlnValIleThrAspSerGlnGlyValProAsnArgTyrGln 74	Qy 35 SerLysProThrTyrAsnSerThrSerGlySerGlySerHisArgThrSerGlySerGly 54	Qy 17 ArgLeuGlyLeuIlePheGlyVallleThrThrCysIleLeuAlaGlyCysAla 34	Qy 1 MetThrValThrIleAlaIleAsnSerĠlnAsnGlnLysProIleLys 16	10-018-706-2 (1-322) x US-08-217-327-7 (1-2077)	Percent Similarity: 34.49% Conservative: 45 Best Local Similarity: 21.45% Mismatches: 125 Query Match: 6.62% Indels: 102 DB: 1 Gaps: 16

•	US-10-018-706-2 (1-322) x US-09-136-574A-2 (1-6416) QY	()	SEQUENCE DESCRI 9-136-574A-2 nment Scores:	; LENGTH: 6416 base pairs ; TYPE: nucleic acid ; STRANDEDNESS: single ; TOPOLOGY: linear	TELEFAX: 215-540-5818 ; TELEX: <unknown> ; INFORMATION FOR SEQ ID NO: 2: ; SEQUENCE CHARACTERISTICS:</unknown>	TRATIC ENCE/D ICATIC HONE:		APPLICATION NUMBER: US/09/136,574A FILING DATE: 19-Aug-1998 CLASSIFICATION: «Unknown» PRIOR APPLICATION DATA:	MEDIUM TYPE: Diskette COMPUTER: IBM Compatible OPERATING SYSTEM: DOS CURRENT APPLICATION DATA:		CORRESPONDENCE ADDRESS: ADDRESSEE: Howson STREET: Spring House Corporate Center, P.O. Box 457 CITY: Spring House	NCES:	Bergquist Daniels, Morgan, I Williams,	ngton, son, F	RESULT 30 US-09-136-574A-2 ; Sequence 2, Application US/09136574A ; Patent No. 6294366	Db 1174 GGTCAGGGCGGT 1186	1166
	Anderson, Paige ; Gibbs, Moreland ; Gibbs, Moreland ; Bergquist, Peter paniels, Roye Morgan, Hugh W. ; Morgan, Diane P. Williams, Diane P. TITLE OF INVENTION: Compositions and Methods for Treating Cellulose Containing Fabrics Using Truncated Cellulase Enzyme Compositions	RESULT 31 US-09-136-574A-46 ; Sequence 46, Application US/09136574A ; Patent No. 6294366 ; GENERAL INFORMATION; APPLICANT: Farrington, Graham K.	Qy 299 SerGlyAlaAlaLeuPheGluPheArgIleSerArgAsnGlyValTyrValAsp 316 . :::	Qy 284 ThrValArgThrGlyGlnArgIleAlaSerMetLysAsnGlnPro 298	Qy 265 AsnGlyPheValSerSerTyrIleHisIleLysAspAlaGlnValLysThrGlyAsp 283	Qy 250 AlaAspHisAsnMetAspGlyAlaSerIleValIleGlnHisThr 264	Qy 245 GlyThr	Qy 225 ThrSerAsnGlyMetTrpPheSerGlyArgAspGlyAspLeuIleAsnAlaSerAsnAla 244	Qy 205 GlyAlaThrAsnProValValArgArgPheGlyThrAlaThrValAlaGlySerThrVal 224	Qy 188AlaProPheAlaThrGlySerSerGlyValMetGlnPheArgTyrProVal 204	Qy 180 ProValAlaProProValThrGlu	Qy 160 ProProValValValValLysLysDroThrProThrProProValValGlnGlnProAla 179	Qy 140 ValAlaValGlnSerSerArgProProValGlnGlnHisProAlaValGlnLysProThr 159	Qy 122 ValArgGluArgSerIleSerSerGlyValAsnThrAlaHisThrProSerPro 139	Qy 102 AsnSerSerTyrThrIleTyrThrGlyGlnTrpLeuThrLeuTrpSerGlyAspLeuLys 121 Db 4159 4173	Oy 82 SerLysIleAlaGlnArgTyrGlyLeuAsnTrpArgGluIleGlyHisileAsnAsnLeu 101	ω

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Best Local Similarity:
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SEQUENCE CHARACTERISTICS:
LENGTH: 2029 base pairs
TYPE: nucleic acid
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NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
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MEDIUM TYPE: Diskette
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                                                                                                                                                                                                          316
                                                                                                                                                                                                                                                                               286
472
                  132 AsnThrAlaHisThrProSerProValAlaValGlnSerSerArgProProValGlnGln 151
                                                                                                                                   433 GGTGTTCTGGTATGGGGG---
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                                                                                                                                                                                                                                       84 IleAlaGlnArgTyrGlyLeuAsn------
                                                                                                                                                                                                                                                                                                            64 ThrAspSerGlnGlyValProAsnArgTyrGlnValLysGlnGlyAspThrValSerLys 83
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ACCCCAACTTCTÁCÁCCCACACCGGTTTCATCATCCACT----
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                                                                                                  TrpLeuThrLeuTrpSerGlyAspLeuLysValArgGluArgSerIleSerSerGlyVal 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/09/136,574A FILING DATE: 19-Aug-1998 CLASSIFICATION: <Unknown>
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TELEFAX: 215-540-5818
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Patent No. 5824508
GENERAL INFORMATION:
APPLICANT: Spaete, Richard and Jackman, Winthrop,
                                                                                                                                             TELEX: 380816 CooleyPA INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
 FEATURE:
NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/229,
FILING DATE: April 18, 1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/
FILING DATE: 25-AUG-199
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: NO NUMBER OF SEQUENCES: 1 CORRESPONDENCE ADDRESS:
                                                       MOLECULE TYPE: CDNA
                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: 415-843-5163
                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patent In Release #1.0,
                                                                                                                                                                                                                                                          NAME: Luann Cserr
REGISTRATION NUMBER: 31,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Cooley Godward STREET: 5 Palo Alto Square CITY: Palo Alto
                                                                          TOPOLOGY:
                                                                                           STRANDEDNESS:
                                                                                                           TYPE: nucleic acid
                                                                                                                                                                                                    TELEFAX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GlySerThrValThrSerAsnGlyMetTrpPheSerGlyArgAspGlyAspLeuIleAsn 240
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                                                                                                                            3833 base pairs
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1014..3734
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                                                                                           double
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Alignment Scores:

Query Match: DB:

Percent Similarity: Best Local Similarity:

1.42 109.00 33.68% 23.16% 6.53%

Pred. No.:

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RESULT 33
PCT-US95-04611A-18
; Sequence 18, Application PC/TUS9504611A
; GENERAL INFORMATION:
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                                                                                                                                                                    ACAGGCCAACATAA-CATAACTTCAAGTTCAACCTCTTCCATGTCACTGAGACCCAGTTC 302
                                                                                                                                                                                                     VallleGlnHisThrAsnGlyPheValSerSerTyrIleHisIleLysAspAlaGlnVal 279
                                                                                                                                                                                                                                            GGAACAAGTCCCACCCCAGTAGTTACCAGCCAACCAAAAAATGCAACCAGTGCTGTTACC 2966
                                                                                                                                                                                                                                                                                                                                                        GlyMetTrpPheSerGlyArgAspGlyAspLeuIleAsnAlaSerAsn------Ala 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCCCAAATGCCACCAGCCCCACC--------TTGGGAAAAACA
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Matches:
Conservative:
Mismatches:
Indels:
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Best Local Similarity:
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Pred. No.:
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; LOCATION: 101
PCT-US95-04611A-18
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04611A
FILING DATE: PLATION DATA:
APPLICATION NUMBER: 08/229,291
FILING DATE: APPLICATION DATA:
APPLICATION NUMBER: 08/229,291
FILING DATE: APPLICATION:
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TELEFAX: 415-857-0663
TELEX: 380816 COOLEYPA
INFORMATION FOR SEQ ID NO.
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: LUANN CSETY
REGISTRATION UNMEER: 31,822
REFERENCE/DOCKET NUMBER: AVIR
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-843-5163
TELEFAX: 415-857-0663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
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ATTORNEY/AGENT IN
NAME: Luann Cs
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STREET: Falo Alto
CITY: Palo Alto
CTATE: California
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TITLE OF INVENTION: Non Splicing Variants of gp350/220
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
STREET: 5 Palo Alto Square
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
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TYPE: nucleic acid
STRANDEDNESS: double
                                                                                         2421
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                                     LeuThr-----LeuTrpSerGlyAspLeuLysValArgGluArgSerIleSer 128
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GTGACACCAAGTCCATCTCCATGGGACAACGGCACAGAAAGTAAGGCCCCCGACATGACC
                                                                                                             ArgGluIleGlyHisIleAsnAsnLeuAsnSerSerTyrThrIleTyrThrGlyGlnTrp
                                                                                                                                                         GCACCTGCAAGCACAGGCCCCACTGTATCC------
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                                                                          ----ACCGCGGATGTCACCAGCCCAACACCAGCCGGCACAACGTCAGGCGCATCACCG 2474
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E: cDNA
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109.00
33.68%
23.16%
6.53%
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Matches:
Conservative:
Mismatches:
Indels:
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RESULT 34
US-08-783-774-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent No. 6054130 GENERAL INFORMATION:
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                   APPLICATION NUMBER: US/08/783,774
PILING DATE: 15-JAN-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, LAUTA A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7682-037
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
                                                                                                                                                                                  OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Spaete, Richard APPLICANT: Jackman, Winthro
                                                                                                                                                                                                                                                                                                                                    STREET: 1155 AV
CITY: New York
STATE: NY
                                                                                                                                                                                                                       COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 10036/2711
                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
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     212-869-8864
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                                                                                                                                                                                                                                                               Diskette
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NON-SPLICING VARIANTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
Best Local Similarity:
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STRANDEDNESS: single
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                                                                       GlyMetTrpPheSerGlyArgAspGlyAspLeuIleAspAlaSerAsp-----Ala
                                                                                                                                            AsnProValValArgArgPheGlyThrAlaThrValAlaGlySerThrValThrSerAsn
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                                    GGCCCTACTGTG----GGAGAAACAAGTCCACAGGCAAATGCCACCAACCACCTTAGGA
                                                                                                             AGCCCC--
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--ValileGlnAlaAspHisAsnMetAspGlyAlaSerile 259
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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patent No. 6458364

GENERAL INFORMATION:
APPLICANT: Speete, Richard

APPLICANT: Jackman, Winthrop

ITILE OF INVENTION: NON SPLICING VARIANTS OF GP350/220

FILE REFERENCE: 7682-050-99

CURRENT APPLICATION NUMBER: US/09/556,706B

CURRENT APPLICATION NUMBER: 08/83,774

PRIOR APPLICATION NUMBER: 08/83,774

PRIOR APPLICATION NUMBER: 08/29,291

PRIOR APPLICATION NUMBER: 08/29,291

PRIOR APPLICATION NUMBER: 08/29,291

PRIOR FILING DATE: 1994-04-18

NUMBER OF SEQ ID NOS: 19

SOFTWARE: Patentin version 3.0

LENGTH: 5931

TYPE: NNA
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Score:
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ORGANISM: Virus
FEATURE:
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         GTGACTACCCCAACCCCAAATGCCACCAGCCCCCACCCCAGCAGTGACTACCCCAACCCCA
                                                                                                                             SerGlyValAsnThrAlaHisThrProSerProValAlaValGlnSerSerArgProPro 148
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                                                                                    ACAGGCCAACATAA-CATAACTTCAAGTTCAACCTCTTCCATGTCACTGAGACCCAGTTC 3025
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Matches:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Vers
OPERATING SYSTEM: US/08/314,309A
FILING DATE: 30-SEP-1994
CLASSIFICATION UMMBER: US/08/314,309A
FILING DATE: 30-SEP-1994
CLASSIFICATION UMBER: US 07/631,906
FILING DATE: 21-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5677141man F.
REGISTRATION UMMBER: 24,618
REGISTRATION UMMBER: 24,618
REGISTRATION UMBER: 18-863-0 CON
TELEPOMOUNICATION INFORMATION:
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APPLICANT: FUKAGAWA, MASAO
APPLICANT: IWANI, MORITA
APPLICANT: IWANI, MORITA
APPLICANT: KOJO, HITOSHI
TITLE OF INVENTION: PROCESS FOR PRODUCING 7-AMINOCEPHEM
TITLE OF INVENTION: COMPOUND OR SALTS THEREOF
NUMBER OF SEQUENCES: 34
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CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
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1755 S. Jefferson Davis Highway, Suite 400
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FITKAGAWA, MASAO
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TOPOLOGY: unknown
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                                                                                                                                                                                                                                                                                                          191 AlaThrGlySerSerGlyValMetGlnPheArgTyrProValGlyAlaThrAsnProVal 210
271 TyrīleHisīleLysAspAlaGlnValLysThrGlyAspThrValArg----- 286
                                                                         251 AspHisAsnMetAspGlyAlaSerIleValIleGlnHisThrAsnGlyPheValSerSer 270
                                                                                                                                                       231 PheSerGlyArgAspGlyAspLeuIleAsnAlaSerAsnAlaGlyThrValIleGlnAla 250
                                                                                                                                                                                                                                 211 ValArgArgPheGlyThrAlaThrValAlaGlySerThrValThrSerAsnGlyMetTrp 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      155 ValGlnLysProThr---ProProValValValLysLysProThrProThrPro--- 172
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Qy 22 PheGlyValileThrThrCysIleLeuAlaGly-CysAlaSerLysBroThrTyrAsn	US-10-018-706-2 (1-322) x US-09-258-371-9 (1-2061)	Alignment Scores: 0.759 Length: 2061 Score: 107.50 Matches: 66 Percent Similarity: 38.03% Conservative: 42 Best Local Similarity: 23.24% Mismatches: 102 Query Match: 6.44% Indels: 74 DB: 2 Gaps: 14	RESULT 37 US-09-258-371-9 US-09-258-371-9 Sequence 9, Application US/09258371 Sequence 9, Application US/09258371 Patent No. 5986078 GENERAL INFORMATION: APPLICANT: Garkavtsev, Igor APPLICANT: Riabowol, Karl TITLE OF INFENTION: DNA SEQUENCE ENCODING THE TUMOR TITLE OF INFENTION: SUPPRESSOR GENE ING1 NUMBER OF SEQUENCES: 23 CORRESPONDENCE ADDRESS: ADDRESSEE: Burns, Doane, Swecker & Mathis STRET: 699 Prince Street CITY: Alexandria STATE: VA COUNTRY: USA COUN	Qy 305 GluPheArgIleSerArgAsnGly 312	Oy 287ThrGlyGlnArgIleAlaSerWetLyBAShGLnProSerGlyAlaAlaLeuPhe	2196 TACCTC
ThrTyrAsn 40 					AlaAlaLeuPhe 304 ::: AGC 2294	

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RESULT 38
US-08-751-230-9
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GENERAL INFORMATION:
APPLICANT: Garkavtsev,
APPLICANT: Riabowol, Ko
                                                                    APPLICANT: Riabowol, Karl
TITLE OF INVENTION: DNA SEQUENCE ENCODING THE TUMOR
TITLE OF INVENTION: SUPPRESSOR GENE ING1
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: 699 Prince Street
COUNTRY: USA
ZIP: 22313-1404
                                   CITY: Alexandria
STATE: VA
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Best Local Similarity:
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; LOCATION:
US-08-751-230-9
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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REFERENCE/DOCKET NUMBER: 02
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-7400
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CURRENT APPLICATION DATA
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MEDIUM TYPE: Floppy
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APPLICATION NUMBER:
FILING DATE: 08-DEC-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: MOOI, Leslie A. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 15-NO
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                                                         AspLeuLysValArqGluArqSerIleSerSerGlyValAsnThrAlaHisThrProSer
                                                                                              AGGCGCAGCAGGAGCTGGGCGACACAGTGGGCAACAGCGGCAAGGTTGGCGCGGACAGGC
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                                                                                                                                                                                                                                                 TGCAGCGCGCTGATCCGCAGCCAGGAGCTGGGCGACGAGAAGATCCAGATCGTGAGCC 340
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08-DEC-1995
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38.03%
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6.44%
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Matches:
Conservative:
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Patent No. 6143522
                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, V
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL
                      TELEPAX: 650-854-8275
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                    ATTORNEY AGENT INFORMATION:
NAME: MOOI, Leslie A.
REGISTRATION NUMBER: 37,047
REFERENCE/DOCKET NUMBER: 0287
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650.854-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                   PRIOR APPLICATION NOWBER: US/08/828,158
APPLICATION NOWBER: US/08/828,158
FILING DATE: 27-MAR-1997
APPLICATION NOWBER: US 08/751230
FILING DATE: 15-NOV-1996
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: METHODS OF MODULATING APOPTOSIS
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                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE: CLASSIFICATION:
                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE: 08-DE
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699 Prince Street
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Johnston, Randall N.
Garkavtsev, Igor
     2061 base pairs
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08-DEC-1995
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DB:
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Best Local Similarity:
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US-09-499-082-9
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STRANDEDNESS: double
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229 MetTrpPheSerGlyArgAspGlyAspLeuIleAsnAlaSerAsnAlaGlyThrValIle
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                                                                                                                                                                                                                                                                              CGGGCACACCCAAGGAGAAGAAGCCAAGACCTCCA-----AGAAGAAGAAGAAGCGCT
                                                                                                                                                                                                                                                                                                               GlnGlnHisProAlaValGlnLysProThrProProValValValValLysLysProThr 169
                                                                                                                                                                                                                                                                                                                                                     GCAACAACGAGAACCGTGAGAACGCGTCCAGCAACCACGACCACGACGACGGCGCCT---
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                                                                                         ProValValArgArgPheGlyThrAlaThrValAlaGlySerThrValThrSerAsnGly
                                                                                                                               -----CCAACGAACCCACGTACTGTCTGTGCAACCAGGTCTCCTATGGGGAGATGATCG
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23.24%
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Matches:
Conservative:
Mismatches:
Indels:
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Best Local Similarity:
Query Match:
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Pred. No.:
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LOCATION: 16..900
JS-09-258-372-9
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REGISTRATION NUMBER: 37,047
REFERENCE/DOCKET NUMBER: 0287
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-7400
TELEFAX: 415-854-7400
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 9, Application US/09258372
Patent No. 6238918
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/751,230
FILING DATE:
ATTORNBY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/258,372
FILING DATE:
FILING DATE:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Garkavtsev, Igor
APPLICANT: Riabowol, Karl
TITLE OF INVENTION: DNA SEQUENCE ENCODING THE TUMOR
TITLE OF INVENTION: SUPPRESSOR GENE ING1
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSE: Burns, Doane, Swecker & Mathis
STREET: 699 Prince Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Burns,
STREET: 699 Prince
CITY: Alexandria
STATE: VA
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TYPE: nucleic acid
STRANDEDNESS: double
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                                    101 CGGACCGCCTCCCCGCGACCCGCGGGCCGGCTCGGAGACAGTTTCAGGCCGCATCTTTGC 160
54 yGlyLeuAlaIleGlySerGlnValIle-----ThrAspSerGlnGly-ValProAsnA 72
                                                                                                         41 TTCCCAGATATAGCAGTAGCAGTGATCCCGGGCCTGTGGCTCGGGGGCCGGGGCTGCAGTT 100
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Mismatches:
Indels:
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Matches:
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Search completed: July 3, 2003, 23:16:08 Job time: 6463 secs

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Result
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Maximum Match 100%
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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9 US-10-098-808-4
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3442.734 Million cell updates/sec
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Sequence 1, Appli
Sequence 4, Appli
Sequence 1, Appli
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Sequence 309, App Sequence 309, App Sequence 309, App Sequence 309, App Sequence 309, App Sequence 309, App Sequence 309, App	, , , , , , , , , , , , , , , , , , ,	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0

ALIGNMENTS

RESULT 1 US-10-329-960-1

Sequence 1, Application US/10329960 Publication No. US20030099277A1

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GENERAL INFORMATION:
APPLICANT: Fleischmann et al.
TITLE OF INVENTION: Nucleotide Sequence of the Haemophilus influenzae Rd Genome, Fragn
TITLE OF INVENTION: Thereof, and Uses Thereof
TITLE OF INVENTION: Thereof, and Uses Thereof
CURRENT APPLICATION NUMBER: US/10/329,960
CURRENT APPLICATION NUMBER: US 09/643,990
PRIOR FILING DATE: 2003-01-02
PRIOR PILING DATE: 2003-01-02
PRIOR PILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: US 08/487,429
PRIOR RILING DATE: 1995-06-07
PRIOR RPLICATION NUMBER: US 08/487,787
PRIOR RPLICATION NUMBER: US 08/426,787
PRIOR RPLICATION NUMBER: US 08/426,787
PRIOR RPLICATION NUMBER: US 08/426,787
PRIOR PILING DATE: 1995-04-21
NUMBER OF SEQ ID NOS: 1
SOFTWARE: Patentin version 3.1
SEQ ID NO 1
LENGTH: 1830121
TYPE: DNA
ORGANISM: Haemophilus influenzae
FEATURE:
NAME/KEY: misc feature
LOCATION: (4747)...(4747)
OTHER INFORMATION: n equals a, t, g or c
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VAME/KEY: misc_feature	r: r: misc feature N: (55369)(55369) NFORMATION: n equals	: v: (51805)(51805) v: (51805)(51805)	NAME/KEY: misc_feature LOCATION: (51786)(51786) TTHER INFORMATION: n equals	NAME/KEY: misc feature LOCATION: (51602)(51602) OTHER INFORMATION: n equals	NAME/KEY: misc_feature LOCATION: (51334)(51334) COTHER INFORMATION: n equals	FAALURE: NAME/KEY: misc_feature LOCATION: (47036)(47036) OTHER INFORMATION: n equals	NAME/KEY: misc_feature LOCATION: (45732)(45732) OTHER INFORMATION: n equals	NAME/KEY: misc_feature LOCATION: (45593)(45593) OTHER INFORMATION: n equals	NAME/KEY: misc_feature LOCATION: (44975)(44975) OTHER INFORMATION: n equals	NAME/KEY: misc_feature LOCATION: (44905)(44905) OTHER INFORMATION: n equals	NAME/KEY: misc feature LOCATION: (44416)(44416) OTHER INFORMATION: n equals	NAME/KEY: misc feature LOCATION: (40808)(40810) COTHER INFORMATION: n equals	NAME/KEY: misc_feature LOCATION: (36636)(36636) OTHER INFORMATION: n equals	NAME/KEY: misc feature LOCATION: (36551)(36551) OTHER INFORMATION: n equals	NAME/KEY: misc feature LOCATION: (36543)(36543) COTHER INFORMATION: n equals	PARTURE: NAME/KEY: misc feature LOCATION: (29298)(29298) OTHER INFORMATION: n equals	NAME/KEY: misc feature LOCATION: (10150)(10150) OTHER INFORMATION: n equals	NAME/KEY: misc feature LOCATION: (9921)(9921) OTHER INFORMATION: n equals
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LOCATION: (150841)..(150841)
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                                           750037 AATGTCGTTGCG-----
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216 ThrAla-----ThrValAlaGlySerThrValThr-----SerAsnGlyMetTrp 230
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                                                                                                ValAsnThrAlaHisThrProSerProValAlaValGlnSerSerArgProProValGln 150
                                                                   GlyValMetGlnPheArgTyrProValGlyAlaThrAsnProValValArgArgPheGly 215
                                                                                                                          GlnGlnProAlaProValAlaProProValThrGluAlaProPheAlaThrGlySerSer 195
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Publication No. US20030007981A1
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CURRENT FILING DATE: 2002-03-13
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/405,728
PRIOR FILING DATE: EARLIER FILING DATE: 1999-09-24
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/267,749
PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: EARLIER PRIOR FILING DATE: EARLIER FILING NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin Ver. 2.0
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TITLE OF INVENTION: CLONING AND EXPRESSION OF HAEMOPHILUS SOMNUS
TITLE OF INVENTION: TRANSFERRIN-BINDING PROTEINS
FILE REFERENCE: 9000-0049.20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
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LOCATION: (872)..(1906)
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TYPE: DNA
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                                                                                                                                                     1289 AAAGAATTGGCCACACTAAATAATATGTCTGAGCCATATCATCTGAGTATTGGACAAGTA 1348
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130 GlyValAsnThrAlaHisThrProSerProValAlaValGlnSerSerArgProProVal 149
                                                                                                                                                                                                93 ArgGluIleGlyHisIleAsnAsnLeuAsnSerSerTyrThrIleTyrThrGlyGlnTrp 112
                                                                                                LeuThrLeuTrpSerGly------AspLeuLysValArgGluArgSerIleSerSer 129
                                                                                                                                                                                                                                                          TACAAAGTACGCAAAGGCGATACCATGTTTCTTATTTGCTTATATTTCAGGCATGGATATA 128
                                                                                                                                                                                                                                                                                        CGCTATAAAGGTAAATCAGTGGATCCAGTACGTTACCTA 750420
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                                                  TTGAAAATTGCAAATAATATTCCCGATAGCAATATGATACCAACACAGACAATAAATGAA 1408
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Pred. No.: 3.23e-05 Length: 9025608 Score: 187.00 Matches: 88	INFO	ORGANISM: Streptomyces avermitilis FEATURE: FEATURE: misc feature FOCAMTION: (4197715)		PELICATION NUMB LLING DATE: 200 PELICATION NUMB LLING DATE: 200	TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES FILE REFERENCE: 249-262 CURRENT APPLICATION NUMBER: US/10/156,761 CURRENT FILING DATE: 2002-05-29	HORIKAWA SHIBA, T. SAKAKI, HATTORI,	, PUDLICATION NO. US20030119018A1 ; GENERAL INFORMATION: ; APPLICANT: OMURA, SATOSHI ; APPLICANT: IKEDA, HARUO ; APPLICANT: IKEDA, HARUO	RESULT 3 US-10-156-761-1/c ; Sequence 1, Application US/10156761	Qy 308 IleSerArgAsnGlyValTyrValAspProLeuThrValLeu 321	Qy 288 GlyGlnArgIleAlaSerMetLy8AsnGlnProSerGlyAlaAlaLeuPheGluPheArg 307 ::: :::	Qy 268 ValSerSerTyrIleHisIleLysAspAlaGlnValLysThrGlyAspThrValArgThr 287	Qy 250 AlaAspHisAsnMetAspGlyAlaSerIleValIleGlnHisThrAsnGlyPhe 267	Qy 230 TrpPheSerGlyArgAspGlyAspLeuIleAsnAlaSerAsnAlaGlyThrValIleGln 249	Qy 210 ValValArgArgPheGlyThrAlaThrValAlaGlySerThrValThrSerAsnGlyMet 229 ::::::::: ::: ::: ::: Db 1571 ATTATTCAAGGATTTTCCAGTGCTGATGGAGGCAATAAAGGTATT 1615	Qy 190 PheAlaThrGlySerSerGlyValMetGlnPheArgTyrProValGlyAlaThrAsnPro 209 Db 1559ACAAATGGAAAA 1570	Qy 170 ProThrProProValValGInGInProAlaProValAlaProProValThrGluAlaPro 189	Db 1466 GAACAAATGAAACCCGTTGCTACACCAACACTTCAACAATGCCAATCAAT	Db 1409 TCAGAGGTGACACAAATACAGTCAATGAGACATGGAATGCTAATAAACCAACAAAT 1465 Oy 150 GlnGlnHisProAlaValGlnLysProThrProValValValValLysEysProThr 169	
Qy 286 ArgThrGlyGlnArgIleAlaSerMetLysAsnGlnProSerGlyAlaAlaLeu 303	Qy 266 GlyPheValSerSerTyrIleHisIleLysAspAlaGlnValLysThrGlyAspThrVal 285	Qy 247 ValIleGlnAlaAspHisAsnMetAspGlyAlaSerIleValIleGlnHisThrAsn 265	Oy 234ArgAspGlyAspLeuIleAsnAlaSerAsnAlaGlyThr 246	Qy 216 ThrAlaThrValAlaGlySerThrValThrSerAsnGlyMetTrpPheSerGly 233 ::: :::	Qy 196 GlyValMetGlnPheArgTyrProValGlyAlaThrAsnProValValArgArgPheGly 215	Qy 176 GlnGlnProAlaProValAlaProProValThrGluAlaProPheAlaThrGlySerSer 195	QY 156 GlnLysProThrProProValValValValLysLysProThrProThrProProValVal 175 Db 2009221ACGGCGAAGCCGGCCACGGGGGTGAAGTCCGCCACGGCG 2009180	Qy 136 ThrProSerProValAlaValGlnSerSerArgProProValGlnGlnHisProAlaVal 155 :::	OY 127 IleSerSerGlyValAsnThr	Oy 107 IleTyrThrGlyGlnTrpLeuThrLeuTrpSerGlyAspLeuLysValArgGluArgSer 126	Qy 87 ArgTyrGlyLeuAsnTrpArgGluIleGlyHisIleAsnAsnLeuAsnSerSerTyrThr 106 :: Db 2009362 GAGCAGAGCGTC 2009351	Qy 73TyrGlnValLysGlnGlyAspThrValSerLysIleAlaGln 86	Qy 67 GlnGlyValProAsnArg72 Db 2009482 GCGGCCGTCTCCGGAAAGGTCTCCGCAGGCCCCCGTTGCCGCGAAGCAGGGGGGCCGCCGAG 2009423	Qy 55 GlyLeuAlaIleGlySerGlnValIleThrAspSer 66	Qy 47 SerHisArg	Qy 27 ThrCysIleLeuAlaGlyCysAlaSerLysProThrTyrAsnSerThrSerGlySerGly 46	US-10-018-706-2 (1-322) x US-10-156-761-1 (1-9025608)	Percent Similarity: 34.35% Conservative: 36 Best Local Similarity: 24.38% Mismatches: 117 Query Match: 11.20% Indels: 120 DB: 9 Gaps: 16	

US-10-018-706-2 (1-322) x US-10-156-761-1629 (1-903) QY 46 GlySerHisArg)03)03)03 : Str : CDS : (1) !-162 !-162 l-162	ISHIKA SHIKA SHIBA, SAKAKI HATTOR HATTOR PLICATION PLICATION I	Oy 304PheGluPheArgIleSerArgAsnGlyValTyrValAspProLeuThrValLeu 321
SULT 5 -10-156-761-4684 Sequence 4684, Appl Publication No. US2 GENERAL INFORMATION APPLICANT: OMURA, APPLICANT: ISHIEA, APPLICANT: HORIGAN APPLICANT: HORIGAN APPLICANT: HATTOO TITLE OF INVENTION FILE REFERENCE: 24 CURRENT FILING DATE FRIOR FILING DATE FRIOR APPLICATION PRIOR FILING DATE PRIOR APPLICATION PRIOR FILING DATE PRIOR APPLICATION PRIOR FILING DATE PRIOR APPLICATION PRIOR FILING DATE PRIOR APPLICATION PRIOR FILING DATE PRIOR APPLICATION PRIOR FILING DATE PRIOR PILING DATE PRIOR APPLICATION REGOR FILING DATE PRIOR APPLICATION PRIOR FILING DATE PRIOR APPLICATION PRIOR FILING DATE PRIOR APPLICATION PRIOR FILING DATE PRIOR APPLICATION PRIOR FILING DATE PRIOR FILING DATE PRIOR APPLICATION PRIOR FILING DATE PRIOR PILING DATE PRIOR PILING DATE PRIOR FILING DATE PRIOR PILING DATE PRIOR FILING DATE PRIOR	TCTCGGCCGGCTGGGGCGGCGCGTACGGCAACGAGGTCGTCGT heValSerSerTyrIleHisIleLysAspAlaGlnValLysTh heValSerSerTyrIleHisIleLysAspAlaGlnValLysTh	Qy 195 SerGlyValMetGlnPheArgTyrProValGlyAlaThrAsnProValValArgArgPhe 214 ::: Db 496 GCCGGCTACACCCTGCCGGTCGACGGC	Qy 126 SerIleSerSerGlyValAsnThr

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RESULT 6
US-10-156-761-1
Sequence 1, Application US/10156761
Publication No. US20030119018A1
GENERAL INFORMATION:
APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: IKEDA, HARUO
APPLICANT: IKEDA, HARUO
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
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HAMP/KEY: CDS
LOCATION: (1)..(609)
US-10-156-761-4684
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T: ISHIKAWA, JUN
T: HORIKAWA, HIROSHI
T: SHIBA, TADAYOSHI
T: SAKAKI, YOSHIYUKI
T: HATTORI, MASAHIRA
INVENTION: NOVEL POLYNUCLEOTIDES
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CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
INUMBER: OF SEQ ID NOS: 15109
SEQ ID NO 1
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                                                                                                                              AlaAlaLeu---PheGluPheArgIleSerArgAsp---GlyValTyrValAspProLeu 318
                                                                                                                                                                CAGGTCGTCGCCÁCCGGTCÁGCACÁTCGCGCTCTCCGGCÁÁCACCGGTAACTCCÁGCGGC 5729209
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Matches:
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; ORGANISM: Xanthomonas campestris
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1001)..(2353)
US-09-927-827-41
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SEQ ID NO 41
LENGTH: 3353
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Publication No.
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TITLE OF INVENTION: Directed Genetic Engineering of Xanthomonas
FILE REFERENCE: 38-10(15824)B
CURRENT APPLICATION NUMBER: US(09/927,827
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: US 60/279,493
PRIOR FILING DATE: 2001-03-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      111 GlnTrpLeuThrLeuTrpSerGlyAspLeuLysValArgGluArgSerIleSerSerGly 130
                                                                                                                                                                                                                                           250 AlaAspHisAsnMetAsp---GlyAlaSerIleValIleGlnHisThrAsnGlyPheVal 268
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PheGluPheArgIleSerArgAsnGlyValTyrValAspProLeuThrValLeuLys 322
                                                                              ValArgThrGlyGlnArgIleAlaSerMet---LysAsnGlnProSerGlyAlaAlaLeu 303
                                                                                                                                                                                                                                                                                                                   TrpPheSerGlyArgAspGlyAspLeuIleAsnAlaSerAsnAlaGlyThrValIleGln
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                                        SerSerTyrTleHis-------IleLysAspAlaGlnValLysThrGlyAspThr 284
                                                                                                                                                                                                       TCCGACTGGATGACCGGCTACGGCATGATCCTGATCGTGGATCACGGCAATGGCTACATG
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10. US20030036176A1
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CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: UP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PATENTIN Ver. 3.0
SEQ ID NO 2741
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US-09-738-626-2741
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Best Local Similarity:
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TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
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376 CCAGCATCCGGCTATGGACAGTGGATCCGCATCCAGCACGACGACGGATCCATCTCCATC 435
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                                                                                                                                                              CCACGTTGGGGAACC---
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TATEISHI, NAOKO
SENOH, AKIHIRO
                                                                            GCAMACTCAATCGGCACCCCAÁTCTACGCCGTCATGGCCGGCÁCTGTCÁTCAGCTCTGGC 375
                                                                                                                SerGlyArgAspGlyAspLeuIleAsnAlaSerAsnAlaGlyThrValIleGlnAlaAsp 251
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ANDO, SEIKO
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US-09-738-626-
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; TYPE: DNA
; ORGANIAM: Corynebacterium glutamicum
US-09-738-626-1
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CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
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APPLICANT: TATEISHI, NAOKO
APPLICANT: SENOH, AKHHIRO
APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO
APPLICANT: OZAKI, AKIO
APPLICANT: OZAKI, OVEL POLYNUCLEOTIDES
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APPLICANT: MIZOGUCHI, HIROSI
APPLICANT: ANDO, SEIKO
APPLICANT: HAYASHI MIKIRO
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ArgArgPheGlyThrAlaThrValAlaGlySerThrValThrSerAsnGlyMetTrpPhe
                                                                                                                  AAGCTGCAGGAGTCGCAACCACCGCCGTC-GCACCAGCCGCCACCGTAGCGCGCCCCAGCA
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                                                                         ThrGlySerSerGlyValMetGlnPheArgTyrProValGlyAlaThrAsnProValVal
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                                                                                                                                                                                              AAACCGACTACGCAGGCCTTTCCTCCGGCGTTG------
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CURRENT APPLICATION NUMBER: US/10/092,243A
CURRENT FILING DATE: 2002-05-21
PRIOR APPLICATION NUMBER: 60/147,551
PRIOR FILING DATE: 1999-08-06
PRIOR APPLICATION NUMBER: US00/21340
PRIOR PILING DATE: 2000-08-04
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 8
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US-10-092-243A-8/c
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APPLICANT: Hillman, Jeffrey D.
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TITLE OF INVENTION: Microbial Polynucleotides Expressed During Infection of
TITLE OF INVENTION: a Host
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
LOCATION: (538)
OTHER INFORMATION: N stands for
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  {\tt ThrAlaHisThrProSerProValAlaValGlnSerSerArgProProValGlnGlnHis}
                                                                       LeuThrLeuTrpSerGlyAspLeuLysValArgGluArgSerIleSerSerGlyValAsn 132
                                                                                                                  AAAGAATTGGCGGCGTTGAATAATATGTCCGAACCTTACAGCTTAAGCGTCGGACAAACC
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US-10-156-761-7229
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                                                         US-10-018-706-2 (1-322) x US-10-156-761-7229 (1-1191)
                                                                                                 Query Match:
DB:
                                                                                                                                   Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                               Alignment Scores:
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US-10-156-761-7229
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SEQ ID NO 7229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Publication No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLECTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILLING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: UF 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
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NAME/KEY: CDS
LOCATION: (1).
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                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Streptomyces
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HORIKAWA, HIROSHI
SHIBA, TADAYOSHI
SAKAKI, YOSHIYUKI
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                                                                                                                                                                                           Sequence 1, Application US/10329960 Publication No. US20030099277A1 GENERAL INFORMATION:
FILE REFERENCE: PB186P1
CURRENT APPLICATION NUMBER: US/10/329,960
CURRENT FILING DATE: 2003-01-02
PRIOR APPLICATION NUMBER: US 09/643,990
PRIOR FILING DATE: 2000-08-23
PRIOR APPLICATION NUMBER: US 08/487,429
PRIOR FILING DATE: 1995-06-07
                                                                                                                                 APPLICANT: Fleischmann et al.
TITLE OF INVENTION: Nucleotide Sequence of the Haemophilus influenzae
TITLE OF INVENTION: Thereof, and Uses Thereof
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PRIOR APPLICATION NUMBER: US 08/426,787
PRIOR FILING DATE: 1995-04-21
NUMBER OF SEQ ID NOS: 1
SOFTWARE: Patentin version 3.1
SEQ ID NO 1
SEQ ID NO 1
TYPE: DNA
ORGANISM: Haemophilus influenzae
FEATURE: Haemophilus influenzae NAME/KEY: misc feature LOCATION: (47036)..(47036) OTHER INFORMATION: n equals a, FEATURE: VAME/KEY: misc_feature LOCATION: (51602)..(51602) OTHER INFORMATION: n equals a, t, g or c NAME/KEY: misc feature LOCATION: (51334)..(51334) OTHER INFORMATION: n equals a, FEATURE:
NAME/KEY: misc_feature
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JOHER INFORMATION: n equals a, NAME/KEY: misc feature LOCATION: (4747)..(4747) OTHER INFORMATION: n equals a, SEATURE: NAME/KEY: misc feature LOCATION: (45593)..(45593) OTHER INFORMATION: n equals a, NAME/KEY: misc_feature LOCATION: (44975)...(44975) OTHER INFORMATION: n equals a, NAME/KEY: misc_feature LOCATION: (36636)..(36636) WITHER INFORMATION: n equals a, EATURE: AME/KEY: misc feature LOCATION: (36551)..(36551) CHER INFORMATION: n equals a, PATURE:

AMME/KEY: misc feature

ACATION: (10150)...(10150)

THER INFORMATION: n equals a, NAME/KEY: misc_feature LOCATION: (9921)..(9921) DIHER INFORMATION: n equals a, NAME/KEY: misc_feature OCATION: (40808)..(40810) THER INFORMATION: n equals a, NAME/KEY: misc_feature OCATION: (36543)..(36543) THER_INFORMATION: n equals a, NAME/KEY: misc feature OCATION: (29298)..(29298) THER INFORMATION: n equals a, AME/KEY: misc feature CCATION: (44905)..(44905) THER INFORMATION: n equals a, E/KEY: misc_feature EXTION: (44416) ..(44416) ER INFORMATION: n equals a, t, g t, g ŗ, ŗ ŗ 'n t, g or t, g or t, g or c t, g or c t, g or t, g or c g or g.or g or Ω Q ø or 9 õ 0 0 ę,

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LOCATION: (147197)..(147197)
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LOCATION: (150841)...(150841)
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LOCATION: (140398)..(140398)
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                                                                                                    AlaHisThrProSerProValAlaValGlnSerSerArgProProVal----GlnGlnHis 152
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 ProValValGlnGlnProAlaProValAlaProProValThrGluAlaProPheAlaThr 192
                                                 ProAlaValGlnLysProThrProProValValValLysLysProThrProThrPro
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US-09-860-846-1/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO
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CURRENT APPLICATION NUMBER: US/09/860,846
CURRENT FILING DATE: 2001-05-18
PRIOR APPLICATION NUMBER: 09/105,537
PRIOR FILING DATE: 1998-06-26
NUMBER OF SEQ ID NOS: 43
SOFTWARE: FastSEQ for Windows Version 3.0
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TITLE OF INVENTION: DNA encoding methymycin and pikromycin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Xue, Y. APPLICANT: Zhao, L
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Streptomyces venezuelae
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Matches:
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Indels:
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    -GlyGlyLeuAlaIleGlySerGlnValIle

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RESULT 14

US-09-988-384B-1/c
; Sequence 1, Application US/09988384B
; Publication No. US20030073824A1
; GENERAL INFORMATION:
; APPLICANT: Sherman, D.H.
; APPLICANT: Xue, Y.
APPLICANT: Zhao, L.
; TITLE OF INVENTION: DNA encoding methymycin and FILE REFERENCE: 600.536US1
; CURRENT APPLICATION NUMBER: US/09/988,384B
; CURRENT FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: ECT/US99/14398
; PRIOR APPLICATION NUMBER: US/09/105,537
; PRIOR PILING DATE: 1998-06-26
; NUMBER OF SEQ ID NOS: 53
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                                                                                                                                                                                                                                                                                                          GCGTCGAGGAAGCGTACGGGCCTGCGG-----ACCTGGTCCACCCAGTACTCGGGATCG
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Pred. No.:
Score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-018-706-2 (1-322) x US-09-988-384B-1 (1-15872)
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LENGTH: 15872
TYPE: DNA
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3150 GTGACGCCGGGGGTAGCGGCAGGCCATGCCGATGATCGCGATGGCTCGGCGGTGGTG 309
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     HisThrAsnGlyPheValSerSerTyrIleHisIleLysAsp---AlaGlnValLysThr
                                      GCGGAGACCGCCGTGGCGGCCTCCTGGTCGCGTACGGAGTCCGCCGCCATCGCGGAGCAG
                                                                  AlaGlyThrValIleGlnAlaAsp---HisAsnMetAspGlyAlaSerIleValIleGln
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                                                                                                                              Ser----AsnGlyMetTrpPheSerGlyArgAspGlyAspLeuIleAsnAlaSerAsn
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US-10-018-706-2 (1-322) x US-09-836-821-1 (1-15872)
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LENGTH: 15872
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT FILING DATE: 2001-04-17
PRIOR APPLICATION NUMBER: 09/105,537
PRIOR FILING DATE: 1998-06-26
NUMBER OF SEQ ID NOS: 43
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: DNA encoding methymycin FILE REFERENCE: 600.438US1
CURRENT APPLICATION NUMBER: US/09/836,821
CURRENT FILING DATE: 2001-04-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Sherman, D.H.
APPLICANT: Liu, H.
APPLICANT: Xue, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Streptomyces venezuelae
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                                                                                                                                                                                                                                                                                                               Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                     Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Sherman, D.H.
APPLICANT: Liu, H.
APPLICANT: Liu, H.
APPLICANT: Xue, Y.
APPLICANT: Zhao, L.
APPLICANT: Zhao, L.
TITLE OF INVENTION: DNA encoding methymycin and pikromycin FILE REPERENCE: 600.438US1
CURRENT APPLICATION NUMBER: US/09/861,289
CURRENT FILING DATE: 2001-05-18
PRIOR APPLICATION NUMBER: 09/105,537
PRIOR FILING DATE: 1998-06-26
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                                            3150 GTGACGCCGCGGGGTAGCGGCAGGCCATGCCGATGATCGCGATGGGCTCGGCGGTGGTG 3091
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Sequence 4, Application US/10087667

| Publication No. US20020194629A1
| GENERAL INFORMATION:
| APPLICANT: Bramley, John A. |
| APPLICANT: Bramley, John A. |
| APPLICANT: Bramley, John A. |
| APPLICANT: Bramley, John A. |
| APPLICANT: Plaut, Karen I. |
| APPLICANT: Kerr, David |
| TITLE OF INVENTION: TREATMENT OF STAPHYLOCOCCUS INFECTIONS |
| FILE REFERENCE: Mastifis |
| CURRENT APPLICATION NUMBER: US/10/087,667 |
| CURRENT FILING DATE: 2002-02-28 |
| NUMBER OF SEQ ID NOS: 10 |
| SOPTWARE: Patentin Ver. 2.1 |
| SEQ ID NO 4 |
| SEQ ID NO 4 |
| TYPE: DNA |
| ORGANISM: Staphylococcus simulans
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US-10-087-667-4
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                                 1009 GACATGTCGCGCGGCGGCGGCTGGGGCAGCAGCAGCAGCAGCAACTGGGTGTCGGCCTCG 1068
243 AsnAlaGlyThrValIleGlnAlaAspHisAsnMetAspGlyAlaSerIleValIleGln
                                                                223 ThrValThrSerAsnGlyMetTrpPheSerGlyArgAspGlyAspLeuIleAsnAlaSer 242
                                                                                                                                     211 ValArgArgPheGlyThrAlaThrValAlaGlySer------ 222
                                                                                                                                                                                                                                                                                                                  778 GCCGGCGGCCGCCGCCGCCGCCGACGCCAGTTCCAGCTGGTCTACGGCCGCCTGTTCAA 837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           658
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                110 GlyGlnTrpLeuThrLeuTrpSerGlyAspLeuLysValArgGluArgSerIleSerSer 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  496 AAGCACTCGGAAGAGATCTCGCAC------
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                                                                                                                                                                                                                                             CGAACCGCGCCAAGGCCAAGGCGGCTTCGGACCGCCTTCGCCAAGGCCGGGCCCGGACGTGCA .897
                                                                                                      AlaThrGlySerSerGlyValMetGlnPheArgTyrProValGlyAlaThrAsnProVal 210
                                                                                                                                                                                                                                                                                   Glu---AlaPro-----
                                                                                                                                                                                                                                                                                                                                                                                     GGTGACGCTGGCCCGCGCCCAATCCGCTGCAGGCGTTTCGAGCGTTCCGGGCGACAACGA 777
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Conservative:
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밁 Ś Б Ś 밁 Ś 밁 Ş 뭥 Ś 밁 Ś 밁 S 밁 Ś 밁 Ş 밁 S В S В S 밁

ThrCysIleLeuAlaGlyCys	; OTHER INFORMATION: us2full US-09-468-147-164 Alignment Scores:	CURRENT FILING DATE: 1999-12-21 EARLIER APPLICATION NUMBER: US/09/468,147A EARLIER FILING DATE: 1999-12-21 EARLIER FILING DATE: 1998-10-15 EARLIER FILING DATE: 1998-10-15 EARLIER FILING DATE: 1997-10-15 EARLIER FILING DATE: 1997-10-15 EARLIER FILING DATE: 1997-10-15 EARLIER FILING DATE: 1997-10-15 SOPTWARE: PastSEQ for Windows Version 3.0 SEQ ID NO 164 ELNGTH: 7277 TYPB: DNA ORGANISM: Hepatitis E Virus FEATURE:	RESULT 18 US-09-468-147-164 ; Sequence 164, Application US/09468147A ; Dequence 164, Application US/09468147A ; Publication No. US20030049601A1 ; GENERAL INFORMATION: APPLICANT: Abbott Laboratories ; APPLICANT: Erker, George G. ; APPLICANT: Erker, James C. ; APPLICANT: Dawson, Suresh M. ; APPLICANT: Dawson, George J. ; APPLICANT: Mushahwar, I. K. ; APPLICANT: Mushahwar, I. K. ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING ; TITLE OF INVENTION: HEPATITIS E VIRUS ; FILE REFERENCE: 623-US-D1	Db 1069 GCCGCCGCTCAAGCGCCACTCTTCGTGCTTCGCGAGATCGTG 1116 Qy 263 HisThrAsmGlyPheValSerSerTyrIleHisIleLysAspAlaGlnValLysThrGly 282
US-09-468-147-165 Sequence 165, Application US/09468147A Sequence 165, Application No. US20030049601A1 GENERAL INFORMATION:	Qy 260 VallleGlnHisThrAsnGlyPheValSerSerTyrIleHisIleLysAspAlaGlnVal 279 ::	OValValArgArgPheGlyThrAlaThrValAAGGTGTAT TTTPPheSerGlyArgAspGlyAspLeuIle	2235 ACT	N N N

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PEATURE:
NAME/KEY: CDS
LOCATION: (5197)...(7176)

LOCATION: (5197)...(7176)

OTHER INFORMATION: orf3 at positions 5159-5527

OTHER INFORMATION: Xaa = Unknown or Other at positions for the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the
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LOCATION: (36)...(5159)
OTHER INFORMATION: Orf1
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ValAlaValGlnSerSerArgProProVal-
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                                                                    TTCTCCCCCCCTGAGGCGGCCGCTCCTGCTTCGGCTGCCGCCCCGGGGGTTGCCCTACCCT
                                                                                                            LeuLysValArgGluArgSerIleSerSerGlyValAsnThrAlaHisThrProSerPro 139
                                                                                                                                                     TTTTGCGGTGAGGGGACTTTGTATACCCGAACCTGGTCAACCTCTGGTTTTTCTAGTGAT
                                                                                                                                                                                             LeuAsnSerSerTyrThrIleTyrThrGlyGlnTrpLeuThrLeu---TrpSerGlyAsp 119
                                                                                                                                                                                                                                        GGGCTGCTGGGTATCTTCCCCCCATTCTCCCCTGGGCATATTTGGGAGTCTGCTAACCCC 211
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                           149
                                                                                          GENERAL INFORMATION

APPLICANT: IKEDA, HARUO

APPLICANT: ISHIKAWA, JUN

APPLICANT: HORIKAWA, HIROSHI

APPLICANT: HORIKAWA, HIROSHI

APPLICANT: SAKAKI, YOSHIYUKI

APPLICANT: SAKAKI, YOSHIYUKI

APPLICANT: BAKKI, YOSHIYUKI

APPLICANT: HATTORI, MASAHIRA

TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES

FILE REFERNCE: 249-262

FURRENT FILING DATE: 2002-05-29

PRIOR APPLICATION NUMBER: JP 2001-204089

PRIOR FILING DATE: 2001-05-30

PRIOR APPLICATION NUMBER: JP 2001-272697

PRIOR FILING DATE: 2001-08-02

NUMBER OF SEQ ID NOS: 15109

SEQ ID NO 2407

LENGTH: 774

TYPE: DNA
ORGANISM: Streptomyces avermitilis
FEATURE:
NAME/KEY: CDS

LOCATION: (1)... (774)

US-10-156-761-2407
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publication No. US20
GENERAL INFORMATION:
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  Length:
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RESULT 21
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APPLICANT:
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                                                                                                 An, Yong-Qiang
Hamilton, Carol M.
Price, Jennifer L.
Raines, Tracy M.
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                                                                                Yu,
   Matthew, Abraham V.
Ledford, Brooke L.
Woessner, Jeffrey P.
                                                  Page, Amy
                                                                     Rameaka, Joshua G.
                                                                                Yang
                                                                                                                                                                 ach, Jorn
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RESULT 22
US-09-468-147-141
; Sequence 141, Application US/09468147A
; Publication No. US20030049601A1
; Publication No. US20030049601A1
; GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
; APPLICANT: Schlauder, George G.
; APPLICANT: Erker, James C.
; APPLICANT: Dessai, Suresh M.
; APPLICANT: Dawson, George J.
; APPLICANT: Mushahwar, I. K.
; TITLE OF INVENTION: METHODS AND COMPOSIT
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Best Local Similarity:
Query Match:
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; OTHER INFORMATION: n =
US-09-770-445-354
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SOFTWARE: FABI
; SEQ ID NO 354
FNGTH: 942
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APPLICANT:
APPLICANT:
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APPLICANT: Hurban, Patrick
APPLICANT: Hurban, Patrick
TITLE OF INVENTION: Expressed Sequences of Arabidopsis
TITLE OF INVENTION: thaliana
FILE REFERENCE: 2023US (PARA-012PRV)
CURRENT APPLICATION NUMBER: US/09/770,445
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: US 60/178,472
PRIOR PILING DATE: 2000-01-27
NUMBER OF SEQ ID NOS: 999
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      OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
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Davis, Keith R.
Allen, Keith
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Kricker, Maja
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Matches:
Conservative:
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Indels:
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625

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FILE OF INVENTION: HEPATITIS E VIRUS
FILE REFERENCE: 6232.US.P1
CURRENT APPLICATION NUMBER: US/09/468,147A
CURRENT FILING DATE: 1999-12-21
EARLIER APPLICATION NUMBER: US 09/173,141
EARLIER APPLICATION NUMBER: US 60/061,199
EARLIER FILING DATE: 1998-10-15
EARLIER FILING DATE: 1997-10-15
NUMBER OF SEQ ID NOS: 258
SOFTMARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 141
ENOTH: 903
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Hepatitis E Virus
FEATURE:
      291
                                                          271
                                                                                     628
                                                                                                         251 AspHisAsnMetAspGlyAlaSerIleValIleGlnHisThrAsnGlyPheValSerSer 270
                                                                                                                                         604
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                                                                                                                                                                                                               211 ValArgArgPheGlyThrAlaThrValAlaGlySerThrValThrSerAsnGlyMetTrp 230
                                                                                                                                                                                                                                                                     191 AlaThrGlySerSerGlyValMetGlnPheArgTyrProValGlyAlaThrAsnProVal 210
                                                                                                                                                                                                                                                                                                      481
                                                                                                                                                                                                                                                                                                                       171 ThrProProValValGlnGlnProAlaProValAlaProProValThrGluAlaProPhe 190
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                                                                                                                                                                                                                                                                                                     CCCCCTCCTCCCGTGCGTAAGCCGGCAACATCCCCGCCTCCCCGCACTCGCCGT-----
                             TATCAACGTTTCCCAGAAGCGTTCTACTCGACTGAATTCATCATGCGCGAGGGCCTTGCA
                                                   TyrIleHisIleLysAspAlaGlnValLysThrGlyAspThrValArgThrGlyGlnArg
                                                                                     ---CATCGCCCCGGGGGTGGC-----CTCTGCCAT--
                                                                                                                                                             PheSerGlyArgAspGlyAspLeuIleAsnAlaSerAsnAlaGlyThrValIleGlnAla
                                                                                                                                                                                                                                                                                                                                                                                                           GATATCTGGGTGTTACCACCGCCCTCAGAGGAATCTCATGTTGATGCGGCATCTGTACCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ValAsnThrAlaHisThrProSerProValAlaValGlnSerSerArgProProVal--- 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGGTCAACCTCTGGTTTTTCTAGTGATTTCTCCCCCCCTGAGGCGGCCGCCCCCTGCTTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              [rpLeuThrLeu---TrpSerGlyAspLeuLysValArgGluArgSerIleSerSerGly 130
                                                                                                                                                                                                                                                                                                                                                                                                                                      0.000388
125.00
35.95%
25.21%
7.49%
                                                                                                                                                                                                                                                 ------CTCCTTTACACCTÁCCCGACGCGCC--------
                                                                                                                                     -----TTAGTCAATGCCTCAAACCCTGGC-------
                                                                                                                                                                                           ----AAGGTGTATGCGGGGTCATTGTKTGAGTCAGACTGTGATTGG
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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nThrAla-HisThrProSerProValAlaValGlnSerSerArgProProVal-----G
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US-10-018-706-2 (1-322) x US-10-063-547-99 (1-2436)
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Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: DNA; Homo; ORGANISM: Homo US-10-063-547-99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 23
US-10-063-547-99
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Publication No. U82002018
GENERAL INFORMATION:
APPLICANT: Eaton, Dan L.
APPLICANT: Filtwaroff, El,
APPLICANT: Gerritsen, Ma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, Christopher. J.

APPLICANT: Grimaldi, Christopher. J.

APPLICANT: Grimaldi, Christopher. J.

APPLICANT: Wood, William I.

APPLICANT: Wood, William I.

APPLICANT: WOOD, WILLIAM I.

APPLICANT: WOOD, WILLIAM I.

APPLICANT: WOOD, WILLIAM I.

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APPLICANT: WOOD, WILLIAM I.

APPLICANT: WOOD, WILLIAM I.

APPLICANTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION. NUMBER: US/10/063,547

CURRENT FILING DATE: 2002-05-02

Prior Application removed - See File Wrapper or Palm

NUMBER OF SEQ ID NOS: 170

SEQ ID NO 99

LENGTH: 2436

TYPEE. NN 4336
1027 CTCCAGTGGGGCCAGCACAGCCACCAACTCTGACTCCAGCACAGTGTCCAGTGGGGGCCAG 1086
                                                                                                   967 TGAGTCCAGAACGACCTCCAATGGGGCTGGCACAGCCAACCTCTGAGTCCAGCACGAC 1026
                                                                                                                                                                                                          907 CACTGCCACCAACTCTGAGTCCAGCACAACCTCCAGTGGGGCCAGCACCACCAACTC 966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            686 GCCACCAACTCTGAGTCCAGCACAGTGTCCAGTAGGGCCAGCACTGCCAACCTCTGAG 745
                                                                                                                                                                                                                                                                                                                                                                                                                     788 GACTCCAGCACAACCTCCAGTGGGGCTAGCACAGCCACCAACTCTGAGTCCAGCACAACC
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                                                                                                                                                                                                                                                                                                                                                           66 SerGlnGlyValProAsnArgTyrGln-------ValLysGlnGlyAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46 GlySerHisArgThrSerGlySerGlyGlyLeuAlaIleGlySerGlnValIleThrAsp 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26 ThrThrCysIleLeuAlaGlyCysAlaSerLysProThrTyrAsnSerThrSerGlySer 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 AlaileAsnSerGlnAsnGlnLysProIleLysArgLeuGlyLeuIlePheGlyValIle
                                                                                                                                                                                                                                                 ThrValSerLysIleAlaGlnArgTyrGlyLeuAsnTrpArgGluIleGlyHis-----
                                                uTrpSerGlyAspLeuLysValArg------GluArgSerIleSerSerGlyValAs 132
                                                                                                                                                    -----IleAsnAsnLeu-AsnSerSerTyrThrIleTyrThrGlyGlnTrpLeuThrLe 115
                                                                                                                                                                                                                                                                                                                 TCCAGTGGGGCCAG-CACAGCCACCAACTCTGAGTCCAGCACAGTGTCCAGTAGGGCCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Application US/10063547
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122.50
39.04%
23.42%
7.34%
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Matches:
Conservative:
Mismatches:
Indels:
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78
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Alignment Scores: 0.00289 Length: 2436 Pred. No.: 122.50 Matches: 78 Percent Similarity: 39.04% Conservative: 52 Best Local Similarity: 23.42% Mismatches: 145		ga a	Smith, Victoria Watanabe, Colin Wood, William I. Zhang, Zemin NVENTION: SECRETE	Chen, Jian Desnoyers, I Goddard, Aud Godowski, Pa Gurney, Aust Pan, James	RESULT 24 US-10-174-590-309 VS-10-174-590-309 VS-10-174-590 VS-10-174-59	Qy 302 laLeuPheGluPheArgIleSerArgAsnGlyVal 313	1485		Qy 226 erAsnGlyMetTrpPheSerGlyArgAspGlyAspLeuIleAsnAlaSerAsnAlaGlyT 246 ::: Db 1344 CCAGTGGG	Db 1246 CACAGTGTCCAGTGGGATCAGCACAGTCAGCACACTCTGAGTCCCAGCACACCCCC-AGTG 1304 Oy 206 laThrAsnProValValArgArgPheGlyThrAlaThrValAlaGlySerThrValThrS 226 Ob 1305 GGGCCAAC	Qy 170 roThrProProValValGlnGlnProAlaProValAlaProProVal	Db 1087 CACTGCCACCACTCTGAGTCCAGCACGACCTCCAGTGGGGCCAG 1131 Oy 150 InGlnHisProAlaValGlnLysProThrProProValValValLysLysProThrP 170 Ill
QY 302 laLeuPheGluPheArgIleSerArgAsmglyVal 313 Oy 1545 CCAACTCTGAGTCTAGCACAGTGTCCAGTGGGATC 1579	264 1425 282	Qy 246 hrVallleGlnAlaAspHisAsnMetAspGlyAlaSerIleVallleGlnHis 263	Db 1305 GGGCCAAC	Qy 186 hrgluAlaProPheAlaThrGlySerSerGlyValMetGlnPheArgTyrProValGlyA 206 :::	Db 1132 CACACCCACTCTGAGTCCAGCACGACCTCCAGTGGGGCTAGCACAGCCACCAACTC 1191 Qy 170 roThrProProValValGlnGlnProAlaProValAlaProProValT 186	Db 1087 CACTGCCACCAACTCTGAGTCCAGCACGACCTCCAGTGGGGCCAG 1131 Oy 150 lnGlnHisProAlaValGlnLysProThrProProValValValValLysLysProThrP 170	Db 1027 CTCCAGTGGGGCCAGCACCAGCCACTCTGACTCCAGTGTGCCAGTGGGGCCAG 1086 Qy 132 nThrAla-HisThrProSerProValAlaValGlnSerSerArgProProValG 150	98IleAsnAsnLeu-AsnSerSerTyrThrIleTyrThrGlyGlnTrpLeuThrLe	Db 848 TCCAGTGGGGCCAG-CACAGCCACTCTGAGTCCAGTGTCCAGTAGGGCCAG 906 Oy 80 ThrValSerLysileAlaGlnArgTyrGlyLeuAsnTrpArgGluIleGlyHis 97 Oy 907 CACTGCCACCAACTCTGAGGTCCAGCACAACCTCCAGTGGGGCAAGCACCAACTC 966	Qy 46 GlySerHisArgThrSerGlySerGlyGlyLeuAlaIleGlySerGlnValIleThrAsp 65	Db 686 GCCACCAACTCTGAGTCAGCACAGTGTCCAGTAGGGCCAGCACCCAACTCTGAG 745 Qy 26 ThrThrCysIleLeuAlaGlyCysAlaSerLysProThrTyrAsnSerThrSerGlySer 45 :::::::::::::::::::::::::::::::::::	Query Match: 7.34% Indels: 60 DB: 9 Gaps: 12 US-10-018-706-2 (1-322) x US-10-174-590-309 (1-2436) Qy 6 AlaileAsmSerGlnAsmGlnLysProlleLysArgLeuGlyLeuIlePheGlyValile 25

1343 226 1304 206 1245

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RESULT 25
US-10-176-758-309
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Best Local Similarity:
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SEQ ID NO 309
LENGTH: 2436
TYPE: DNA
ORGANISM: Homo Sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 309, Applic
Publication No. US20
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P343 CRICI04
CURRENT APPLICATION NUMBER: US/10/176,758
CURRENT FILING DATE: 2002-06-21
CURRENT FILING DATE: 2002-06-21
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APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audre
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APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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150 lnGlnHisProAlaValGlnLysProThrProProValValValLysLysProThrP 170
                                                                                                                                                                                                                                                   115 uTrpSerGlyAspLeuLysValArg------GluArgSerIleSerSerGlyValAs 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                848
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                                                                                                                                                                                                                                                                                                                                                                                                                   907
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                                                                                      CACTGCCACCAACTCTGAGTCCA-
                                                                                                                                      nThrAla-HisThrProSerProValAlaValGlnSerSerArgProProVal-----G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ThrValSerLysIleAlaGlnArgTyrGlyLeuAsnTrpArgGluIleGlyHis-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCCAGTGGGGCCAG-CACAGCCACCAACTCTGAGTCCAGCACAGTGTCCAGTAGGGCCAG
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Goddard, Audrey
Godowski, Paul
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5. US20030008353A1
                                                                                                                                                                                                                                                                                                                                                         ----IleAsnAsnLeu-AsnSerSerTyrThrIleTyrThrGlyGlnTrpLeuThrLe 115
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122.50
39.04%
23.42%
7.34%
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Matches:
Conservative:
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                                                                                      -GCACGÁCCTCCÁGTGGGGCCAG
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APPLICANT: Eaton Dan L.

APPLICANT: Edeton Mary E.

APPLICANT: Gerritsen, Mary E.

APPLICANT: Goodward, Audrey

APPLICANT: Goodward, Paul J.

APPLICANT: Goodward, Paul J.

APPLICANT: Grimaldi, Christopher J.

APPLICANT: Grimaldi, Christopher J.

APPLICANT: Grimaldi, Christopher J.

APPLICANT: Watanabe, Colin K.

APPLICANT: Watanabe, Colin K.

APPLICANT: Wood, William I.

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US-10-063-616-99
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                                                                                   US-10-018-706-2 (1-322) x US-10-063-616-99 (1-2436)
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                                                                                                                                                                                            Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-616-99
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Publication No
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6 AlalleAsnSerGlnAsnGlnLysProlleLysArgLeuGlyLeuIlePheGlyVallle 25
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Matches:
Conservative:
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RESULT: 27
US-10-175-737-309
Sequence 309, Application US/10175737
Publication No. US20030013153A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
                                                                                                                                                                                                                                                            1485
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                                                                                                                                                                       CCAACTCTGAGTCTAGCACAGTGTCCAGTGGGATC 1579
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TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P343BRIC50
CURRENT APPLICATION NUMBER: US/10/175,737
CURRENT FILING DATE: 2002-06-19
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 309
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TYPE: DNA
ORGANISM: Homo
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  hrGluAlaProPheAlaThrGlySerSerGlyValMetGlnPheArgTyrProValGlyA 206
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                                          TGACTCCA-----GCACAACCTCCAGTGGGGCCGGCACCACCACCAACTCTGAGTCCAG 1245
                                                                                  roThrProProValValGlnGlnPro---AlaProValAlaProProVal------T 186.
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Watanabe, Colin K.
Wood, William I.
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Goddard, Audrey
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US-10-063-502-99
j. Sequence 99, Application US/10063502
j. Publication No. US20030023042A1
j. Publication No. US20030023042A1
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; ORGANISM: Homo Sapien
US-10-063-502-99
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CURRENT FILING DATE: 2002-05-01
Prior Application removed - See File Wrapy
NUMBER OF SEQ ID NOS: 170
SEQ ID NO 99
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APPLICANT: Filvar
APPLICANT: Gerrit
APPLICANT: Goddar
APPLICANT: Goddows
APPLICANT: Grimal
APPLICANT: Grimal
APPLICANT: Gurimal
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Goddard, Audrey
Godowski, Paul J.
Grimaldi, Christopher J
Gurney, Austin L.
Watanabe, Colin K.
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                                                                    ThrThrCysIleLeuAlaGlyCysAlaSerLysProThrTyrAsnSerThrSerGlySer 45
                                                                                                           AlaIleAsnSerGlnAsnGlnLysProIleLysArgLeuGlyLeuIlePheGlyValIle
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                                                 Sequence 309, Application Us
Publication No. US2003002223
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Goddwski, Paul (
APPLICANT: Godwski, Paul (
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                                                                                                                                                                                                                                                                                                                                                                                                                           GCACAACCTCCAGTGGGGTCAGCACAGCCACCAACTCTGAGTCCAGCACAACCTCCAGTG
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                                                     Desnoyers, Luc
Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
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    Smith, Victoria
Watanabe, Colin
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; LENGTH: 2436
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CURRENT FILING DATE: 2002-06-17
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                                                                       CACAGTGTCCAGTGGGATCAGCACAGTCACCAATTCTGAGTCCAGCACCACCCTCC-AGTG 1304
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                                                                                                          hrGluAlaProPheAlaThrGlySerSerGlyValMetGlnPheArgTyrProValGlyA 206
                                                                                                                                                TGACTCCA-----GCACAACCTCCAGTGGGGCCGGCACAGCCACCAACTCTGAGTCCAG 1245
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TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P9430R1C45
CURRENT APPLICATION NUMBER: US/10/175,738
CURRENT FILING DATE: 2002-06-19
Prior application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 309
LENGTH: 2436
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Homo
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66 SerGlnGlyValProAsnArgTyrGln---
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Godowski, Paul J.
Gurney, Austin L.
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RESULT 31
US-10-175-752-309
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T: Zhang, Zemin
INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES
INVENTION: ACIDS ENCODING THE SAME
ERENCE: P3430R1C60
                                                                  Pan, James
Smith, Victoria
Watanabe, Colin K.
Wood, William I.
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Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
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CURRENT FILTM DATE: 2002-06-19
Prior Application removed - See File Wrapp
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 309
LENGTH: 2436
TYPE: DNA
ORGANIZM: Homo Sapien
US-10-175-752-309
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US-10-176-482-309
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LENGTH: 2436
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CURRENT FILING DATE: 2002-06-20
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Watanabe, Colin K.
Wood, William I.
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FILE REFERENCE: P3430NIC86
CURRENT APPLICATION NUMBER: US/10/176,757
CURRENT FILING DATE: 2002-06-20
Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 612
SEQ ID NO 309
                                                                                                                                                                                                                                                                                                                                                                                Sequence 309, Application US/10176757 Publication No. US20030022297A1
                                                                                                                                                                                                                                                                                                                                                                   GENERAL
                                                                                                               APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
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Watanabe, Colin K.
Wood, William I.
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US-10-176-913-309
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CURRENT FILING DATE: 2002-06-20
Prior Application removed - See file Wrapper
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 309
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TYPE: DNA
ORGANISM: Homo Sapien
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Gurney, Austin L.
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; Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 612 ; SEQ ID NO 309 ; LENGTH: 2436 ; TYPE: DNA ORGANISM: Homo Sapien US-10-180-552-309
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US-10-180-552-309
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: 99430R1C153
CURRENT APPLICATION NUMBER: US/10/180,552
CURRENT FILING DATE: 2002-06-25
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                                                                                GCACAACCTCCAGTGGGGTCAGCACAGCCACCAACTCTGAGTCCAGCACAACCTCCAGTG
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GGGCTAGCACAGCCAACTCTGACTCCAGCACAACCTCCAGTGAGGCCAGCACAGCCA 154
                                                                                                                                                                                                         hrValIleGlnAlaAspHisAsnMetAspGlyAlaSerIleValIleGlnHis-----
                                                                                                                                                                                                                                                                                              erAsnGlyMetTrpPheSerGlyArgAspGlyAspLeuIleAsnAlaSerAsnAlaGlyT 246
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                                                                                                                                                                 CCAACTCTGAGTCCAGCACAGTGTCCAGTGGGGCCAGCACTGCCACCCAACTCTGAGTCCA 142
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                                   lyAspThrValArgThrGlyGlnArgIleAlaSerMetLysAsnGlnProSerGlyAlaA 302
                                                                                                                         ----ThrAsnGlyPheValSerSerTyrIleHisIleLysAspAlaGlnValLysThrG
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; ORGANISM: Homo Sapien
US-10-180-557-309
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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430RLC147
CURRENT EPILICATION NUMBER: US/10/180,557
CURRENT FILING DATE: 2002-06-25
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 309
LENGTH: 2436
TYPE: NUMBER: NO 309
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nThrAla-HisThrProSerProValAlaValGlnSerSerArgProProVal-----G
                                   CTCCAGTGGGGCCAGCACAGCCACCCAACTCTGACTCCAGCACAGTGTCCAGTGGGGCCAG
                                                                                                       TGAGTCCAGAACGACCTCCAATGGGGCTGGCACAGCCACCAACTCTGAGTCCAGCACGAC 102
                                                                                                                                                                             CACTGCCACCAACTCTGAGTCCAGCACAACCTCCAGTGGGGCCAGCACAGCCACCAACTC 966
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Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
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Watanabe, Colin K.
Wood, William I.
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5. US20030022301A1
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Prior Application removed - See File Wrapper NUMBER OF SEQ ID NOS: 612
SEQ ID NO 309
LENGTH: 2436
TYPE: DNA
ORGANISM: Homo Sapien
US-10-173-700-309
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US-10-173-700-309
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Publication No. US20030027262A1
                                                                                                                                                                                                                                                                         APPLICANT: Zhang,Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C14
                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/173,700
CURRENT FILING DATE: 2002-06-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Baker, Kevin P.
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Godowski, Paul J.
Gurney, Austin L.
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                      CCAACTCTGAGTCTAGCACAGTGTCCAGTGGGATC 1579
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                                                          laLeuPheGluPheArgIleSerArgAsnGlyVal 313
                                                                                                GGGCTAGCACAGCCACCAACTCTGACTCCAGCACAACCTCCAGTGAGGCCAGCACAGCCA
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CURRENT FILING DATE: 2002-06-18
Prior Application removed - See File Wrapper NUMBER OF SEQ ID NOS: 612
SEQ ID NO 309
LENGTH: 2436
TYPE: DNA
ORGANISM: Homo Saplen
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APPLICANT: Baker, Kevin P.
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lnGlnHisProAlaValGlnLysProThrProProValValValUysLysProThrP 170
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Goddard, Audrey
Godowski, Paul
                                                            CACTGCCACCAACTCTGAGTCCA-------GCACGACCTCCAGTGGGGCCCAG 1131
                                                                                              nThrAla-HisThrProSerProValAlaValGlnSerSerArgProProVal-----G
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LENGTH: 2436
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GENERAL INFORMATION
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APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
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Watanabe, Colin K.
Wood, William I.
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RESULT 40
US-10-174-582-309
US-10-174-582-309
; Sequence 309, Application US/10174582
; Publication No. US20030027265A1
; GENERAL INFORMATION:
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; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-174-582-309
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CURRENT APPLICATION NUMBER: US/10/174,582
CURRENT FILING DATE: 2002-06-18
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TGACTCCA-----GCACAACCTCCAGTGGGGCCGGCACAGCCACCAACTCTGAGTCCAG 1245
                                                                    CACAGCCACCAACTCTGAGTCCAGCACGACCTCCAGTGGGGCCTAGCACCACCAACTC 1191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AlaIleAsnSerGlnAsnGlnLysProIleLysArgLeuGlyLeuIlePheGlyValIle
                               roThrProProValValGlnGlnPro---AlaProValAlaProProVal------- 186
                                                                                                    lnGlnHisProAlaValGlnLysProThrProProValValValValLysLysProThrP 170
                                                                                                                                       CACTGCCACCAACTCTGAGTCCA-------GCACGACCTCCAGTGGGGCCAG 113:
                                                                                                                                                                          nThrAla-HisThrProSerProValAlaValGlnSerSerArgProProVal-----G
                                                                                                                                                                                                               CTCCAGTGGGGCCAGCACCACCAACTCTGACTCCAGCACAGTGTCCAGTGGGGCCAG
                                                                                                                                                                                                                                             uTrpSerGlyAspLeuLysValArg------GluArgSerIleSerSerGlyValAs 132
                                                                                                                                                                                                                                                                                  TGAGTCCAGAACGACCTCCAATGGGGCTGGCACAGCCAACTCTGAGTCCAGCACGAC 1026
                                                                                                                                                                                                                                                                                                                   -----IleAsnAsnLeu-AsnSerSerTyrThrIleTyrThrGlyGlnTrpLeuThrLe 115
                                                                                                                                                                                                                                                                                                                                                                                                                             TCCAGTGGGGCCAG-CACAGCCACCAACTCTGAGTCCAGCACAGTGTCCAGTAGGGCCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                laThrAsnProValValArgArgPheGlyThrAlaThrValAlaGlySerThrValThrS
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                                   laLeuPheGluPheArgIleSerArgAsnGlyVal 313
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Search completed: July 4, 2003, 00:39:18
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Copyright
GenCore version 5.1.6 (c) 1993 - 2003 Compugen Ltd.
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Minimum
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-MODEL-frame+ p2n.model -DEV=xlh
-MODEL-frame+ p2n.model -DEV=xlh
-Q-/Ggn2 1/USPTO_spool/US10018706/runat_30062003_091105_23805/app_query.fasta_1.519
-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS-blits -START=1 -END=-1 -MAXRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DCCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=40 -mODE=LOCAL
-OUTFMT=pto -NORM-ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER-US10018706_@CGN_1 1_1456_@runat_30062003_091105_23805_NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -MAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -LOAPEXT=0.5 -FGAPOP=6
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ALIGNMENTS

REFERENCE AUTHORS		ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION		DEFINITION	LOCUS	BF866446/c	RESULT 1
<pre>1 (bases 1 to 784) Grossman,A., Davies,J., Federspiel,N., Harris,E., Hauser,C., Lefebvre,P., McDermott,J.P., Shrager,J., Silflow,C. and Stern,D.</pre>	Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales; Chlamydomonadaceae; Chlamydomonas.	Chlamydomonas reinhardtii	Chlamydomonas reinhardtii.	EST.	BF866446.1 GI:12256590	BF866446	, Lambda Zap II Chlamydomonas reinhardtii cDNA, mRNA sequence.	963069A11.x1 C. reinhardtii CC-1690, Stress condition I, normalized	BF866446 784 bp mRNA linear EST 19-JAN-2001		

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JOURNAL COMMENT
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DCMB Box 9100
Duke University
Durham, NC 27708-1000
Tel: 919 613 8159
Fax: 919 613 8177
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ATRATCACCTGACGGACTTGCATTCCTTGAGCTGGCGGTTAGGCGAAAGGATACTATA 536
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       Pro---
                                                                                                                             ProProValValValVaLysLysProThrProThrProProValValGlnGlnProAla 179
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XhoI; This library, constructed by John Davies and Jeffrey
McDermott, combines cDNAs from CC-1690 cells grown to
McDermott, combines cDNAs from CC-1690 cells grown to
mid-log phase in TAP-N (30 min, lhr, 4hr), TAP-S (30 min,
mid-log phase in TAP-P (30 min, lhr, 4hr), TAP-S (30 min,
lhr, 4hr) and NH4 to NO3 (30 min, lhr, 4hr), PolyA mRNA was
/hr) and NH4 to NO3 (30 min, lhr, 4hr). PolyA mRNA was
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Direct Submission
Submitted (16-FEB-2000) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (B-mail : seqrefægenoscope.cns.fr)
- Web : www.genoscope.cns.fr)
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Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
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/organism="Anopheles
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High quality sequence start: 30
High quality sequence stop: 4784
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Fax: 33 1 34 65 25 21
Email: sorokine@jouy.inra.fr
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Lactococcus lactis subsp. cremoris
Bacteria; Firmicutes; Lactobacillales;
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                                                                                           quality sequence start: 30 quality sequence stop: 478
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/organism="Lactococcus lactis subsp. cremoris"
/strain="MG153"
/db xref="taxon:1159"
/clone_lib="MG1363 Random Sequence Tag Library"
                                                                               Location/Qualifiers
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    rVal---
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                                  TTCTTCTAACTCAAATGCCTCAATTCAT------AAGGTCGTTAAAGGAGATAC
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Contact: Lim, C.O.
Contact: Lim, C.O.
Plant Molecular Biology & Biotechnology Research Centre
Gyeongsang National University
#900 Gazwa-dong, Jinju 660-701, Korea
Tel: 82 55 751 625
Fax: 82 55 759 9363
Email: colimonongae.gsmu.ac.kr
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Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicot;
Spermatophyta; Magnoliophyta; eudicotyledons; Brassica.
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B3832 Chinese cabbage etiolated seedling library Brassica rapa
subsp. pekinensis cDNA clone E3832, mRNA sequence.
BQ791034 GI:22005996
EST.
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Ryu.S.H., Yang, K.A., Lee, S.Y., Kim, H.-I., Cho, M.J. and Lim, C.O.
Expressed Sequence Tags of Chinese Cabbage Etiolated Seedling cDNA
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                                                      AlaThrAsnProValVal·211
                                                                                                                         ---GlualaprophealaThrGlySerSerGlyValMetGlnPheArgTyrproValGly 205
                                                                                                                                                                              ProThrProThrProProValValGlnGlnProAlaProValAlaProProValThr--- 186
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/cultivar="Jangwon"
/db_xref="taxon:51351"
/clone="m3832"
/clone="m3832"
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/tissue_type="Etiolated seedling"
/lab_host="XL-1 Blue"
/note="Vsctor: pspRRT 1; Site_1: Sal I; Site_2: Not I"
209 c 50 g 49 t
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155 alGlnLysProThrFroProValValValValLysLysProThrPro 170	 711 GGGGGACTGGGTCAACAGTCTGCTGAAAGGTACGGTAGGGGGTAGCTTTGTCGCCAGCGC 652	146 rgProPro141GlnGlnHisProAlaV 155	1 TGAAACGCGTACCTACGATCGCACTGCCAACGGTTTTAAAATGAGCAGTGAAATGCAGCA 71	130 yValAsnThrAlaHisThrProSer-ProValAlaValGlnSerSerA 146	110 yGlnTrpLeuThrLeuTrpSerGlyAspLeuLysValArgGluArgSerIleSerSerGl 130	882 ACTTGCCGCTTCTGATAAGGGACTGCGCAATCTGAAAATTGGCCCAACAGCTT 831	leAsnAsnLeuAsnSerSerTyrThrI	942 AGGCGATACGTTAAGCAGCATTCTGAATCAGTACGGCATCGATATGAGCGATATTAGCCG 883	77 nGlyAspThrValSerLysIleAlaGlnArgTyrGlyLeuAsnTrpArgGluIleGlyHi 97	9 TGAGCTGGACGATAAAACCGCAGGCGAAGTCGGCGTCCATGAATACGTCGTCTCCA	rAspSerGlnGlyValProAsnArgTyrGlnValLysGl	42 ThrSerGlySerGlySerHisArgThrSerGlySerGly-GlyLeuA	706-2 (1-322) x AF094939 (1-1096)	: Scores: 0.0998	/note="Vector: Lambda DASH II; sequenced using Li-Cosequencer" 239 a 323 c 272 g 262 t	/organism="Salmonella typhimurium" /strain="LT2" /db_xref="taxon:602" /clone="226-T3" /clone_1ib="Salmonella typhimurium LT2, Lambda DASH	CTORR: RII	Notecular Blology Sidney Kimmel Cancer Center 3099 Science Park Road, San Diego, CA 92121, USA Email: mcclelland@lifsci.sdsu.edu	Unpublished (1999) Contact: McClelland M	1 (bases 1 to 1096) 1 (bases 1 to 1096) Wong,R.M.Y. and McClelland,M. End Sequences of Salmonella typhimurium LT2 Lambda DASHII Clones,		AF094939 AF094939.1 GI:4322781	

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RESULT 6
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                                                                                                                                                                                       Brassica rapa subsp. pekinensis.
Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Busasica rapa subsp. pekinensis
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Bukaryota, Viridiplantae, eudicotyledons; core eudicots;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
                            Gyeongsang National University
#900 Gazwa-dong, Jinju 660-701, Korea
Tel: 82 55 751 6555
Fax: 82 55 759 9363
                                                                                  Contact: Lim, C.O.
Plant Molecular Biology & Biotechnology
                                                                                                                 Ryu,S.H., Kang,J.S., Kang,C.-h., Kim,C.Y., Bahk,J.D., Lee,S.Y., Cho,M.J. and Lim,C.O. Expressed Sequence Tags of Chinese Cabbage Unpublished (2001)
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GAAAGAGGCCGGTTTAACCAGCAGCGAAATCAGCGCAGTGATAAAAGCCATGCAGTGGCA
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                                                                                                                                                                         (bases 1 to 596)
primer:
          colim@nongae.gsnu.ac.kr
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US-10-018-706-2 (1-322) x BG543924 (1-596)
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                                                                                                                                                                                                                                                  Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1306 bp
AGENCOURT 6626294 NIH MGC_115 Homo
5', mRNA sequence.
                                                                                                                                     found through the I.M.A.G.E. Consonttp://image.11n1.gov
Plate: LLAM12787 row: p column:
High quality sequence start: 90
High quality sequence stop: 471.
                                                                                                                                                                                                                                                                                                                                                                                                                     NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACGCCACCGACACCAACCCCTCCTGTCGTAACACCTCCAACACCACCGGTCGTAACG---
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5752955"
/clone_lib="NIH_MGC_115"
                                                                                                                  location/Qualifiers
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/clone="B1673"
/clone | type="Etiolated seedling"
/tissue type="Etiolated seedling"
/lab_host="XL-1 Blue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           db_xref="taxon:51351"
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sapiens cDNA clone IMAGE:5752955
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:

0.158 131.00 39.60% 26.73% 7.84% .84%

BASE COUNT ORIGIN

US-10-018-706-2 (1-322) x BM921488

(1-1306)

147

42

61

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BO791640 398 bp mRNA linear EST 30 EO791640 ilnear EST 30 E3323 Chinese cabbage etiolated seedling library Brassica subsp. pekinensis cDNA clone E3323, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                               oValAlaProProValThrGluAlaProPheAlaThrGlySerSerGlyValMetGlnPh
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                                                                                                                                                                                                                                                                                        eArgTyrProVal-----GlyAlaThrAsnProValValArgArgPheGlyThrAlaTh 218
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/note="Organ: pooled brain, lung, testis; Vector:
/note="Organ: pooled brain, lung, testis; Vector:
pCWV-SPORT6; Site 1: Not1; Site 2: EcoRV (destroyed); RNA
source anonymous pool of 6 male brains, age range 23-27; 1
male lung, age 27; and I male testis, age 69. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021, Note: this is a NIH MGC Library."
a 213 t 2 others
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CNS03DYV/c
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BQ791640.1
EST.
ALC39728.1 GI:7898863
GSS; genome survey sequence.
Tetraodon nigroviridis.
Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Lim, C.O.
Plant Molecular Biology & Biotechnology
Gyeongsang National University
#900 Gazwa-dong, Jinju 660-701, Korea
Tel: 82 55 751 6255
Fax: 82 55 759 9363
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Brassica rapa subsp. pekinensis.
Brassica rapa subsp. pekinensis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; eudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
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Ryu.S.H., Yang, K.A., Lee, S.Y., Kim, H.-I., Cho, M.J. and Lim, C.O.
Expressed Sequence Tags of Chinese Cabbage Etiolated Seedling of Chinese Cabbage Etiolated Seedling of Chinese Cabbage Etiolated Seedling
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Brassica rapa subsp. pekinensis"
/cultivar="Jangwon"
/db xref="taxon:51351"
/clone="mg323"
/clone="mg323"
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/tissue_type="Etiolated seedling"
/lab host="XI-1 Blue"
/note="Vector: pspRRT 1; Site_1: Sal I; Site_2: Not I"
165 c 67 g 61 t
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This sequence is a single read and was generated as scale clone-end sequencing project of the Tetraodon genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bernot, A., Fizames, C., Wincker, P., Brottier Saurin, W. and Weisenbach, J.
Human gene number estimate provided by geno Tetraodon nigrouserising.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tetraodon nigroviridis DNA sequence Unpublished
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Roest-Crollius, H., Jaillon, O.,
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                                                                                                                                                                                                                                                                                                                                         TIGACCCTCTGCAGCGTCTCCGGCTGCAGGCGGAAGCTGGCAGCATCTGAGGCAGCGTCC 706
                                                                                                                                                         AsnAsnLeuAsnSerSerTyrThrIleTyrThrGlyGlnTrpLeuThrLeuTrpSerGly
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                                                                                                                                                                                                                                                                                                                Ser-----GlySerHisArgThrSerGlySerGlyGlyLeuAlaIleGlySerGlnVal 62
                                                                                                     AspLeuLysValArgGluArgSerIleSerSerGlyValAsnThrAlaHisThrProSer
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                         CCGTGGGGCTGTCAGTCCCCCAGTCCCCAGTCCCCAGTCCCCAGTCCTCCCCAGT
                                                   ProValAlaValGlnSerSerArgProProValGlnGlnHisProAlaVal------
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/clone_lib="G"
/note="Genoscope sequence
/note="Genoscope sequence
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|db_xref="taxon:99883"
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GlnLysProThrProProValValValLysLys 167
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Contact: Singh, J.A.
Eastern Cereal and Oilseed Research Centre
Agriculture and Agri-food Canada
KW Neatby Bldg., Central Experimental Farm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Singh, J., Allard, G., Tinker, N., Robert, L., Lacroix, C., De Moors, Chagnon, J., Farah, S., Couroux, P. and Hattori, J.

Expressed Sequence Tags from constitutively frost tolerant
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Bn01_AAFC ECORC_transgenic_Brassica_napus_overexpressing_BNCBF17.
nstitutively_frost_tolerant_Brassica_napus_cDNA_clone_Bn01_03006.
mRNA_sequence.
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BQ704548.1 GI:21843967
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (613) 759-1662
(613) 759-1701
l: singhja@em.agr.ca
                                                                                                                                                                                                    /tissue_type="fourth leaf"
/dev.stage="3 weeks seedling grown at room temperature"
/note="Vector: Bluescript SK+/XhoI-EcoRI; Site 1: EcoRI,
Site 2: XhoI; Germinated in soil flats and seedlings gro
for 3 weeks in a Conviron E-15 cabinet set at 200C /16 l
light (250 Em-2sec-1) and 16 oC / 8 hr dark. Fourth leav
collected at 9 am and immediately frozen."
203 c 124 g 168 t 7 others
                                                                                                                                                                                                                                                                                                                                                                                    /clone="Bn01_03006"
/clone_lib="Bn01_AAFC_ECORC_transgenic_Brassica_napus_overexpressing_BNCBF17_constitutively_frost_tolerant"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Brassica napus"
cultivar="Westar"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                db_xref="taxon:3708"
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eudicots;
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                    131 ValAsnThrAlaHisThrProSerProValAlaValGlnSerSerArgProProValGln 150
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Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AV520U24 Arabidopsis thaliana aboveground organs two to six-week old Arabidopsis thaliana clone APZ04g09F 3', mRNA sequence. AV520024
                                                                                                                                                                                                                                                                                                                                                                                                                       The First Laboratory for Plant Kazusa DNA Research Institute Yana 1532-3, Kisarazu, Chiba i Email: asamizu@kazusa.or.jp, U Email: asamizu@kazusa.or.jp, U Location/Qualifiers 1.628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 628)
Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.
A large scale analysis of cDNA in Arabidopsis thaliana: Generation of 12,028 non-redundant expressed sequence tags from normalized and size-selected cDNA libraries
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                                                                                                                                                                                                                                                        /tissue_type="aboveground organs"
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XhoI"
                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:3702"
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six-week old"
                                                                                                                                                                                                                                                                                                                                                                                       organism="Arabidopsis thaliana"
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AGENCOURT_6613368 NIH_MGC_98
5', mRNA sequence.
BM911051
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Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLCM1951 row: c column: 03
High quality sequence stop: 259.
Location/Qualifiers
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="IMAGE:545034"
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/note: potB7; Site_1
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/db_xref="taxon:9606"
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EST492606 CSTS
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Contact: Cathy Ronning
The Institute for Genomic Research
For clone info: please contact Research Genetics,
Division tel 1-800-711-6195, email cdna@resgen.com
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1 (bases 1 to 666)
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Bougri,O., Buell,C.R., Ronning,C., Tanksley,S. and
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                                                                                                  /clone="cSTS5N16"
/clone lib="cSTS"
/tissue_type="sprouting e
/dev stage="12-14 weeks p
/lab_host="SOLR"
/note-"Vector: pBluescript SK(-); Site 1: EcoRI; Site 2: XhoI; Various sizes of sprouting eyes (7mm to 15mm) were taken from tubers. The tubers were incubated at 26C in the dark for 2-3 weeks prior to sprouting. The eyes were
                                                                                                                                                                                                                             organism="Solanum tuberosum"
|cultivar="Kennebec"
|db_xref="taxon:4113"
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analyses mixed potato tissues
                                                                      Buell, C.R., Hart, A., Baker, B., Restrepo, S., Griffiths, H., van Karamycheva, S.A.
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RESULT 15
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The Institute for Genomic Research
9712 Medical Center Dr. Rockville, MD 20850,
Email: potato@tigro.org
This clone is available through the Pessarch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: potato@tigr.org
This clone is available through the Research Genetics, contact the Research Genetics for further information 1-800-711-6195 or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LeuTrpSerGlyAspLeuLysValArgGluArgSerIleSerSerGlyValAsn-----
                                                     TCTGGGTGCTCCGTC---
                                                                                      AspGlyAlaSerIleValIleGlnHisThrAsnGlyPheValSerSerTyrIle
                                                                                                                                                                                                       AspGlyAspLeuIleAsnAlaSerAsnAlaGlyThrValIleGlnAlaAspHisAsnMet
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/cultivar="Kennebec or Binjte"
/db_xref="taxon:4113"
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AUTHORS
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Pred. No.:
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Unpublished (2000)
Contact: Charles Hauser
DCMB Box 91000
Duke University
Durham, NC 27708-1000
Tel: 919 613 8179
Fax: 919 613 8179
Email: chauser@duke.edu.
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Bukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.

1 (bases 1 to 839)
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963001C10.y3 C. reinhard
, Lambda Zap II Chlamydd
BF859163
BF859163.1 GI:12249254
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                                               SerTyrThrIleTyrThrGlyGlnTrpLeuThrLeuTrpSerGlyAspLeuLysValArg
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                                                                                                                                                 {\tt IleAlaGlnArgTyrGlyLeuAsnTrpArgGluIleGlyHisIleAsnAsnLeuAsnSer}
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C. reinhardtii CC-1690, Stress condition I, normalized
II Chlamydomonas reinhardtii cDNA, mRNA sequence.
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AUTHORS
TITLE
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BH705150/c
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                                                                                                                       US-10-018-706-2 (1-322) x BH705150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cdtown@tigr.org
DNA is from a doubled haploid
Seq primer: TF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 285)
Town, C.D., Van Aken, S., Utterback, T. and Fraser, C.M.
Whole genome shotgun sequencing of Brassica oleracea
Unpublished (2001)
Other_GSSs: BOMKT37TR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
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Brassica oleracea
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BOMKT37TF BO_2_3_KB
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Class: sheared ends.
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                    GlnLysProThr-----ProProValValValLysLysProThrProThrProPro
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ACGCCACCAACACCAGCCCCACCTGTTGTAACGCCACCAACACCAACACCAACACCACCG
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                                                                                                                                                                                                                                                                                          /clone_lib="BO_2_3 KB"
//clone_TVector: pHOS1; Site_1: BstXI; 2-3 kb sheared
/note="Vector: pHOS1; Site_1: BstXI 2-3 kb sheared
genomic DNA inserted into pHOS1 using BstXI linkers"
1 26 c 143 g 89 t
                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:3712"
/clone="BOMKT37"
                                                                                                                                                                                                                                                                                                                                                                                   organism="Brassica oleracea"
/strain="TO1000DH3"
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124.00
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Brassica
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BOMKT37,
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AZ187441
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seq primer: SP6
Class: BAC ends
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California Institute of Technology
Pasadena California 91125, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strongylocentrotus purpuratus
Eukaryota; Metazoa; Echinodermata; Eleutherozoa;
Echinoidea; Euchinoidea; Echinacea; Echinoida;
Strongylocentrotidae; Strongylocentrotus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: acameron@caltech.edu
Plate: 1009 row: G column
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Fax: (626) 793-3047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20402566
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GlyAspLeuLysValArgGluArgSerIleSerSerGlyValAsn-ThrAlaHisThrPr
                                                                                          IleAsnAsnLeuAsnSerSerTyrThrIleTyrThrGlyGlnTrpLeuThrLeuTrpSer
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                                                                                                                                                                                                                                                                                                                                                                                   /organism="Strongylocentrotus purpuratus"
/db_xref="taxon:7668"
/clone="plate=1009 Col=18 Row=G"
/clone=!ib="Strongylocentrotus purpuratus,
urchin, sperm genomic BAC library"
/note="Organ: sperm; Vector: BACe3.6; BAC CDH10B"
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BM913728
LOCUS
DEFINITION
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                                                                            Percent Similarity:
Best Local Similarity:
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                                       US-10-018-706-2 (1-322) x BM913728
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  21 IlePheGlyValIleThrThrCysIleLeuAlaGlyCysAlaSerLysProThrTyrAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D.
Email: cgapbs r@mail.nih.gov
Tissue Procurement: ATCC

CDNA Library Preparation: Rubin Laboratory

CDNA Library Preparation: Rubin Laboratory

CDNA Sequencing by: Agenocurt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
Plate: LLCM1995 row: g column: 24

High quality sequence stop: 398.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1252)
11 (hases 1 to 1252)
12 (hational Institutes of Health, Mammalian Gene Collection (MGC)
13 (1999)
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                                                                                                                                                                                                                                                              218
                                                                                                                                                                                                                                                    /clone="IMAGE:5477423"
/clone lib="NIH McG298"
/clone lib="NIH McG98"
/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: brain; Vector: pOTB7; Site 1: XhoI; Site_2: CORI, CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5; adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH MGC Library."

18 a 568 c 230 g 235 t 1 others
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                                                         Suaeda maritima subsp. salsa.

Suaeda maritima subsp. salsa.

Suaeda maritima subsp. salsa.

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Spermatophylidae; Caryophyllales; Chenopodiaceae; Suaeda.

Tel: (Bases 1 to 538)

Expressed sequence tags from a halophyte Suaeda salsa cDNA library

Lupublished (2000)

Contact: Hui Zhang

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The Biology Department of Shandong Normal University

No.88, Wenhua East Road, Jinan, Shandong province, 250014, PRC

Tel: (86)531-296084

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         zhangh@sdnu.edu.cn.
  Location/Qualifiers
  1. .538
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                                                                                                          1 (bases 1 to 1002)
Roest-Crollus, H., Jaillon, O., Dasilva, C., Bou
Bernot, A., Fizames, C., Wincker, P., Brottier, P.
Saurin, W. and Weissenbach, J.
Human gene number estimate provided by genome
Tetraodon nigroviridis DNA sequence
                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthopterygii; Percomorpha; Tetraodontiformes;
                                                                                                                                                                                                                                                                                   GSS; genome survey sequence. Tetraodon nigroviridis.
Charaterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
                                  Bouneau, L., Billault, A., Weissenbach, J.
                                                               2 (bases 1 to 1002)
Roest-Crollius, H., J
                                                                                                                                                                                                                                                                       Tetraodon nigrovirid:
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library G from Tetraodon nigroviridis, genom
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                                             on,O., Dasilva,C., Fizar
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                                                  Bernot,
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COUNT

REFERENCE AUTHORS

JOURNAL REFERENCE AUTHORS

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RESULT 20 CNS01SZG LOCUS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (12-APR-2000)
This sequence is a single read and was generated as scale clone-end sequencing project of the Tetraodon genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genoscope
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                                                                                                                                                                                                                                                                      SerGlyArgAspGlyAspLeuIleAsnAla-----SerAsnAlaGlyThrValIle
                                                                                                                                                                                                                                                                                                            AAATWAGGCCACAGCCTCACCCTTGCCGGCAGC-----GGTGGGGGGCATTGGGAGC 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --- AGACCCAAACCTCCATCGCGCCCTTGCCAACCTGCCCGCAGCTTTGTACGCAACAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GlnGlnProAlaProValAlaProProValThrGluAla---ProPheAla-----Thr 192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AATTACACCACATACGAGGATCAT-----ACGGTGTGGGATTTGGACTACTTTGAGAGA
                                    LysThrGlyAspThrValArgThrGlyGlnArgIleAlaSerMetLysAsnGlnProSer 299
                                                                                                            IleGlnHis---ThrAsnGlyPheValSerSerTyrIleHisIleLysAspAlaGlnVal
                                                                                                                                                     ATTGGGAGAAGTGCAACTCTTGGTCGTACTACGTTCAACAGCAGCMAGGGCCAGAMCAGT
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/db_xref="taxon:99883"
/clone="170H14"
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/note="Genoscope sequence
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BJ220947 Y. Ogihara unpublished cDNA library, Wh Triticum aestivum
cDNA clone wh22h09 3', mRNA sequence.
BJ220947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Tadasu Shin-i
Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6855
Feax: 81-559-81-6855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Expressed genes in Unpublished (2002)
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Triticem.
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Ogihara, Y. and Murai, K.
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                                                                                                                        GlyValProAsnArgTyrGlnValLysGlnGlyAspThrValSerLysIleAlaGlnArg 87
TyrThrGlyGlnTrpLeuThrLeuTrpSerGlyAspLeuLysValArgGluArgSerIle ::::::
                                                      ATGGGGCTC:
                                                                                     TyrGlyLeuAsnTrpArgGluIleGlyHisIleAsnAsnLeuAsnSerSerTyrThrIle 107
                                                                                                                                                                                                                                                                                                                                                                                             160
                                                                                                                                                                                                                                                                                                                                                                                   /clone lib="". Ogihara unpublished cDNA library, wh"
/clone lib="". Ogihara unpublished cDNA library, wh"
/tissue typee "spike at meiosis"
/dev_stage="peekes' scale 9"
/dev_stage="leekes' scale 9"
/note="Vector: Lambda Uni-ZAP XR, excised phagemid;
Site_1: EcoRI; Site_2: XhoI; Plants were grown under hydroponic conditions at UC Davis, salt stressed for 12 hours, and for 7 days, then dissected and frozen (Akhunov in J Dvorak Lab). Total RNA was prepared from sheath tissue, equal quantities of RNA were pooled RNA, a cDNA inbrary was made, and the cDNA clones were in vivo excised to give psluescript phagemids in the TJ Close lab at the University of California, Riverside (Akhunov, Chin Choi, Close, Fenton, Kianian, Otto, Simons, Zhang).
Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Triticum aestivum"
/cultivar="Chinese Spring"
/cultivar="thinese Spring"
/chone="wh22h09"
/clone="wh22h09"
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                                                                                                                                                                                                                                                                                                                                                                            Dictyostelium discoideum.

Dictyostelium discoideum

Bukaryota, Mycetozoa, Dictyosteliida; Dictyostelium.

1 (bases 1 to 500)

Trushihara, H., Morio, T., Saito, T., Koriki, E., Ochiai, H.,

Takeuchi, I., Kohara, Y. and Tanaka, Y.

Population analysis of cDNAs from unicellular and multice stages of Dictyostelium discoideum

Unpublished (2002)

Contact: Hideko Urushihara

Contact: Hideko Urushihara
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                                                                                                                                                                                                                                                                                                                             University of Tsukuba
1-1-1 Tennoudai, Tsuk
                                                                                                                                                                                                                                                                                           Tel: 81-298-53-4664 Fax: 81-298-53-6614
                                                                                                                                                                                                                                                                                                                                                            institute of Biological Sciences
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                                                                                             212
                                                                                                                                                                                                                                                                          hideko@biol
                                                                                           /organism="Dictyostelium
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                                                                                                                                                                                                                                               Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                               2 (bases 1 to 722)
Fujiyama, A., Hattori, M., Toyoda, A., 'Totoki, Y., Watanabe, H. and Sakaki, Y. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fujiyama,A., Hattori,M., Toyoda,A., Totoki,Y., Watanabe,H. and Sakaki,Y. BAC end sequences of Library PTB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pan troglodytes DNA, clone: AG130154
AG130154.1 GI:16659319
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pan troglodytes
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                                                                                                                                                                                Sequencing: M13Rev
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GlyValMetGlnPheArgTyrProValGlyAlaThrAsnProValValArgArgPheGly 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ThrAlaHisThrProSerProValAlaVal-------GlnSerSer 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   troglodytes male lymphoblast DNA, Library clone:PTB-141N09.R.
                                                                                                                           R.Site 1
R.Site 2
                                                                                                                                                                                                                                  tracking errors.
                                 organism="Pan troglodytes"
/db_xref="taxon:9598"
/clone="PTB-141N09.R"
                                                                                                        Location/Qualifiers
cell_type="lymphoblast"
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36.61%
7.34%
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    bp DNA
    PTB-141N09.R,
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REFERENCE
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AG054509
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                357
                                                                                                                                                                                           Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp/, URL:hhttp://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170

Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                     Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                              BAC end sequences of Library PTB Unpublished
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GSS.
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                                                                                                                                                                              clone tracking errors.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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                                                                                                                           Sequencing: -21M13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CACACCACCCGCCACGACTGTCGATGCGCCACCAACACCCCCCA-----CCGCACCCG
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                                                                         R.Site 1
R.Site 2
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397 c 89 g 65 t 5 others
                                                    Location/Qualifiers
organism="Pan troglodytes"
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PTB-040D10.F,
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survey sequence. GSS 02-NOV-2001

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168 251 153

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ORIGIN
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                                                                                                                                                                                                                                                                                   710 AATGACAGGTCGANGGACCGCGGTGGTTCGCGA---CGCCGGTCGCGGACTCCCTCGCAC 766
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36 LysProThrTyrAsnSerThrSerGlySerGlySerHisArgThrSerGlySerGlyGly 55
                                                                                                                                              AlaGlyThrvalIleGlnAla--------AspHisAsnMetAspGly 256
                                                                                                                                                                                                                                                                                                           ThrGluAlaProPheAlaThrGlySerSerGlyValMetGlnPheArqTyrProValGly 205
                                                                                                                                                                                                                                                                                                                                       TTCCCCTATTACCCGCGCCCCGTTACTATGCACCATCCACACCCCAACCACCCCGAACATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCACTCTCCTTTGCCTCACCTATTCGTGTCCAGCGTCGCTCAGCGATAACGGGGACGGTC 541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LeuThrLeuTrpSerGlyAspLeuLysValArgGluArgSerIleSerSerGly----- 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGCGGCTTATATAGGGATACGCGCTTCTTCATCACGTTATTCGCTCGAGTATGTGCGTGG 481
                                                                                                                     ValThrSerAsnGlyMetTrpPheSerGlyArgAspGlyAspLeuIleAsnAlaSerAsn 243
                                                                                                                                                                                                                                                                                                                                                                                      GCTCCG------CCCCGAGTTCCCGTGCCGGTTCCCACCGCTATCCTTTCGTTTCG
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            TGTACACATCCTGACGGATCGCAGGGGGGTTGCCTCCGCCATCACGAATCCGCAGCGTAAA 102
                                                                                                                                                                                                                           GCCTCCGGTCATCCACCGTTATGTCGCCAATACGGTGCGGCTACCTGCGGAGGGACGCGT 826
                                                                                                                                                                                                                                              AlaThrAsn-----ProValValArgArgPheGlyThrAlaThrValAlaGlySerThr 223
                                                                                                                                                                                                                                                                                                                                                                LysPro---ThrProThrProProValValGlnGlnProAlaProValAlaProProVal 185
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                                                                GCGTCGACTGCTTTGCGCTTGTCTTTAGCCGTCCAAACTCGGGCGCGATGTTTCCACTGT 967
                                                                                           AlaSerIleValIleGln-----
                                    -----HisThrAsnGly-----PheValSerSerTyrIle-------
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/Bex="male"
/Bex="Almphoblast"
/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
/clone_lib="PTB Chimpanzee Male BAC Library"
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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265 CCACCTATTGTGTCACCTCCAATCATTCCAACACCACCTATTGTTTCTCCACCTTTTGTC 324
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13 Gaps: (8-706-2 (1-322) x BM109778 (1-450) 136 ThrProSerProValAlaValGInSerSerArgProProValAlaValGInSerSerArgProProValAlaValIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
/(lspue_type="roots" //dev_stage="in vitro grown stem cuttings" //dev_stage="in vitro grown stem cuttings" //lab_host="soltR" /
Email: cdna@resgen.com Email: cdna@resgen.com For clone info: please contact Research Genetics, Libraries Division tel 1-800-711-6195, email cdna@resgen.com Seq primer: T3: Location/Qualifiers Location/Qualifiers 1. 450 1. 450 1. 450 1. 450 1. cultivar="Kennebec" /cultivar="Kennebec" /db xref="taxon:4111" /clone="cpR0564" /clone lib="optato roots"
ABTERIAGE, ABGININGINGER, ENGINEER ENGINEER ENGINEER ABTERIAGE, ENGINEER I, (bases 1 to 450) AUTHORS van der Hoeven, R., Sun, H., Karamycheva, S.A., Tsai, J., Van Aken, S., Utterback, T., Chiemingo, A., Bougri, O., Buell, C.R., Ronning, C., Tanksley, S. and Baker, B. TITLE Generation of ESTs from potato roots JOURNAL Contact: Research Genetics, Libraries Division Tel. 1, 2007, 711, 2105.
RESULT 25 BM109778 BM109778 BM109778 BM109778 BM109778 BM109778 ACCESSION ACCESSION BM109778 ACCESSION BM109778 ACCESSION CREATION BM109778 BM109778 BM109778 AM10977
Qy 291 IleAlaSerMetLysAsnGlnProSerGlyAlaAlaLeuPheGluPheArgIleSerArg 310
Qy 273HislleLysAspAlaGlnValLysThrGlyAspThrValArgThrGlyGlnArg 290 Db 1028 GATCGGCGCTACGCGACGCACGCACGTGGACAGCANATAACTCTCAGCGT 107

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1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:chimpbes@sc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library RPCI-43 This BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fujiyama,A., Hattori,M., Toyoda,A.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library RPCI-43
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347 c 476 g 282 t
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Reboul, J., Vaglio, P., Tzellas, N., Thierry-Mieg, N., Moore, T., Jackson, C., Shin-i, T., Kohara, Y., Thierry-Mieg, D., Thierry-Mieg, J., Lee, H., Hitti, J., Doucette-Stamm, L., Hartley, J.L., Temple, G.F., Brasch, M.A., Vandenhaute, J., Lamesch, P.E., Hill, D.E. and Vidal, M. Open-reading-frame sequence tags (OSTs) support the existence of at least 17,300 genes in C. elegans
Nat. Genet. 27 (3), 332-336 (2001)
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Sequence tag of Gateway entry clones. The primers used were
designed on the predicted protein encoding ORF. C. elegans (
cloning project : Contact jerome_reboul@dfci.harvard.edu or
philippe_vaglio@dfci.harvard.edu
POLYA=No.
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44 Binney Street, Boston, MA
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cDNAs were cloned into pPC86"
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AL552396.1 GI:7973408
AL252396.1 GI:7973408
S GSS; genome survey sequence.
Tetraodon nigroviridis.

ISM Tetraodon nigroviridis.

Actinopterygi; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygi; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;

Tetraodontidae; Tetraodon.

I (bases 1 to 969)
RORS Roest-Crollius, H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C., Hornot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F., Saurin,W. and Weissenbach,J. Saurin,W. and Weissenbach,J. Saurin,W. and Weissenbach,J. Saurin,W. and Weissenbach,J. Saurin,W. and Weissenbach,J. Saurin,W. and Weissenbach,J. Saurin,W. and Weissenbach,J. Saurin,W. and Weissenbach,J. Saurin,W. and Weissenbach,J. Saurin,W. and Weissenbach,J. Saurin,W. and Weissenbach,J. Saurin,W. and Weissenbach,J. Saurin,W. and Weissenbach,J. Saurin,W. and Weissenbach,J. Saurin,W. and Weissenbach,J. Saurin,W. and Weissenbach,J. Saurin,W. and Weissenbach,J. Saurin,W. and Weissenbach,J. Saurin,W. and Weissenbach,J. Saurin,W. and Weissenbach,J. Saurin,W. and Weissenbach,J. Saurin,W. and Weissenbach,J. Saurin,W. and Weissenbach,J. Saurin,W. and Weissenbach,J. Saurin,W. and Weissenbach,J. Saurin,W. Saurin,W. Saurin,W. Saurin,W. Saurin,W. Saurin,W. Saurin,W. Saurin,W. Saurin,W. Saurin,W. Saurin,W. Saurin,W. Saurin,W. Saurin,W. Saurin,W. Saurin,W. Saurin,W. Saurin,W. Saurin,W. Saurin,W. Saurin,W. Saurin,W. Saurin,W. Saurin,W. Saurin,W. Saurin,W. Saurin,W. Saurin,W. Saurin,W. Saurin,W. Saurin,W. Saurin,W. Saurin,W. Saurin,W. Saurin,W. Saurin,W. Saurin,W. Saurin,W. Saurin,W. Saurin,W. Saurin,W. Saurin,W. Saurin,W. Saurin,W. Saurin,W. Saurin,W. Saurin,W. Saurin,W. Saurin,W. Saurin,W. Saurin,W. Saurin,W. Saurin,W. Saurin,W. Saurin,W. Saurin,W. Saurin,W. Saurin,W. Saurin,W. Saurin,W. Saurin,W. Saurin,W. Saurin,W. Saurin,W. Saurin,W. Saurin,W. Saurin,W. Saurin,W. Saurin,W. Saurin,W. Saurin,W. Saurin,W. Saurin,W. Saurin,W. Saurin,W. Saurin,W. Saurin,W. Saurin,W. Saurin,W. Saurin,W. Saurin,W. Sa
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                                      Medicago.
1 (bases 1 to 365)
Journet, E.P., Crespeau,
Niebel, A., Carreau, V.,
                                                                                                                   Medicago truncatula
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
                                                                                                                                                                                                                                                         sequence.
AL377972
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This sequence is a single read and was generated as scale clone-end sequencing project of the Tetraodon genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                AL377972
MtBB35B07F1 MtBB Medicago
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2 (bases 1 to 969)
Roest-Crollius,H., Jaillo
Bouneau,L., Billault,A.,
Weissenbach,J.
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/db_xref="Tetraon:99883"
/clome="040D21"
/clome="040D21"
/clome_lib="G"
/note="Genoscope sequence ID : COB
/note="Genoscope sequence ID : COB
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                                        .H., van-Tuinen,D., Gouzy,J., Jaillon,O., Chatagnier,O., Kahn,D., Gianinazzi-Pearson
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                                                                            EST318546 MHAM Medicago truncatula/Glomus versiforme library cDNA clone pMHAM-56C5, mRNA sequence. AM586923 AM586923.1 GI:7266437
              Medicago truncatula/Glomus versiforme mixed Medicago truncatula/Glomus versiforme mixed
Eukaryota; mixed EST libraries.
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Medicago truncatula ESTs from Sinorhizobium meliloti-induced root
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                                                                                                                                                                                                                                         CCTCCTTTGGTGAAAACACCACCTTATCAATCACCACCTATAGTGAAGGCACCA 247
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/tissue_type="symbiotic root nodules"
/dev_stage="harvested 4 days post inoc
Sinorhizobium meliloti"
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/clone="MtBB35B07"
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REFERENCE
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NF049E09FL 5', n
BQ147993
BQ147993.1 GI::
EST.
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MF049E09FL1F1070 Developing flower Medicago
MF049E09FL 5', mRNA sequence.
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More information is available at..
'http://chrysie.tamu.edu/medicago'
Seq primer: SKmod (CTA gAA CTA gtg gAT CC).
Location/Qualifiers
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Tel: 580-223-5810
Fax: 580-221-7380
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                                                                                                    RESULT 32
BI271940
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BI271940 710 bp mRNA linear EST 18-JUL-2001
NF016F08FL1F1074 Developing flower Medicago truncatula cDNA clone
NF016F08FL 5', mRNA sequence.
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Contact: May GD
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Insert Length: 650 Std Error: 0.00
Plate: 049 row: E column: 09
Seq primer: TCACACAGGAAACAGCTATGAC.
Location/Qualifiers
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Spermatophyta; Magnoliopyta; eudiootyledons; core eudioti;
Rosidae; eurosids I; Fabales; Fabaccae; Papilionoideae; Trifolieae;
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Eukaryota; Viridipl
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580 221 7391
580 221 7380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="NP049809FL"
/clone_lib="Developing flowers"
/tissue_type="Developing flowers"
/dev_stage="Developmentally pooled. Contains a mixture of
/dev_stage="Developmentally pooled flowers and flowers
in early transition into pods."
/note="Vector: Lambda Zap; cDNA was prepared from polyA+
enriched, pooled samples of equivalent amounts of total
RNA from very young, developing, fully-opened flowers and
flowers transitioning into pods. The cDNA was
directionally ligated into the Uni-Zap XR vector
(Stratagene) and packaged using the Gigapack III Gold
packaging extracts. Phagemids containing cDNA inserts were
in vivo excised from the recombinant Uni-ZAP XR vector
using Exassist helper phage and the E. coli strain
XL1-Blue MRF* (Stratagene). Excised plasmids were plated
using SOLR cells."

97 a 198 C 77 g 175 t 3 others
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|db_xref="taxon:3880"
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Contact: May GD
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magmoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae
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Insert Length: 710 Std Error: 0.00
Plate: 016 row: F column: 08
Seq primer: TCACACAGGAAACAGCTATGAC.
Location/Qualifiers
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The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK
Tel: 580 221 7391
Fax: 580 221 7380
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BI271940.1 GI:14880858
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                                                                                                    CCTCCTTTGGTGAAAACACCACCTTATCAATCACCACCTATAGTGAAGGCACCA
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/clone="NR016F08FL"
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/clone="Stage="Developing, fully-opened flowers and flowers
in exrly transition into pods. The character and
flowers transitioning into pods. The cDNA was
firectionally ligated into the Uni-Zap XR vector
(Stratagene) and packaged using the Gigapack III Gold
packaging extracts. Phagemids containing cDNA inserts were
in vivo excised from the recombinant Uni-Zap XR vector
using ExAssist helper phage and the E. coli strain
XL1-Blue MRF' (Stratagene). Excised plasmids were plated
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      199
                                             627
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                                                                                      187
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National Institutes of Health, Mammalian
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM12346 row: m column: 21
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Tissue Procurement: ATCC
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                              TrpLeuThrLeuTrpSerGlyAspLeuLysValArgGluArgSerIleSerSerGlyVal 131
                                                                                 GluAlaProPheAlaThrGlySerSerGlyValMet-----
                                                                                                                                                               LysProThrProThrProValValGlnGlnProAlaProValAlaProProValThr 186
GlnPheArgTyrProValGlyAlaThrAsnProValValArgArgPheGlyThrAla 217
                                                                                                                                                                                                                                               ProProValGlnGlnHisProAlaValGlnLysProThrProProValValValValLys 166
                                                                                                                                                                                                          (bases 1 to 1460)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:9666"
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/note="Organ: testis, Vector: pCRV-SPORT6; Site_1: Not1;
Site_2: Sall; Cloned unidirectionally; oligo-dT primed.
Average insert size 2.5 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
33 a 669 c 208 g 350 t
                                                                                                                          ACACCCGCCCCCAATACTTCCACCCCCGCCCCCCTT---CCCCCGTTTCT 626
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: oandersn@pw.usda.gov
Sequence have been trimmed to remove vector
quality sequence with phred score less than
Seq primer: Stratagene SK primer.
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Anderson,O.D., Chao,S., Dubcovsky,J., Echenique,V., Han,P.S., Hsi,C.C., Kang,Y., Lazo,G.R., Miller,R., Rausch,C.J., Seaton,C.L., Stamova,B. and Tong,J.C.
The structure and function of the expressed portion of the wheat genomes - Early reproductive apex cDNA library from Triticum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (2001)
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                                       SerLysProThrTyrAsnSerThrSerGlySerGlySerHisArgThrSerGly-SerGl
                                                                                   (1-322)
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                                                                                                                                                                                                                                                                                                                                         /note="Vector: Lambda Uni-ZAP XR, excised phagemid; 3ite 1 ECORI; Site 2: Xhol; The tissue, total RNA, and poly(A) RNA were prepared from apex at double-ridge stage to terminal-spikelet stage during transition from vegetative state to flower state, a cDNA library was made, and the cDNA clones were in vivo excised at the University of California, Davis (V. Echenique, B. Stamova, J. Dubcovsky). Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="Early reproductive apex"
/dev_stage="Seven week-old plants"
/lab_host="E. coli XLOLR"
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/clone_lib="Triticum monococcum early reproductive
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Bukaryota; Metazoa; Chordata; Craniata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 909)

1 (bases 1 to 909)

National Institutes of Health, Mammalian Gene Collection (MGC)

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: CGAP (Stanford)

Tissue Procurement: CGAP (Stanford)

CDNA Library Preparation: Rubin Laboratory

CDNA Library Preparation: Rubin Laboratory

CDNA Library Preparation (MC Colone Corporation

Clone distribution: MGC Colone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLCM2512 row: c column: 15

High quality sequence stop: 589.
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        179
  Library."
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/notc="organ: liver; Vector: poTB7; Site_1: XhoI; Site_2:
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                                                                                                                                                                                                                                                                                   organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:629462"

/clone_lib="NIH_MGC_100"
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                                                                                                                                                                                   AI484465
AI3 bp mRNA linear EST EST242475 tomato ovary, TAMU Lycopersicon esculentum cDN CLED1H16 similar to proline rich protein, mRNA sequence.
  Lycopersicon esculentum

Lycopersicon esculentum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
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AI484465.1 GI:4379836
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Generation of ESTs from tomato carpel tissue Unpublished (1999)

Other_ESTs; EST242465
                                                                                      esculentum
BE460175
                                                                                                   BE460175

443 bp mRNA linear EST 18-MAY
EST415467 tomato developing/immature green fruit Lycopersicon
esculentum cDNA clone cLEM9019, mRNA sequence.
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Alcala,J., Vrebalov,J., White,R., Matern,A.L., Vision,T., H., Liang,F., Upton,J., Romning,C.M., Craven,M.B., Fujii,C.Y., C.L., Nierman,W., Fraser,C.M., Venter,J.C., Martin,G.B., T
 Lycopersicon
Eukaryota; Vi
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Location/Qualifiers
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Clemson University
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/tissue_type="carpel"
/dev_stage="5 days post-anthesis"
/lab_host="XL1-Blue MRR?"
/note="Yector: pBlueScript SK(-); Site 1: EcoR1; Site 2:
Xho1; CLED - Tomato Carpel EST Library. OligodT-primed and directionally cloned cDNA in vector Lamda ZAP II with 5' and 3' ends located at the EcoRI and XhoI sites,
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 Streptophyta; Embryophyta; Tracheophyta;
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Y., Bowman
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Email: http://www.genome.clemson.edu/orders/index.html
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Alcala,J., Vrebalov,J., White,R., van der Hoeven,R.S., Holt,I.E., Liang,F., Hansen,T.S., Craven,M.B., Bowman,C.L., Ronning,C.M., Nierman,W., Fraser,C.M., Martin,G.B., Giovannoni,J.J. and Tanksle,
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ACCCATAGTT 402
                                                                  CCCCAATCCTCCCGTGGTAATACCACCACCCTACGTGCCAAGTCCTCCGGTTGTTACTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="tomato developing/immature green fruit"
/tlssue_type="fruit"
/dev_stage="immature green (5-35 days post-anthesis
/lab_host="sOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   db_xref="taxon:4081"
clone="cLEM9019"
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Genes galore: a summary of methods for accessing results from large-scale partial sequencing of anonymous Arabidopsis cDNA clones plant physiol. 106, 1241-1255 (1994)
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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17899 Lambda-PRL2
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                                                                                                                                                                                                                                                                                                          134 AlaHisThrProSerProValAlaValGlnSerSerArgProProValGlnGlnHisPro 153
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MSU-DDE Plant Research Laboratory
Michigan State University
MSU-DDE-PRL, Michigan State University, Plant Biology Bldg.,E.
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                                                                                                               ProThrProProValValGlnGlnProAlaProValAla---ProProValThrGluAla 188
ProPheAlaThrGlySerSerGlyVal-MetGlnPheArgTyrProValGlyAlaThrAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : 517-353-0854
: 517-353-9168
il: 22313tcn@ibm.cl.msu.edu
primer: T7 dye primer.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    / Clone | 15 "Lambda-PRL2" | / Clone | 15 "Lambda-PRL2" | / Clone | 15 "Lambda-PRL2" | / Clone | 15 "Lambda | Fig. Lox; Site_1: Sal; Site_2: Not; / notee "Vector: lambda | Fig. Lox; derived from equal | / Lambda | PRL2 is a CDNA | 1ibrary derived from equal | / (Fig. Lox) | / (Fig. Lox) | / (Fig. Lox) | / (Fig. Lox) | / (Fig. Lox) | / (Fig. Lox) | / (Fig. Lox) | / (Fig. Lox) | / (Fig. Lox) | / (Fig. Lox) | / (Fig. Lox) | / (Fig. Lox) | / (Fig. Lox) | / (Fig. Lox) | / (Fig. Lox) | / (Fig. Lox) | / (Fig. Lox) | / (Fig. Lox) | / (Fig. Lox) | / (Fig. Lox) | / (Fig. Lox) | / (Fig. Lox) | / (Fig. Lox) | / (Fig. Lox) | / (Fig. Lox) | / (Fig. Lox) | / (Fig. Lox) | / (Fig. Lox) | / (Fig. Lox) | / (Fig. Lox) | / (Fig. Lox) | / (Fig. Lox) | / (Fig. Lox) | / (Fig. Lox) | / (Fig. Lox) | / (Fig. Lox) | / (Fig. Lox) | / (Fig. Lox) | / (Fig. Lox) | / (Fig. Lox) | / (Fig. Lox) | / (Fig. Lox) | / (Fig. Lox) | / (Fig. Lox) | / (Fig. Lox) | / (Fig. Lox) | / (Fig. Lox) | / (Fig. Lox) | / (Fig. Lox) | / (Fig. Lox) | / (Fig. Lox) | / (Fig. Lox) | / (Fig. Lox) | / (Fig. Lox) | / (Fig. Lox) | / (Fig. Lox) | / (Fig. Lox) | / (Fig. Lox) | / (Fig. Lox) | / (Fig. Lox) | / (Fig. Lox) | / (Fig. Lox) | / (Fig. Lox) | / (Fig. Lox) | / (Fig. Lox) | / (Fig. Lox) | / (Fig. Lox) | / (Fig. Lox) | / (Fig. Lox) | / (Fig. Lox) | / (Fig. Lox) | / (Fig. Lox) | / (Fig. Lox) | / (Fig. Lox) | / (Fig. Lox) | / (Fig. Lox) | / (Fig. Lox) | / (Fig. Lox) | / (Fig. Lox) | / (Fig. Lox) | / (Fig. Lox) | / (Fig. Lox) | / (Fig. Lox) | / (Fig. Lox) | / (Fig. Lox) | / (Fig. Lox) | / (Fig. Lox) | / (Fig. Lox) | / (Fig. Lox) | / (Fig. Lox) | / (Fig. Lox) | / (Fig. Lox) | / (Fig. Lox) | / (Fig. Lox) | / (Fig. Lox) | / (Fig. Lox) | / (Fig. Lox) | / (Fig. Lox) | / (Fig. Lox) | / (Fig. Lox) | / (Fig. Lox) | / (Fig. Lox) | / (Fig. Lox) | / (Fig. Lox) | / (Fig. Lox) | / (Fig. Lox) | / (Fig. Lox) | / (Fig. Lox) | / (Fig. Lox) | / (Fig. Lox) | / (Fig. Lox) | / (Fig. Lox) | / (Fig. Lox) | / (Fig. Lox) | / (Fig. Lox) | / (Fig. Lox) | / (Fig. Lox) | / (Fig. Lox) | / (Fig. Lox) | /
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/strain="var columbia"
/db_xref="taxon:3702"
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Kaul,S., Town,C.D., Bowman,C.L., Van Aken,S.E., Utterback,T.V.,
Feldblyum,T.V. and Fraser,C.M.
Survey sequencing of Arabidopsis thaliana BAC T6J16
Unpublished (2001)
Contact: Chris Town
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tlgr.org
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Class: sheared ends.
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From Wash. U contig 1144. C
some non-Arabidopsis source
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                                                                           ProProValValGlnGlnProAlaProValAlaProProValThrGluAlaProPheAla 191
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/clone=1b="ATZE"
/note="Vector: phOS2; Site 1: BstXI; 2-3 kb sheared
/note="Vector: phOS2; Site 1 BstXI linkers"
DNA inserted into phOS2 using BstXI linkers"
DNA inserted into phOS2 using BstXI linkers"
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/strain="Columbia"
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Conservative:
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c clone ATZEC82, DNA
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AUTHORS
Search completed: July 3, 2003, 21:28:26 Job time: 1155 secs
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JOURNAL
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                                                                                                           171 ThrProProValValGlnGlnProAlaProValAlaPro---ProValThrGlu 187
                                                                                                                                                                                      151 GlnHisProAlaValGlnLysProThrProProValValValValLysLysProThrPro 170
                                                                                                                                                                                                                                                                131 ValAsnThrAlaHisThrProSerProValAlaValGlnSerSerArgProProValGln 150
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Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Rosidae; euroside II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Kyeong Tae Pih
Department of Plant Molecular Biology
Gyeongsang National Univ., Plant Molecular Biology and
Biotechnology Research Center
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Pih,K.T., Park,J.M., Jang,H.J., Kang,S.G., Piao,H.L. and Hwang,I.
EST of salt inducible mRNA in Arabidopsis thaliana
Unpublished (1997)
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ATU74096 NaCl-treated Arabidopsis subtraction library Arabidopsis
thaliana cDNA clone OS001, mRNA sequence.
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Location/Qualifiers
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Tel: 82-591-751-5193
Fax: 82-591-759-9363
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/note="Subtracted cDNA library from salt(NaCl)-treated
whole plants"
130 c 46 g 53 t 9 others
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